

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:49:29 ; Search time 150.277 Seconds  
(without alignments)  
978.085 Million cell updates/sec

Title: US-10-087-631B-9

Perfect score: 28  
Sequence: 1 cgtctggatagtcgcatggtgtt 28

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 3992700

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : N\_Geneseq\_23Sep04.\*

- 1: Geneseqn1980s.\*
- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	21	75.0	21	9	ADAI13880 Short int
2	21	75.0	21	9	ADAI13871 Short int
3	21	75.0	21	9	ADAI13872 Short int
4	21	75.0	21	9	ADAI13873 Short int
5	21	75.0	21	10	ADFS2874 Hepatitis
6	21	75.0	21	10	ADFS2876 Hepatitis
7	21	75.0	21	10	ADFS2883 Hepatitis
8	21	75.0	21	10	ADFS2875 Hepatitis
9	20	71.4	21	9	ADAI13879 Short int
10	20	71.4	21	9	ADAI13824 Short int
11	20	71.4	21	10	ADFS2882 Hepatitis
12	20	71.4	21	10	ADFS2848 Hepatitis
13	20	71.4	21	10	ADFS2996 Hepatitis
14	20	71.4	23	10	ADFS2938 Hepatitis
15	19.4	69.3	21	9	ADAI13825 Short int
16	19.4	69.3	21	10	ADFS2849 Hepatitis
17	19.4	69.3	23	10	ADFS2995 Hepatitis
18	19.4	69.3	23	10	ADFS2937 Hepatitis
19	19.4	69.3	23	10	ADFS2997 Hepatitis
20	19.4	69.3	23	10	ADFS2999 Hepatitis
21	19.4	69.3	23	10	ADFS2939 Hepatitis

c 95	14.4	51.4	38	3	AAZ35481	Aax35481 Human cel	168	13.6	48.6	26	2	AAT36369	Aat36369 Beta-iono
c 96	14.4	51.4	38	3	AAZ35482	Aax35482 Primer fo	169	13.6	48.6	27	6	ABL99556	ABL99556 Canine BR
c 97	14.4	51.4	38	3	AAZ35462	Aax35462 Human C-H	170	13.6	48.6	27	10	ABZ83650	ABZ83650 Toxicolog
c 98	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	171	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 99	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	172	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 100	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	173	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 101	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	174	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 102	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	175	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 103	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	176	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 104	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	177	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 105	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	178	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 106	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	179	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 107	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	180	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 108	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	181	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 109	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	182	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 110	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	183	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 111	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	184	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 112	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	185	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 113	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	186	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 114	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	187	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 115	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	188	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 116	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	189	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 117	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	190	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 118	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	191	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 119	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	192	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 120	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	193	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 121	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	194	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 122	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	195	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 123	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	196	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 124	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	197	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 125	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	198	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 126	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	199	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 127	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	200	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 128	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	201	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 129	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	202	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 130	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	203	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 131	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	204	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 132	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	205	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 133	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	206	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 134	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	207	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 135	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	208	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 136	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	209	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 137	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	210	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 138	14.4	51.4	38	3	AAZ35340	Aax35340 Human H-r	211	13.6	48.6	28	2	AAV23035	AAV23035 HG3100A-2
c 139	14.2	50.7	20	2	AAT29692	Aat29692 beta-acti	212	13.6	48.6	23	5	AAH47146	Aah47146 B1466 gen
c 140	14.2	50.7	24	10	ADC59541	Adc59541 Mouse bet	213	13.6	48.6	24	12	ADN59638	Adn59638 Beta-gluc
c 141	14.2	50.7	46	2	AAZ22928	Aax22928 DE1973659	214	13.6	48.6	25	6	ABV80911	Abv80911 Human HTP
c 142	14.2	50.7	48	3	AAZ64783	Aax64783 C. tracho	215	13.6	48.6	25	6	ABV80912	Abv80912 Human HTP
c 143	14.2	50.7	48	3	AAZ64783	Aax64783 C. tracho	216	13.6	48.6	25	6	ABV80913	Abv80913 Human HTP
c 144	14.2	50.7	48	3	AAZ64783	Aax64783 C. tracho	217	13.6	48.6	25	6	ABV80910	Abv80910 Human HTP
c 145	14.2	50.7	49	12	ADI80447	Adi80447 Anti-tumo	218	13.6	48.6	25	6	ABV80909	Abv80909 Human HTP
c 146	14.2	50.7	49	12	ADI80447	Adi80447 Anti-tumo	219	13.6	48.6	25	6	ABV80910	Abv80910 Human HTP
c 147	14.2	50.7	49	12	ADI80447	Adi80447 Anti-tumo	220	13.6	48.6	25	6	ABV80911	Abv80911 Human HTP
c 148	14.2	50.7	49	12	ADI80447	Adi80447 Anti-tumo	221	13.6	48.6	25	6	ABV80912	Abv80912 Human HTP
c 149	14.2	50.7	49	12	ADI80447	Adi80447 Anti-tumo	222	13.6	48.6	25	6	ABV80913	Abv80913 Human HTP
c 150	14.2	50.7	49	12	ADI80447	Adi80447 Anti-tumo	223	13.6	48.6	25	6	ABV80910	Abv80910 Human HTP
c 151	14.2	50.7	49	12	ADI80447	Adi80447 Anti-tumo	224	13.6	48.6	25	6	ABV80909	Abv80909 Human HTP
c 152	13.8	49.3	25	9	ACK22303	Ack22303 Human mic	225	13.6	48.6	25	9	ACK22303	Ack22303 Human mic
c 153	13.8	49.3	25	12	AQO30807	Aaq30807 A fumigat	226	13.6	48.6	25	9	ACK22303	Ack22303 Human mic
c 154	13.8	49.3	26	5	AAI62009	Aai62009 Soybean 2	227	13.6	48.6	25	9	ACK22303	Ack22303 Human mic
c 155	13.8	49.3	30	12	ADE85726	Ad85726 Human Eph	228	13.6	48.6	25	9	ACK22303	Ack22303 Human mic
c 156	13.8	49.3	40	2	AAZ44878	Aat44878 HPV linke	229	13.6	48.6	26	2	ABA99190	Ab99190 Human RCC
c 157	13.8	49.3	40	2	AAZ78099	Aat78099 Human pap	230	13.6	48.6	30	2	AAT39272	Aat39272 Human bet
c 158	13.8	49.3	41	8	ABZ25604	Abz25604 Human pre	231	13.6	48.6	30	2	AAV26823	Aav26823 3'RACE Hu
c 159	13.8	49.3	41	8	ABZ25604	Abz25604 Human pre	232	13.6	48.6	30	10	ADC55441	Adc55441 Oligonucl
c 160	13.6	48.6	20	3	AAZ86971	Aaz86971 35S promo	233	13.6	48.6	30	12	ADO79802	Ado79802 CENPC1 PC
c 161	13.6	48.6	20	3	AAZ86971	Aaz86971 35S promo	234	13.6	48.6	36	2	AAV99646	Aav99646 Human tis
c 162	13.6	48.6	20	8	AAZ93200	Aaz93200 35S promo	235	13.6	48.6	36	4	AAO03473	Aao03473 Human t-p
c 163	13.6	48.6	25	9	ACD45238	Acd45238 Molecular	236	13.6	48.6	36	4	AAO03471	Aao03471 Human t-p
c 164	13.6	48.6	25	9	ACI61431	Aci61431 Human mic	237	13.6	48.6	38	2	AAT73348	Aat73348 Probe for
c 165	13.6	48.6	25	9	ACK27910	Ack27910 Human mic	238	13.6	48.6	40	10	AAQ12194	Aaq12194 as-1b mut
c 166	13.6	48.6	25	9	ACK27910	Ack27910 Human mic	239	13.6	48.6	40	10	ADH11033	Adh11033 Human bet
c 167	13.6	48.6	25	9	ACK27910	Ack27910 Human mic	240	13.6	48.6	43	2	AAO1306	Aao1306 PCR prime



241	13	46.4	45	2	AA88768	Aax88768 SV40 olig	C 314	12.8	45.7	38	3	AAA9597	Aaa9597 C-K-ras-V
242	13	46.4	45	2	AA88772	Aax88772 SV40 olig	C 315	12.8	45.7	38	4	AAF82137	Aaf82137 Human C-K
243	13	46.4	47	8	ABT1441	Abt1441 HCV envel	C 316	12.8	45.7	38	4	AAF82140	Aaf82140 Human C-K
244	13	46.4	47	8	AD50591	Ad50591 pGEMTEIsh	C 317	12.8	45.7	38	4	AAH13524	Aah13524 Human C-K
245	13	46.4	47	10	ABQ84199	Abq84199 HCV EI-H6	C 318	12.8	45.7	38	4	AAH47355	Aah47355 Human C-K
246	12.8	45.7	20	3	AA29852	Aaa29852 Human jun	C 319	12.8	45.7	38	4	AAH47355	Aah47355 Human C-K
247	12.8	45.7	20	6	AB194656	Abi94656 Capture o	C 320	12.8	45.7	38	4	AAH47355	Aah47355 Human C-K
248	12.8	45.7	20	11	ADP75359	Adp75359 Human ADA	C 321	12.8	45.7	38	4	AAH47355	Aah47355 Human C-K
249	12.8	45.7	21	3	AAZ44473	Aaz44473 H. pylori	C 322	12.8	45.7	38	4	AAH47355	Aah47355 Human C-K
250	12.8	45.7	24	4	AA506943	Aaa506943 PCR prime	C 323	12.8	45.7	38	4	AAH47355	Aah47355 Human C-K
251	12.8	45.7	24	6	AB185883	Abi85883 Capture o	C 324	12.8	45.7	38	4	AAH47355	Aah47355 Human C-K
252	12.8	45.7	24	6	AB185882	Abi85882 Capture o	C 325	12.8	45.7	38	4	AAH47355	Aah47355 Human C-K
253	12.8	45.7	25	9	ACK13357	Ack13357 Human mic	C 326	12.8	45.7	38	4	AAH47355	Aah47355 Human C-K
254	12.8	45.7	25	9	AC129108	Ac129108 Human mic	C 327	12.8	45.7	38	4	AAH47355	Aah47355 Human C-K
255	12.8	45.7	25	9	AC166658	Ac166658 Human mic	C 328	12.8	45.7	38	4	AAH47355	Aah47355 Human C-K
256	12.8	45.7	25	9	AC166658	Ac166658 Human mic	C 329	12.8	45.7	38	4	AAH47355	Aah47355 Human C-K
257	12.8	45.7	25	9	AC178480	Ac178480 Human mic	C 330	12.8	45.7	38	4	AAH47355	Aah47355 Human C-K
258	12.8	45.7	25	9	AC166659	Ac166659 Human mic	C 331	12.8	45.7	38	4	AAH47355	Aah47355 Human C-K
259	12.8	45.7	25	9	AC166659	Ac166659 Human mic	C 332	12.8	45.7	38	4	AAH47355	Aah47355 Human C-K
260	12.8	45.7	25	9	AC151673	Ac151673 Human mic	C 333	12.8	45.7	38	4	AAH47355	Aah47355 Human C-K
261	12.8	45.7	25	9	ACK16635	Ack16635 Human mic	C 334	12.8	45.7	38	4	AAH47355	Aah47355 Human C-K
262	12.8	45.7	25	9	ADAL14320	Ada14320 Human Skp	C 335	12.8	45.7	38	4	AAH47355	Aah47355 Human C-K
263	12.8	45.7	26	12	ADP12302	Adp12302 Tagman pr	C 336	12.8	45.7	38	5	AAF23767	Aaf23767 Human C-K
264	12.8	45.7	27	6	ABK27861	Abk27861 Corin male	C 337	12.8	45.7	38	5	AAF23767	Aaf23767 Human C-K
265	12.8	45.7	31	12	ADO56802	Ado56802 Human CAR	C 338	12.8	45.7	38	5	AAF23767	Aaf23767 Human C-K
266	12.8	45.7	33	12	ADK67297	Adk67297 RT-PCR pr	C 339	12.8	45.7	38	5	AAF23767	Aaf23767 Human C-K
267	12.8	45.7	34	4	AAF58375	Aaf58375 Human cel	C 340	12.8	45.7	38	5	AAF23767	Aaf23767 Human C-K
268	12.8	45.7	34	4	AAF59717	Aaf59717 Human C-K	C 341	12.8	45.7	38	5	AAF23767	Aaf23767 Human C-K
269	12.8	45.7	38	2	AAH43982	Aah43982 Octopine	C 342	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
270	12.8	45.7	38	2	AAH43984	Aah43984 Octopine	C 343	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
271	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 344	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
272	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 345	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
273	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 346	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
274	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 347	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
275	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 348	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
276	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 349	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
277	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 350	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
278	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 351	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
279	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 352	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
280	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 353	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
281	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 354	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
282	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 355	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
283	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 356	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
284	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 357	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
285	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 358	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
286	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 359	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
287	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 360	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
288	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 361	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
289	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 362	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
290	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 363	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
291	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 364	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
292	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 365	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
293	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 366	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
294	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 367	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
295	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 368	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
296	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 369	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
297	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 370	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
298	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 371	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
299	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 372	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
300	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 373	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
301	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 374	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
302	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 375	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
303	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 376	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
304	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 377	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
305	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 378	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
306	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 379	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
307	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 380	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
308	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 381	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
309	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 382	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
310	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 383	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
311	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 384	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
312	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 385	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR
313	12.8	45.7	38	2	AAH43983	Aah43983 Octopine	C 386	12.8	45.7	38	6	ABK52793	Abk52793 H-ras PCR

387	12.6	45.0	35	5	AAD04347	Aad04347	Complemen	460	12.4	44.3	40	2	AAT87164
388	12.6	45.0	36	2	AAV33725	Aav33725	Human chy	C 461	12.4	44.3	40	12	ADi82369
389	12.6	45.0	36	5	AAV33725	Aav33725	Human chy	C 462	12.4	44.3	41	6	ABz49616
390	12.6	45.0	36	12	ADAD04341	Adm04341	MLV parti	C 463	12.4	44.3	42	5	Adf16714
391	12.6	45.0	36	12	ADAD04341	Adm04341	MLV parti	C 464	12.4	44.3	44	10	AdG17428
392	12.6	45.0	38	2	AAQ34772	Aaq34772	PCR prime	C 465	12.4	44.3	44	10	AdG17428
393	12.6	45.0	38	2	AAQ37233	Aaq37233	PCR prime	C 466	12.4	44.3	47	3	AzG58897
394	12.6	45.0	38	2	AAQ37233	Aaq37233	PCR prime	C 467	12.4	44.3	47	3	AzG58897
395	12.6	45.0	38	2	AAQ37233	Aaq37233	PCR prime	C 468	12.4	44.3	50	4	AAL33751
396	12.6	45.0	38	6	AAQ37233	Aaq37233	PCR prime	C 469	12.4	44.3	50	6	AAL33751
397	12.6	45.0	39	6	AAQ37233	Aaq37233	PCR prime	C 470	12.4	44.3	50	6	AAL33751
398	12.6	45.0	39	6	AAQ37233	Aaq37233	PCR prime	C 471	12.4	44.3	50	6	AAL33751
399	12.6	45.0	41	3	AAQ37233	Aaq37233	PCR prime	C 472	12.4	44.3	50	6	AAL33751
400	12.6	45.0	42	2	AAQ37233	Aaq37233	PCR prime	C 473	12.4	44.3	50	6	AAL33751
401	12.6	45.0	42	3	AAQ37233	Aaq37233	PCR prime	C 474	12.4	44.3	50	6	AAL33751
402	12.6	45.0	42	3	AAQ37233	Aaq37233	PCR prime	C 475	12.4	44.3	50	6	AAL33751
403	12.6	45.0	42	6	AAQ37233	Aaq37233	PCR prime	C 476	12.4	44.3	50	6	AAL33751
404	12.6	45.0	42	6	AAQ37233	Aaq37233	PCR prime	C 477	12.4	44.3	50	6	AAL33751
405	12.6	45.0	42	6	AAQ37233	Aaq37233	PCR prime	C 478	12.4	44.3	50	6	AAL33751
406	12.6	45.0	47	3	AAQ37233	Aaq37233	PCR prime	C 479	12.4	44.3	50	8	ABs55681
407	12.6	45.0	47	3	AAQ37233	Aaq37233	PCR prime	C 480	12.4	44.3	50	8	ABs55681
408	12.6	45.0	50	6	AAQ37233	Aaq37233	PCR prime	C 481	12.4	44.3	50	8	ABs55681
409	12.6	45.0	50	6	AAQ37233	Aaq37233	PCR prime	C 482	12.4	44.3	50	9	ABs55681
410	12.4	44.3	20	2	AAQ37233	Aaq37233	PCR prime	C 483	12.4	44.3	50	9	ABs55681
411	12.4	44.3	24	6	AAQ37233	Aaq37233	PCR prime	C 484	12.4	44.3	50	9	ABs55681
412	12.4	44.3	24	6	AAQ37233	Aaq37233	PCR prime	C 485	12.4	44.3	50	9	ABs55681
413	12.4	44.3	24	6	AAQ37233	Aaq37233	PCR prime	C 486	12.4	44.3	50	10	ABs55681
414	12.4	44.3	24	6	AAQ37233	Aaq37233	PCR prime	C 487	12.4	44.3	50	10	ABs55681
415	12.4	44.3	25	9	AAQ37233	Aaq37233	PCR prime	C 488	12.4	44.3	50	10	ABs55681
416	12.4	44.3	25	9	AAQ37233	Aaq37233	PCR prime	C 489	12.4	44.3	50	10	ABs55681
417	12.4	44.3	25	9	AAQ37233	Aaq37233	PCR prime	C 490	12.4	44.3	50	10	ABs55681
418	12.4	44.3	25	9	AAQ37233	Aaq37233	PCR prime	C 491	12.4	44.3	50	10	ABs55681
419	12.4	44.3	25	9	AAQ37233	Aaq37233	PCR prime	C 492	12.4	44.3	50	10	ABs55681
420	12.4	44.3	25	9	AAQ37233	Aaq37233	PCR prime	C 493	12.4	44.3	50	10	ABs55681
421	12.4	44.3	25	9	AAQ37233	Aaq37233	PCR prime	C 494	12.4	44.3	50	10	ABs55681
422	12.4	44.3	25	9	AAQ37233	Aaq37233	PCR prime	C 495	12.4	44.3	50	10	ABs55681
423	12.4	44.3	25	9	AAQ37233	Aaq37233	PCR prime	C 496	12.4	44.3	50	12	ADp42975
424	12.4	44.3	25	9	AAQ37233	Aaq37233	PCR prime	C 497	12.4	44.3	50	12	ADp42975
425	12.4	44.3	25	9	AAQ37233	Aaq37233	PCR prime	C 498	12.4	44.3	50	12	ADp42975
426	12.4	44.3	25	9	AAQ37233	Aaq37233	PCR prime	C 499	12.2	43.6	18	2	AAQ92187
427	12.4	44.3	25	9	AAQ37233	Aaq37233	PCR prime	C 500	12.2	43.6	18	10	ADf13511
428	12.4	44.3	25	9	AAQ37233	Aaq37233	PCR prime	C 501	12.2	43.6	19	2	AAQ82287
429	12.4	44.3	25	9	AAQ37233	Aaq37233	PCR prime	C 502	12.2	43.6	20	4	AAQ82287
430	12.4	44.3	25	9	AAQ37233	Aaq37233	PCR prime	C 503	12.2	43.6	20	6	AAQ82287
431	12.4	44.3	25	9	AAQ37233	Aaq37233	PCR prime	C 504	12.2	43.6	21	3	AAQ82287
432	12.4	44.3	25	9	AAQ37233	Aaq37233	PCR prime	C 505	12.2	43.6	22	3	AAQ82287
433	12.4	44.3	25	9	AAQ37233	Aaq37233	PCR prime	C 506	12.2	43.6	22	6	AAQ82287
434	12.4	44.3	25	9	AAQ37233	Aaq37233	PCR prime	C 507	12.2	43.6	22	10	AAQ82287
435	12.4	44.3	25	9	AAQ37233	Aaq37233	PCR prime	C 508	12.2	43.6	23	3	AAQ82287
436	12.4	44.3	25	12	ADP15504	Adp15504	Renal cel	C 509	12.2	43.6	23	3	AAQ82287
437	12.4	44.3	26	4	AAH01109	Aah01109	vancI/2/3	C 510	12.2	43.6	24	9	ACA90136
438	12.4	44.3	27	4	AAH47525	Aah47525	Human Her	C 511	12.2	43.6	24	9	ACA90136
439	12.4	44.3	30	2	AAQ99481	Aaq99481	OligonucI	C 512	12.2	43.6	24	10	ADG72943
440	12.4	44.3	30	2	AAQ99481	Aaq99481	OligonucI	C 513	12.2	43.6	25	2	AAQ71850
441	12.4	44.3	30	5	AAQ84633	Aaq84633	SIV gene	C 514	12.2	43.6	25	4	AAQ71850
442	12.4	44.3	30	6	ABK931124	Abk931124	IRE5 muta	C 515	12.2	43.6	25	9	ACI75382
443	12.4	44.3	30	12	ADP46285	Adp46285	PCR prime	C 516	12.2	43.6	25	9	ACI75382
444	12.4	44.3	31	2	AAQ30195	Aaq30195	p53 gene	C 517	12.2	43.6	25	9	ACI75382
445	12.4	44.3	31	2	AAQ30195	Aaq30195	p53 gene	C 518	12.2	43.6	25	9	ACI75382
446	12.4	44.3	32	2	AAQ80042	Aaq80042	5' flankI	C 519	12.2	43.6	25	9	ACI75382
447	12.4	44.3	32	2	AAQ80042	Aaq80042	5' flankI	C 520	12.2	43.6	25	9	ACI75382
448	12.4	44.3	33	6	ABK48050	Abk48050	Heliothis	C 521	12.2	43.6	25	9	ACI75382
449	12.4	44.3	35	10	ADF75325	Adf75325	PCR prime	C 522	12.2	43.6	25	9	ACI75382
450	12.4	44.3	36	3	AAQ35687	Aaq35687	Permutin	C 523	12.2	43.6	25	9	ACI75382
451	12.4	44.3	36	4	AAQ35687	Aaq35687	Permutin	C 524	12.2	43.6	25	9	ACI75382
452	12.4	44.3	36	4	AAQ35687	Aaq35687	Permutin	C 525	12.2	43.6	25	9	ACI75382
453	12.4	44.3	37	3	AAQ65800	Aaq65800	Nucleotid	C 526	12.2	43.6	25	9	ACI75382
454	12.4	44.3	37	3	AAQ65800	Aaq65800	Nucleotid	C 527	12.2	43.6	25	9	ACI75382
455	12.4	44.3	37	4	AAH43906	Aah43906	Human apc	C 528	12.2	43.6	26	2	AAH43906
456	12.4	44.3	37	5	AAH43906	Aah43906	Human apc	C 529	12.2	43.6	26	6	AAH43906
457	12.4	44.3	37	5	AAH43906	Aah43906	Human apc	C 530	12.2	43.6	26	6	AAH43906
458	12.4	44.3	38	4	AAH21383	Aah21383	Human his	C 531	12.2	43.6	26	6	AAH21383
459	12.4	44.3	39	4	AAH21383	Aah21383	Human his	C 532	12.2	43.6	26	6	AAH21383

C 533	12.2	43.6	26	11	ADP68350	Adp68350 DNA probe	606	12.2	43.6	50	6	ABZ05683	Abz05683 Human leu
C 534	12.2	43.6	26	11	ADP68353	Adp68353 DNA probe	C 607	12	42.9	20	2	AAQ50842	AAQ50842 HTLV-1 de
C 535	12.2	43.6	26	12	ADL25704	Adl25704 Human NOV	608	12	42.9	20	2	AAQ63653	AAQ63653 Anti-HTLV
C 536	12.2	43.6	26	12	ADL25701	Adl25701 Human NOV	609	12	42.9	20	2	AAV63222	AAV63222 Reverse p
C 537	12.2	43.6	27	10	ADF50351	Adf50351 PCR prime	C 610	12	42.9	20	2	AZ202028	Az202028 PCR prime
C 538	12.2	43.6	28	6	ABK66286	Abk66286 Human gen	611	12	42.9	20	3	AAQ93194	AAQ93194 Human STA
C 539	12.2	43.6	28	10	ABS58319	Abs58319 Baees 380	612	12	42.9	20	6	AAQ96811	AAQ96811 Human STA
540	12.2	43.6	29	3	AAA04442	Aaa04442 Polymorph	C 613	12	42.9	20	10	ABZ86119	Abz86119 Human oli
C 541	12.2	43.6	29	6	ABA99925	AbA99925 NDV HN PC	C 614	12	42.9	20	11	ABD22429	ABD22429 Human cat
C 542	12.2	43.6	30	2	AAAT31857	Aat31857 Primer fo	C 615	12	42.9	20	12	ADI37414	Adi37414 M. tuberc
C 543	12.2	43.6	30	6	ABT03850	Abt03850 Human RFL	C 616	12	42.9	20	12	ADK96487	Adk96487 Primer of
C 544	12.2	43.6	30	9	ADA19166	Ada19166 Human koh	C 617	12	42.9	20	12	ADL22948	Adl22948 Human gra
C 545	12.2	43.6	31	2	AAAT80047	Aat80047 Primer IG	618	12	42.9	20	12	ADK73270	Adk73270 Chimeric
C 546	12.2	43.6	31	2	AAAX06483	Aax06483 Human bia	619	12	42.9	20	12	ADK73535	Adk73535 Chimeric
C 547	12.2	43.6	31	4	AAI29870	Aai29870 Human sin	620	12	42.9	21	10	ADF39601	Adf39601 EST gene
C 548	12.2	43.6	33	2	AAQ63306	Aaq63306 Canine ho	C 621	12	42.9	21	10	ACC43493	Acc43493 PCR prime
C 549	12.2	43.6	33	2	AAQ69065	Aaq69065 Primer fo	622	12	42.9	21	11	ADL70122	Adl70122 Human GIP
C 550	12.2	43.6	33	2	AAQ85502	Aaq85502 PCR prime	623	12	42.9	21	11	ADL70130	Adl70130 Human GIP
C 551	12.2	43.6	33	2	AAAX28918	Aax28918 5' PCR pr	624	12	42.9	21	11	ADL70138	Adl70138 Human GIP
C 552	12.2	43.6	33	3	AAA48956	Aaa48956 PCR prime	625	12	42.9	22	2	AAQ36858	Aaq36858 Human XLI
C 553	12.2	43.6	33	3	AAA48955	Aaa48955 PCR prime	626	12	42.9	22	8	AAQ56067	AAQ56067 Primer #2
C 554	12.2	43.6	33	6	ABA92442	AbA92442 Human per	627	12	42.9	22	9	ADA09280	Ada09280 Mouse 14-
C 555	12.2	43.6	35	10	ABV74520	Abv74520 Human G p	628	12	42.9	22	10	ADC23485	Adc23485 Human imm
C 556	12.2	43.6	35	12	ADN11790	Adn11790 PCR prime	629	12	42.9	23	12	ADM74245	Adm74245 Human NOV
C 557	12.2	43.6	36	5	AAH78962	Aah78962 Antisense	630	12	42.9	24	5	AAF85529	Aaf85529 Salmonell
C 558	12.2	43.6	36	5	AAH78961	Aah78961 Antisense	631	12	42.9	24	6	ABI83975	Abi83975 Capture o
C 559	12.2	43.6	37	10	ADF50463	Adf50463 PCR prime	C 632	12	42.9	24	6	ABI83974	Abi83974 Capture o
C 560	12.2	43.6	38	3	AAA62474	Aaa62474 Human SEC	633	12	42.9	24	8	ABZ69862	Abz69862 Human gly
C 561	12.2	43.6	38	4	AAH22717	Aah22717 Human sec	634	12	42.9	24	10	ADG17439	Adg17439 PCR prime
C 562	12.2	43.6	38	6	AAQ30544	Aaq30544 Human B7-	635	12	42.9	24	10	ADG17440	Adg17440 PCR prime
C 563	12.2	43.6	38	6	AAAL0540	Aal0540 Human B7-	C 636	12	42.9	25	6	ADG17476	Adg17476 Interleuk
C 564	12.2	43.6	40	5	AAAF31477	Aaf31477 Primer #3	C 637	12	42.9	25	6	ABV80908	Abv80908 Human HTP
C 565	12.2	43.6	40	6	AAAL40251	Aal40251 Isoprenoi	C 638	12	42.9	25	6	ABV80914	Abv80914 Human HTP
C 566	12.2	43.6	40	10	ADF18589	Adf18589 Mouse zal	639	12	42.9	25	9	ACI07359	Act07359 Human mic
C 567	12.2	43.6	40	10	ADG63342	Adg63342 Human wil	640	12	42.9	25	9	ACI85532	Act85532 Human mic
C 568	12.2	43.6	41	2	AAQ53758	Aaq53758 Ligand fo	641	12	42.9	25	9	ACI85682	Act85682 Human mic
C 569	12.2	43.6	41	2	AAAT07959	Aat07959 Bacteriop	642	12	42.9	25	9	ACI39290	Act39290 Human mic
C 570	12.2	43.6	41	2	AAV00975	Aav00975 SELEX lig	643	12	42.9	25	9	ACI84993	Act84993 Human mic
C 571	12.2	43.6	41	2	AAV14760	Aav14760 Clone 5,	644	12	42.9	25	9	ACK27911	Ack27911 Human mic
C 572	12.2	43.6	41	2	AAV79835	Aav79835 RNA ligan	645	12	42.9	25	9	ACI56843	Act56843 Human mic
C 573	12.2	43.6	41	3	AAQ92935	Aaq92935 High-affi	646	12	42.9	25	9	ACI61430	Act61430 Human mic
C 574	12.2	43.6	41	4	AAH78919	Aah78919 Human spe	647	12	42.9	25	9	ACI56215	Act56215 Human mic
C 575	12.2	43.6	41	4	AAH78920	Aah78920 Human spe	648	12	42.9	25	9	ACK08450	Ack08450 Human mic
C 576	12.2	43.6	41	6	ABK61311	Abk61311 SELEX pro	C 649	12	42.9	25	9	ACI32628	Act32628 Human mic
C 577	12.2	43.6	41	6	ABL61505	AbL61505 Vector pG	650	12	42.9	25	9	ACI37287	Act37287 Human mic
C 578	12.2	43.6	41	6	ABZ44662	Abz44662 Human ATP	C 651	12	42.9	25	9	ACI43865	Act43865 Human mic
C 579	12.2	43.6	41	6	ABZ47159	Abz47159 Human ATP	C 652	12	42.9	25	9	ACI25083	Act25083 Human mic
C 580	12.2	43.6	41	10	ADF67699	Adf67699 Bacteriop	C 653	12	42.9	25	9	ACI76831	Act76831 Human mic
C 581	12.2	43.6	41	12	ADG39247	Adg39247 RNA clone	C 654	12	42.9	25	9	ACK30936	Ack30936 Human mic
C 582	12.2	43.6	42	6	AAAD41168	Aad41168 Human HGP	655	12	42.9	25	9	ACK38282	Act38282 Human mic
C 583	12.2	43.6	42	9	ACC58890	Acc58890 Human G-p	656	12	42.9	25	9	ACK08451	Ack08451 Human mic
C 584	12.2	43.6	43	2	AAQ53769	Aaq53769 Ligand fo	C 657	12	42.9	25	12	ADP15850	Adp15850 Renal cel
C 585	12.2	43.6	43	2	AAAT07970	Aat07970 Bacteriop	C 658	12	42.9	25	12	ADP17205	Adp17205 Renal cel
C 586	12.2	43.6	43	2	AAV00986	Aav00986 SELEX lig	C 659	12	42.9	25	12	ADP17204	Adp17204 Renal cel
C 587	12.2	43.6	43	2	AAV14771	Aav14771 Clone 16,	C 660	12	42.9	26	2	AAA70661	Aaa70661 Comamonas
C 588	12.2	43.6	43	2	AAV79846	Aav79846 RNA ligan	C 661	12	42.9	26	12	ADN01564	Adn01564 Enterococ
C 589	12.2	43.6	43	3	AAQ92946	Aaq92946 High-affi	C 662	12	42.9	27	10	ACC43497	Acc43497 PCR prime
C 590	12.2	43.6	43	6	ABK61322	Abk61322 SELEX pro	663	12	42.9	27	10	ABZ84245	Abz84245 Toxicolog
C 591	12.2	43.6	43	9	ACD07848	Act07848 Human con	664	12	42.9	27	10	ADO31399	Ado31399 Human CFT
C 592	12.2	43.6	43	9	ACD07849	Act07849 Human con	665	12	42.9	29	3	AAA16765	Aaa16766 Human sec
C 593	12.2	43.6	43	10	ADF67710	Adf67710 Bacteriop	666	12	42.9	29	10	ADD40784	Add40784 Human ten
C 594	12.2	43.6	43	12	ADG39258	Adg39258 RNA clone	667	12	42.9	30	4	AAN20232	Aan20232 Human ADA
C 595	12.2	43.6	44	2	AAV66743	Aav66743 PCR prime	C 668	12	42.9	30	4	AAH41475	Aah41475 Trichosan
C 596	12.2	43.6	44	6	ADG69920	Adg69920 Aspergill	C 669	12	42.9	30	6	ABA95173	AbA95173 Trichosan
C 597	12.2	43.6	44	10	AAD64573	Aad64573 N-vp16-78	C 670	12	42.9	30	10	ADC77570	Adc77570 Zebrafish
C 598	12.2	43.6	44	11	ADN88854	Adn88854 FAE-N5 pr	671	12	42.9	30	12	ADP08887	Adp08887 PCR prime
C 599	12.2	43.6	45	2	ABK70067	Abk70067 Antibody	672	12	42.9	30	12	ADP45978	Adp45978 PCR prime
C 600	12.2	43.6	45	6	ABK70067	Abk70067 Antibody	673	12	42.9	31	3	AAA40389	Aaa40389 A. thalia
C 601	12.2	43.6	45	10	ADL18019	Adl18019 Anti-I-lect	C 674	12	42.9	32	10	ADC03036	Adc03036 Ex vivo s
C 602	12.2	43.6	45	11	ADL35283	Adl35283 Anti-Pcga	C 675	12	42.9	32	12	ADI58711	Adi58711 Human int
C 603	12.2	43.6	48	2	AAQ24496	Aaq24496 CC49/218	676	12	42.9	33	2	AAT47659	Aat47659 Primer fo
C 604	12.2	43.6	50	2	AAV66651	Aav66651 Anti-huma	677	12	42.9	33	2	AAT45437	Aat45437 Human tra
605	12.2	43.6	50	3	AAA78342	Aaa78342 Humanised	678	12	42.9	33	2	AAT45431	Aat45431 Human tra

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679	12	42.9	33	2	AAx25991	Reverse p	C 752	12	42.9	49	9	ADAl3269	Human sec
680	12	42.9	33	3	Az87136	Human TRA	C 753	12	42.9	49	9	ADAl3127	Human sec
681	12	42.9	34	3	Az57969	D-JH and	C 754	12	42.9	49	9	ADAl2137	Human sec
682	12	42.9	34	6	AA143729	Immunoglo	C 755	12	42.9	49	9	ADAl1995	Human sec
683	12	42.9	34	6	AA143729	Immunoglo	C 756	12	42.9	49	9	ADAl17342	Human sec
684	12	42.9	35	2	ADA24367	Murine th	C 757	12	42.9	49	9	ADAl17484	Human sec
685	12	42.9	35	2	AA163640	Anti-HrLV	C 758	12	42.9	49	9	ADAl42987	Human sec
686	12	42.9	35	2	AA178011	Chimeric	C 759	12	42.9	49	9	ADAl42845	Human sec
687	12	42.9	35	2	AA178011	Chimeric	C 760	12	42.9	49	9	ADAl42845	Human sec
688	12	42.9	36	2	AA178011	Chimeric	C 761	12	42.9	49	9	ADAl42845	Human sec
689	12	42.9	36	2	AA178011	Chimeric	C 762	12	42.9	49	9	ADAl42845	Human sec
690	12	42.9	36	2	AA178011	Chimeric	C 763	12	42.9	49	9	ADAl42845	Human sec
691	12	42.9	37	10	AD158712	Human int	C 764	12	42.9	49	9	ADAl42845	Human sec
692	12	42.9	37	10	AD158712	Human int	C 765	12	42.9	49	9	ADAl42845	Human sec
693	12	42.9	38	1	AA151708	Primer TO	C 766	12	42.9	49	9	ADAl42845	Human sec
694	12	42.9	38	1	AA151708	Primer TO	C 767	12	42.9	49	9	ADAl42845	Human sec
695	12	42.9	38	12	AD134325	Primer of	C 768	12	42.9	49	9	ADAl42845	Human sec
696	12	42.9	39	2	AA170993	Mouse his	C 769	12	42.9	49	9	ADAl42845	Human sec
697	12	42.9	39	2	AA170993	Mouse his	C 770	12	42.9	49	9	ADAl42845	Human sec
698	12	42.9	40	1	AA171243	Recombina	C 771	12	42.9	49	9	ADAl42845	Human sec
699	12	42.9	40	2	AA171243	Recombina	C 772	12	42.9	49	9	ADAl42845	Human sec
700	12	42.9	41	5	AA171243	Recombina	C 773	12	42.9	49	9	ADAl42845	Human sec
701	12	42.9	41	5	AA171243	Recombina	C 774	12	42.9	49	9	ADAl42845	Human sec
702	12	42.9	41	5	AA171243	Recombina	C 775	12	42.9	49	9	ADAl42845	Human sec
703	12	42.9	41	5	AA171243	Recombina	C 776	12	42.9	49	9	ADAl42845	Human sec
704	12	42.9	41	5	AA171243	Recombina	C 777	12	42.9	49	9	ADAl42845	Human sec
705	12	42.9	41	5	AA171243	Recombina	C 778	12	42.9	49	9	ADAl42845	Human sec
706	12	42.9	41	5	AA171243	Recombina	C 779	12	42.9	49	9	ADAl42845	Human sec
707	12	42.9	41	5	AA171243	Recombina	C 780	12	42.9	49	9	ADAl42845	Human sec
708	12	42.9	41	5	AA171243	Recombina	C 781	12	42.9	49	9	ADAl42845	Human sec
709	12	42.9	41	5	AA171243	Recombina	C 782	12	42.9	49	9	ADAl42845	Human sec
710	12	42.9	41	5	AA171243	Recombina	C 783	12	42.9	49	9	ADAl42845	Human sec
711	12	42.9	41	5	AA171243	Recombina	C 784	12	42.9	49	9	ADAl42845	Human sec
712	12	42.9	41	5	AA171243	Recombina	C 785	12	42.9	49	9	ADAl42845	Human sec
713	12	42.9	41	5	AA171243	Recombina	C 786	12	42.9	49	9	ADAl42845	Human sec
714	12	42.9	41	5	AA171243	Recombina	C 787	12	42.9	49	9	ADAl42845	Human sec
715	12	42.9	41	5	AA171243	Recombina	C 788	12	42.9	49	9	ADAl42845	Human sec
716	12	42.9	41	5	AA171243	Recombina	C 789	12	42.9	49	9	ADAl42845	Human sec
717	12	42.9	41	5	AA171243	Recombina	C 790	12	42.9	49	9	ADAl42845	Human sec
718	12	42.9	41	5	AA171243	Recombina	C 791	12	42.9	49	9	ADAl42845	Human sec
719	12	42.9	41	5	AA171243	Recombina	C 792	12	42.9	49	9	ADAl42845	Human sec
720	12	42.9	41	5	AA171243	Recombina	C 793	12	42.9	49	9	ADAl42845	Human sec
721	12	42.9	41	5	AA171243	Recombina	C 794	12	42.9	49	9	ADAl42845	Human sec
722	12	42.9	41	5	AA171243	Recombina	C 795	12	42.9	49	9	ADAl42845	Human sec
723	12	42.9	41	5	AA171243	Recombina	C 796	12	42.9	49	9	ADAl42845	Human sec
724	12	42.9	41	5	AA171243	Recombina	C 797	12	42.9	49	9	ADAl42845	Human sec
725	12	42.9	41	5	AA171243	Recombina	C 798	12	42.9	49	9	ADAl42845	Human sec
726	12	42.9	41	5	AA171243	Recombina	C 799	12	42.9	49	9	ADAl42845	Human sec
727	12	42.9	41	5	AA171243	Recombina	C 800	12	42.9	49	9	ADAl42845	Human sec
728	12	42.9	41	5	AA171243	Recombina	C 801	12	42.9	49	9	ADAl42845	Human sec
729	12	42.9	41	5	AA171243	Recombina	C 802	12	42.9	49	9	ADAl42845	Human sec
730	12	42.9	41	5	AA171243	Recombina	C 803	12	42.9	49	9	ADAl42845	Human sec
731	12	42.9	41	5	AA171243	Recombina	C 804	12	42.9	49	9	ADAl42845	Human sec
732	12	42.9	41	5	AA171243	Recombina	C 805	12	42.9	49	9	ADAl42845	Human sec
733	12	42.9	41	5	AA171243	Recombina	C 806	12	42.9	49	9	ADAl42845	Human sec
734	12	42.9	41	5	AA171243	Recombina	C 807	12	42.9	49	9	ADAl42845	Human sec
735	12	42.9	41	5	AA171243	Recombina	C 808	12	42.9	49	9	ADAl42845	Human sec
736	12	42.9	41	5	AA171243	Recombina	C 809	12	42.9	49	9	ADAl42845	Human sec
737	12	42.9	41	5	AA171243	Recombina	C 810	12	42.9	49	9	ADAl42845	Human sec
738	12	42.9	41	5	AA171243	Recombina	C 811	12	42.9	49	9	ADAl42845	Human sec
739	12	42.9	41	5	AA171243	Recombina	C 812	12	42.9	49	9	ADAl42845	Human sec
740	12	42.9	41	5	AA171243	Recombina	C 813	12	42.9	49	9	ADAl42845	Human sec
741	12	42.9	41	5	AA171243	Recombina	C 814	12	42.9	49	9	ADAl42845	Human sec
742	12	42.9	41	5	AA171243	Recombina	C 815	12	42.9	49	9	ADAl42845	Human sec
743	12	42.9	41	5	AA171243	Recombina	C 816	12	42.9	49	9	ADAl42845	Human sec
744	12	42.9	41	5	AA171243	Recombina	C 817	12	42.9	49	9	ADAl42845	Human sec
745	12	42.9	41	5	AA171243	Recombina	C 818	12	42.9	49	9	ADAl42845	Human sec
746	12	42.9	41	5	AA171243	Recombina	C 819	12	42.9	49	9	ADAl42845	Human sec
747	12	42.9	41	5	AA171243	Recombina	C 820	12	42.9	49	9	ADAl42845	Human sec
748	12	42.9	41	5	AA171243	Recombina	C 821	12	42.9	49	9	ADAl42845	Human sec
749	12	42.9	41	5	AA171243	Recombina	C 822	12	42.9	49	9	ADAl42845	Human sec
750	12	42.9	41	5	AA171243	Recombina	C 823	12	42.9	49	9	ADAl42845	Human sec
751	12	42.9	41	5	AA171243	Recombina	C 824	12	42.9	49	9	ADAl42845	Human sec

C 825	12	42.9	49	12	ADP74057	Adf74057 Human sec	898	11.8	42.1	23	6	ABK97004	Abk97004 Synthetic
C 826	12	42.9	49	12	ADF73633	Adf73633 Human sec	899	11.8	42.1	23	6	ABK97020	Abk97020 Synthetic
C 827	12	42.9	49	12	ADF73491	Adf73491 Human sec	900	11.8	42.1	23	6	ABK96988	Abk96988 Synthetic
C 828	12	42.9	49	12	ADG92334	Adg92334 Human sec	901	11.8	42.1	23	6	ABK97032	Abk97032 Synthetic
C 829	12	42.9	49	12	ADG92476	Adg92476 Human sec	902	11.8	42.1	23	12	ADJ95881	Adj95881 Cell prol
C 830	12	42.9	49	12	ADG92903	Adg92903 Human sec	903	11.8	42.1	23	12	ADJ95791	Adj95791 Cell prol
C 831	12	42.9	49	12	ADG92761	Adg92761 Human sec	904	11.8	42.1	23	12	ADJ95803	Adj95803 Cell prol
C 832	12	42.9	49	12	ADH20692	Adh20692 Human sec	905	11.8	42.1	23	12	ADJ95839	Adj95839 Cell prol
C 833	12	42.9	49	12	ADH20550	Adh20550 Human sec	906	11.8	42.1	23	12	ADJ95759	Adj95759 Cell prol
C 834	12	42.9	49	12	ADH07547	Adh07547 Human sec	907	11.8	42.1	23	12	ADJ95775	Adj95775 Cell prol
C 835	12	42.9	49	12	ADH07405	Adh07405 Human sec	908	11.8	42.1	24	2	AAT43346	Aat43346 Primer GS
C 836	12	42.9	49	12	ADH60092	Adh60092 Human sec	C 909	11.8	42.1	24	2	AAT95061	Aat95061 Primer fo
C 837	12	42.9	49	12	ADH59950	Adh59950 Human sec	910	11.8	42.1	24	2	AAX90069	Aax90069 Fervidoba
C 838	12	42.9	49	12	ADH06978	Adh06978 Human sec	911	11.8	42.1	24	6	ABK97006	Abk97006 Synthetic
C 839	12	42.9	49	12	ADH07120	Adh07120 Human sec	912	11.8	42.1	24	6	ABK97022	Abk97022 Synthetic
C 840	12	42.9	49	12	ADI18720	Adi18720 Human sec	913	11.8	42.1	24	6	ABK96990	Abk96990 Synthetic
C 841	12	42.9	49	12	ADI18862	Adi18862 Human sec	914	11.8	42.1	24	6	ABK97112	Abk97112 Synthetic
C 842	12	42.9	49	12	ADI65582	Adi65582 Human sec	915	11.8	42.1	24	6	ABK97034	Abk97034 Synthetic
C 843	12	42.9	49	12	ADI65540	Adi65540 Human sec	916	11.8	42.1	24	6	ABK97070	Abk97070 Synthetic
C 844	12	42.9	49	12	ADI37841	Adi37841 Human sec	C 917	11.8	42.1	24	6	ABI89312	Abi89312 Capture o
C 845	12	42.9	49	12	ADI37699	Adi37699 Human sec	918	11.8	42.1	24	6	ABI89313	Abi89313 Capture o
C 846	12	42.9	49	12	ADH97499	Adh97499 Human sec	919	11.8	42.1	24	12	ADJ95761	Adj95761 Cell prol
C 847	12	42.9	49	12	ADH97641	Adh97641 Human sec	920	11.8	42.1	24	12	ADJ95805	Adj95805 Cell prol
C 848	12	42.9	49	12	ADI65867	Adi65867 Human sec	921	11.8	42.1	24	12	ADJ95883	Adj95883 Cell prol
C 849	12	42.9	49	12	ADI66009	Adi66009 Human sec	922	11.8	42.1	24	12	ADJ95777	Adj95777 Cell prol
C 850	12	42.9	49	12	ADH60610	Adh60610 Human sec	923	11.8	42.1	24	12	ADJ95841	Adj95841 Cell prol
C 851	12	42.9	49	12	ADH60752	Adh60752 Human sec	924	11.8	42.1	24	12	ADJ95793	Adj95793 Cell prol
C 852	12	42.9	49	12	ADJ99667	Adj99667 Human sec	C 925	11.8	42.1	25	2	AAT65132	Aat65132 Primer 31
C 853	12	42.9	49	12	ADJ99809	Adj99809 Human sec	C 926	11.8	42.1	25	2	AAT74103	Aat74103 Oligonuc
C 854	12	42.9	49	12	ADL08860	Adl08860 Human sec	927	11.8	42.1	25	6	ABK89633	Abk89633 Chimeric
C 855	12	42.9	49	12	ADL09002	Adl09002 Human sec	928	11.8	42.1	25	6	ABN13636	Abn13636 Human GDM
C 856	12	42.9	49	12	ADM25201	Adm25201 Human sec	929	11.8	42.1	25	6	ABN13635	Abn13635 Human GDM
C 857	12	42.9	49	12	ADM25343	Adm25343 Human sec	930	11.8	42.1	25	6	ABN13634	Abn13634 Human GDM
C 858	12	42.9	49	12	ADM29951	Adm29951 Human sec	931	11.8	42.1	25	6	ABK96992	Abk96992 Synthetic
C 859	12	42.9	49	12	ADM30093	Adm30093 Human sec	C 932	11.8	42.1	25	6	ABK97037	Abk97037 Synthetic
C 860	12	42.9	49	12	ADM06415	Adm06415 Human PRO	933	11.8	42.1	25	6	ABK97036	Abk97036 Synthetic
C 861	12	42.9	49	12	ADO06273	Ado06273 Human SNP	934	11.8	42.1	25	6	ABK97072	Abk97072 Synthetic
C 862	12	42.9	50	4	AAL31007	Aal31007 Human SNP	C 935	11.8	42.1	25	6	ABK97115	Abk97115 Synthetic
C 863	12	42.9	50	6	ABZ06873	Abz06873 Human leu	936	11.8	42.1	25	6	ABK97008	Abk97008 Synthetic
C 864	12	42.9	50	6	ABZ04772	Abz04772 Human leu	937	11.8	42.1	25	6	ABK97024	Abk97024 Synthetic
C 865	12	42.9	50	6	ABZ06483	Abz06483 Human leu	938	11.8	42.1	25	6	ABK97114	Abk97114 Synthetic
C 866	12	42.9	50	6	ABZ01039	Abz01039 Human leu	939	11.8	42.1	25	8	ACD00055	Acdo0055 G-protein
C 867	12	42.9	50	6	ABZ00259	Abz00259 Human leu	940	11.8	42.1	25	8	ACD00056	Acdo0056 G-protein
C 868	12	42.9	50	6	ABZ03066	Abz03066 Human leu	941	11.8	42.1	25	8	ACD00057	Acdo0057 G-protein
C 869	12	42.9	50	6	ABZ02986	Abz02986 Human leu	942	11.8	42.1	25	9	ACI15692	Acti15692 Human mic
C 870	12	42.9	50	10	ADD31791	Add31791 Anti-CEA	C 943	11.8	42.1	25	9	ACI17719	Acti17719 Human mic
C 871	12	42.9	50	12	ADP10275	Adp10275 50-mer ol	C 944	11.8	42.1	25	9	ACI56965	Acti56965 Human mic
C 872	11.8	42.1	17	8	ACD59071	Acd59071 HCV DNaz	945	11.8	42.1	25	9	ACI09842	Acti09842 Human mic
C 873	11.8	42.1	17	8	ACD63598	Acd63598 HCV minus	946	11.8	42.1	25	9	ACI73063	Acti73063 Human mic
C 874	11.8	42.1	17	12	ADI86156	Adi86156 HCV DNaz	947	11.8	42.1	25	9	ACK25403	Actk25403 Human mic
C 875	11.8	42.1	17	12	ADI83907	Adi83907 HCV DNaz	948	11.8	42.1	25	9	ACK05762	Actk05762 Human mic
C 876	11.8	42.1	18	2	AZ41099	Aaz41099 Human G-a	C 949	11.8	42.1	25	9	ACI37838	Acti37838 Human mic
C 877	11.8	42.1	18	2	AZ19470	Aaz19470 Human G-a	C 950	11.8	42.1	25	9	ACI38426	Acti38426 Human mic
C 878	11.8	42.1	19	5	AAF26278	Aaf26278 Human egf	C 951	11.8	42.1	25	9	ACK00994	Actk00994 Human mic
C 879	11.8	42.1	19	5	AAF26269	Aaf26269 Human egf	C 952	11.8	42.1	25	9	ACK20213	Actk20213 Human mic
C 880	11.8	42.1	19	12	ADQ27840	Adq27840 RNA inter	C 953	11.8	42.1	25	9	ACI50116	Acti50116 Human mic
C 881	11.8	42.1	20	2	AAQ53932	Aaq53932 Synthetic	C 954	11.8	42.1	25	9	ACI17059	Acti17059 Human mic
C 882	11.8	42.1	20	3	AAAS1711	Aas1711 R17 ligan	C 955	11.8	42.1	25	9	ACI32119	Acti32119 Human mic
C 883	11.8	42.1	20	5	AAF90588	Aaf90588 Human zap	C 956	11.8	42.1	25	9	ACI12041	Acti12041 Human mic
C 884	11.8	42.1	20	6	AAF36758	Aaf36758 Human RIN	C 957	11.8	42.1	25	9	ACI45908	Acti45908 Human mic
C 885	11.8	42.1	20	6	AD28215	Ad28215 Alphaviru	C 958	11.8	42.1	25	9	ACI56964	Acti56964 Human mic
C 886	11.8	42.1	20	10	ABZ92478	Abz92478 Human oli	C 959	11.8	42.1	25	9	ACI88756	Acti88756 Human mic
C 887	11.8	42.1	20	11	ABD28708	Abd28708 AA48261-	C 960	11.8	42.1	25	9	ACI43709	Acti43709 Human mic
C 888	11.8	42.1	20	12	ADK96098	Adk96098 Primer of	C 961	11.8	42.1	25	9	ACK23753	Actk23753 Human mic
C 889	11.8	42.1	21	3	AA16736	Aa16736 Human sec	C 962	11.8	42.1	25	9	ACI09566	Acti09566 Human mic
C 890	11.8	42.1	21	8	ABZ81891	Abz81891 Primer Ba	C 963	11.8	42.1	25	9	ACI79116	Acti79116 Human mic
C 891	11.8	42.1	21	12	ADG64974	Adg64974 Primer #5	C 964	11.8	42.1	25	9	ACI42014	Acti42014 Human mic
C 892	11.8	42.1	21	12	ADK96320	Adk96320 Primer of	C 965	11.8	42.1	25	9	ACI78057	Acti78057 Human mic
C 893	11.8	42.1	22	2	AAQ88191	Aaq88191 C1 inhibi	C 966	11.8	42.1	25	9	ACK04749	Actk04749 Human mic
C 894	11.8	42.1	22	2	AAQ90141	Aaq90141 Transthyr	C 967	11.8	42.1	25	9	ACK05136	Actk05136 Human mic
C 895	11.8	42.1	22	10	ADA43545	Add43545 Mouse PAP	C 968	11.8	42.1	25	9	ACI08930	Acti08930 Human mic
C 896	11.8	42.1	23	6	ABK97110	Abk97110 Synthetic	C 969	11.8	42.1	25	9	ACI39054	Acti39054 Human mic
C 897	11.8	42.1	23	6	ABK97068	Abk97068 Synthetic	970	11.8	42.1	25	9	ACI47841	Acti47841 Human mic

c	971	11.8	42.1	25	9	ACI89056	AcI89056 Human mic
c	972	11.8	42.1	25	9	ACI91715	AcI91715 Human mic
c	973	11.8	42.1	25	9	ACI23114	AcI23114 Human mic
c	974	11.8	42.1	25	9	ACI39682	AcI39682 Human mic
c	975	11.8	42.1	25	9	ACH64079	ACH64079 DNA target
c	976	11.8	42.1	25	10	ADF63356	ADF63356 Human PCC
c	977	11.8	42.1	25	10	ADF63357	ADF63357 Human PCC
c	978	11.8	42.1	25	10	ADF63358	ADF63358 Human PCC
c	979	11.8	42.1	25	12	ADJ95808	ADJ95808 Cell prol
c	980	11.8	42.1	25	12	ADJ95886	ADJ95886 Cell prol
c	981	11.8	42.1	25	12	ADJ95795	ADJ95795 Cell prol
c	982	11.8	42.1	25	12	ADJ95763	ADJ95763 Cell prol
c	983	11.8	42.1	25	12	ADJ95885	ADJ95885 Cell prol
c	984	11.8	42.1	25	12	ADJ95779	ADJ95779 Cell prol
c	985	11.8	42.1	25	12	ADJ95807	ADJ95807 Cell prol
c	986	11.8	42.1	25	12	ADJ95843	ADJ95843 Cell prol
c	987	11.8	42.1	26	6	AAI47432	AAI47432 Human Slo
c	988	11.8	42.1	26	6	ADJ17407	ADJ17407 PCR prime
c	989	11.8	42.1	26	12	ADN42496	ADN42496 Human NOV
c	990	11.8	42.1	27	2	AAQ53402	AAQ53402 Mouse bet
c	991	11.8	42.1	28	3	AAJ98365	AAJ98365 D. vulgar
c	992	11.8	42.1	28	6	ABL35176	ABL35176 Immunosti
c	993	11.8	42.1	28	8	ADJ53890	ADJ53890 PCR prime
c	994	11.8	42.1	28	8	ADJ53889	ADJ53889 PCR prime
c	995	11.8	42.1	28	10	ADB89206	ADB89206 Human Gal
c	996	11.8	42.1	28	10	ADC24553	ADC24553 Human Gal
c	997	11.8	42.1	28	10	ADG67823	ADG67823 Human Gia
c	998	11.8	42.1	28	10	ADE10536	ADE10536 Minicell
c	999	11.8	42.1	28	10	ADE11458	ADE11458 Human Gal
c	1000	11.8	42.1	28	10	ADE12636	ADE12636 Human Gal

ALIGNMENTS

RESULT 1  
ADAI3880/c  
ID ADAI3880 standard; RNA; 21 BP.  
XX  
AC ADAI3880;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Short interfering nucleic acid (siNA) oligonucleotide SEQ ID NO:217.  
XX  
KW double-stranded short interfering nucleic acid;  
KW short interfering nucleic acid; siNA; expression; replication;  
KW inhibition; RNA interference; virucide; anti-HIV; hepatotropic;  
KW antiinflammatory; plant; antiviral; vasotropic; neuroprotective;  
KW cytostatic; cardiovascular; immunosuppressive; respiratory; nephrotropic;  
KW endocrine; viral infection; hepatitis B; hepatitis C; HIV;  
KW herpes simplex; cytomegalovirus; human papillomavirus;  
KW respiratory syncytial virus; influenza virus; restenosis;  
KW neurodegeneration; cancer; neurological; prion; inflammatory; autoimmune;  
KW pulmonary; renal; liver; mitochondrial; reproductive disease;  
KW chemical modification; ss.  
XX  
OS Synthetic.  
XX  
XX WO2003070918-A2.  
XX  
XX 28-AUG-2003.  
XX  
XX 20-FEB-2003; 2003WO-US005346.  
XX  
XX 20-FEB-2002; 2002US-0358580P.  
XX 11-MAR-2002; 2002US-0363124P.  
XX 06-JUN-2002; 2002US-0386782P.  
XX 29-AUG-2002; 2002US-0406784P.  
XX 03-SEP-2002; 2002US-0408378P.  
XX 03-SEP-2002; 2002US-0409293P.  
XX 15-JAN-2003; 2003US-0440129P.  
XX

PA (RIBO-) RIBOZYME PHARM INC.  
XX Mcswiggen J, Beigelman L, Macejak D, Zinnen S, Pavco P;  
PI Morrissey D, Fosnaugh K, Mokler V, Jamison S;  
XX WPI; 2003-689785/65.  
XX New short interfering nucleic acid containing no ribonucleotides, useful  
PT e.g. for treating viral infection, downregulates expression of target  
PT gene or RNA.  
XX  
XX Example 4; Page 139; 204pp; English.  
XX The present invention describes a double-stranded short interfering  
XX nucleic acid (siNA) that downregulates expression of a target gene, where  
CC the siNA molecule comprises no ribonucleotides and each strand of the  
CC double-stranded siNA comprises about 21 nucleotides. Also described: (1)  
CC a siNA molecule that inhibits expression of target RNA; (2) a siNA  
CC molecule that inhibits replication of a virus and optionally does not  
CC require presence of a ribonucleotide for inhibition; (3) a siNA molecule  
CC that inhibits expression of a target gene and does not require presence  
CC of a ribonucleotide for inhibition; (4) a siNA molecule that inhibits  
CC expression of a target gene by mediating RNA interference; and (5) a  
CC method for modulating expression of a gene in a cell using siNA  
CC molecules. siNA's can have virucide, anti-HIV, hepatotropic,  
CC antiinflammatory, plant antiviral, vasotropic, neuroprotective,  
CC cytostatic, cardiovascular, immunosuppressive, respiratory, nephrotropic  
CC and endocrine activities. The siNA's are useful for downregulating  
CC expression of target genes, inhibiting expression of target RNA, and  
CC inhibiting replication of a virus. siNA molecules can be used: (a) for  
CC therapy of any disorder that responds to modulation of gene expression,  
CC especially animal and plant viral infections, specifically hepatitis B or  
CC C; HIV; herpes simplex; cytomegalovirus; human papilloma; respiratory  
CC syncytial or influenza viruses, and also many other diseases such as  
CC restenosis, neurodegeneration, cancers, and cardiovascular, neurological,  
CC prion, inflammatory, autoimmune, pulmonary, renal, liver, mitochondrial,  
CC endocrine or reproductive diseases; and (b) for diagnosis, target  
CC validation, genomic discovery, genetic engineering, pharmacogenomics and  
CC analysis of gene function. Chemical modification of siNA molecules  
CC improves interfering activity; stability; cellular uptake; binding  
CC affinity and/or mediates increased polymerase activity. siNA may be  
CC designed to target many related genes containing a conserved sequence.  
CC The present sequence represents a siNA oligonucleotide sequence, which is  
CC used in the exemplification of the present invention.  
XX  
XX Sequence 21 BP; 7 A; 8 C; 3 G; 0 T; 3 U; 0 Other;

Query Match 75.0%; Score 21; DB 9; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.4;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 GGGATAGTCGTCATGGGTT 28  
DB 21 GGGATAGTCGTCATGGGTT 1  
RESULT 2  
ADAI3871  
ID ADAI3871 standard; RNA; 21 BP.  
XX  
XX ADAI3871;  
XX  
XX 20-NOV-2003 (first entry)  
XX  
XX Short interfering nucleic acid (siNA) oligonucleotide SEQ ID NO:208.  
XX double-stranded short interfering nucleic acid;  
XX short interfering nucleic acid; siNA; expression; replication;  
XX inhibition; RNA interference; virucide; anti-HIV; hepatotropic;  
XX antiinflammatory; plant; antiviral; vasotropic; neuroprotective;  
XX cytostatic; cardiovascular; immunosuppressive; respiratory; nephrotropic;  
XX endocrine; viral infection; hepatitis B; hepatitis C; HIV;  
XX herpes simplex; cytomegalovirus; human papillomavirus;  
XX

KW respiratory syncytial virus; influenza virus; restenosis;  
 KW neurodegeneration; cancer; neurological; prion; inflammatory; autoimmune;  
 KW pulmonary; renal; liver; mitochondrial; reproductive disease;  
 KW chemical modification; ss.  
 OS Synthetic.  
 XX  
 PN WO2003070918-A2.  
 XX  
 XX 28-AUG-2003.  
 XX  
 XX 20-FEB-2003; 2003WO-US005346.  
 XX  
 XX 20-FEB-2002; 2002US-0358580P.  
 PR 11-MAR-2002; 2002US-0363124P.  
 PR 06-JUN-2002; 2002US-0386782P.  
 PR 29-AUG-2002; 2002US-0406784P.  
 PR 05-SEP-2002; 2002US-0408378P.  
 PR 09-SEP-2002; 2002US-0409293P.  
 PR 15-JAN-2003; 2003US-0440129P.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX  
 XX McSwiggen J, Beigelman L, Macejak D, Zinnen S, Pavco P;  
 PI Morrissey D, Fosnaugh K, Mokler V, Jamison S;  
 XX  
 XX WPI; 2003-689785/65.  
 XX  
 XX New short interfering nucleic acid containing no ribonucleotides, useful  
 PT e.g. for treating viral infection, downregulates expression of target  
 PT gene or RNA.  
 XX  
 XX Example 4; Page 138; 204pp; English.  
 XX  
 CC The present invention describes a double-stranded short interfering  
 CC nucleic acid (siNA) that downregulates expression of a target gene, where  
 CC the siNA molecule comprises no ribonucleotides and each strand of the  
 CC double-stranded siNA comprises about 21 nucleotides. Also described: (1)  
 CC a siNA molecule that inhibits expression of target RNA; (2) a siNA  
 CC molecule that inhibits replication of a virus and optionally does not  
 CC require presence of a ribonucleotide for inhibition; (3) a siNA molecule  
 CC that inhibits expression of a target gene and does not require presence  
 CC of a ribonucleotide for inhibition; (4) a siNA molecule that inhibits  
 CC expression of a target gene by mediating RNA interference; and (5) a  
 CC method for modulating expression of a gene in a cell using siNA  
 CC molecules. siNA's can have virucide, anti-HIV, hepatotropic,  
 CC antiinflammatory, plant antiviral, vasotropic, neuroprotective,  
 CC cytotostatic, cardiovascular, immunosuppressive, respiratory, nephrotropic  
 CC and endocrine activities. The siNA's are useful for downregulating  
 CC expression of target genes, inhibiting expression of target RNA, and  
 CC therapy of any disorder that responds to modulation of gene expression,  
 CC especially animal and plant viral infections, specifically hepatitis B or  
 CC C; HIV; herpes simplex; cytomegalovirus; human papilloma; respiratory  
 CC syncytial or influenza viruses, and also many other diseases such as  
 CC restenosis, neurodegeneration, cancers, and cardiovascular, neurological,  
 CC prion, inflammatory, autoimmune, pulmonary, renal, liver, mitochondrial,  
 CC endocrine or reproductive diseases; and (b) for diagnosis, target  
 CC validation, genomic discovery, genetic engineering, pharmacogenomics and  
 CC analysis of gene function. Chemical modification of siNA molecules  
 CC improves interfering activity; stability; cellular uptake; binding  
 CC affinity and/or mediates increased polymerase activity. siNA may be  
 CC designed to target many related genes containing a conserved sequence.  
 CC The present sequence represents a siNA oligonucleotide sequence, which is  
 CC used in the exemplification of the present invention.  
 XX  
 SQ Sequence 21 BP; 3 A; 3 C; 8 G; 0 T; 7 U; 0 Other;  
 Query Match 75.0%; Score 21; DB 9; Length 21;  
 Best Local Similarity 66.7%; Pred. No. 3.4;  
 Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;  
 8 GGGATAGTCGCTCAGGTGTT 28

Db  
 1 GCGAUGACGCCGCAUGGUGUU 21  
 ||||:||||:||||:||||:||||:  
 RESULT 3  
 ADA13872  
 ID ADA13872 standard; RNA; 21 BP.  
 XX  
 AC ADA13872;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Short interfering nucleic acid (siNA) oligonucleotide SEQ ID NO:209.  
 XX  
 XX double-stranded short interfering nucleic acid;  
 KW short interfering nucleic acid; siNA; expression; replication;  
 KW inhibition; RNA interference; virucide; anti-HIV; hepatotropic;  
 KW antiinflammatory; plant; antiviral; vasotropic; neuroprotective;  
 KW cytotostatic; cardiovascular; immunosuppressive; respiratory; nephrotropic;  
 KW endocrine; viral infection; hepatitis B; hepatitis C; HIV;  
 KW herpes simplex; cytomegalovirus; human papillomavirus;  
 KW respiratory syncytial virus; influenza virus; restenosis;  
 KW neurodegeneration; cancer; neurological; prion; inflammatory; autoimmune;  
 KW pulmonary; renal; liver; mitochondrial; reproductive disease;  
 KW chemical modification; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX WO2003070918-A2.  
 XX  
 XX 28-AUG-2003.  
 XX  
 XX 20-FEB-2003; 2003WO-US005346.  
 XX  
 XX 20-FEB-2002; 2002US-0358580P.  
 PR 11-MAR-2002; 2002US-0363124P.  
 PR 06-JUN-2002; 2002US-0386782P.  
 PR 29-AUG-2002; 2002US-0406784P.  
 PR 05-SEP-2002; 2002US-0408378P.  
 PR 09-SEP-2002; 2002US-0409293P.  
 PR 15-JAN-2003; 2003US-0440129P.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 XX  
 XX McSwiggen J, Beigelman L, Macejak D, Zinnen S, Pavco P;  
 PI Morrissey D, Fosnaugh K, Mokler V, Jamison S;  
 XX  
 XX WPI; 2003-689785/65.  
 XX  
 XX New short interfering nucleic acid containing no ribonucleotides, useful  
 PT e.g. for treating viral infection, downregulates expression of target  
 PT gene or RNA.  
 XX  
 XX Example 4; Page 138; 204pp; English.  
 XX  
 CC The present invention describes a double-stranded short interfering  
 CC nucleic acid (siNA) that downregulates expression of a target gene, where  
 CC the siNA molecule comprises no ribonucleotides and each strand of the  
 CC double-stranded siNA comprises about 21 nucleotides. Also described: (1)  
 CC a siNA molecule that inhibits expression of target RNA; (2) a siNA  
 CC molecule that inhibits replication of a virus and optionally does not  
 CC require presence of a ribonucleotide for inhibition; (3) a siNA molecule  
 CC that inhibits expression of a target gene and does not require presence  
 CC of a ribonucleotide for inhibition; (4) a siNA molecule that inhibits  
 CC expression of a target gene by mediating RNA interference; and (5) a  
 CC method for modulating expression of a gene in a cell using siNA  
 CC molecules. siNA's can have virucide, anti-HIV, hepatotropic,  
 CC antiinflammatory, plant antiviral, vasotropic, neuroprotective,  
 CC cytotostatic, cardiovascular, immunosuppressive, respiratory, nephrotropic  
 CC and endocrine activities. The siNA's are useful for downregulating  
 CC expression of target genes, inhibiting expression of target RNA, and  
 CC therapy of any disorder that responds to modulation of gene expression,  
 CC especially animal and plant viral infections, specifically hepatitis B or  
 CC C; HIV; herpes simplex; cytomegalovirus; human papilloma; respiratory  
 CC syncytial or influenza viruses, and also many other diseases such as  
 CC restenosis, neurodegeneration, cancers, and cardiovascular, neurological,  
 CC prion, inflammatory, autoimmune, pulmonary, renal, liver, mitochondrial,  
 CC endocrine or reproductive diseases; and (b) for diagnosis, target  
 CC validation, genomic discovery, genetic engineering, pharmacogenomics and  
 CC analysis of gene function. Chemical modification of siNA molecules  
 CC improves interfering activity; stability; cellular uptake; binding  
 CC affinity and/or mediates increased polymerase activity. siNA may be  
 CC designed to target many related genes containing a conserved sequence.  
 CC The present sequence represents a siNA oligonucleotide sequence, which is  
 CC used in the exemplification of the present invention.



Wed Nov 24 08:46:11 2004

CC especially animal and plant viral infections, specifically hepatitis B or  
CC C; HIV; herpes simplex; cytomegalovirus; human papilloma; respiratory  
CC syncytial or influenza viruses, and also many other diseases such as  
CC restenosis, neurodegeneration, cancers, and cardiovascular, neurological,  
CC prion, inflammatory, autoimmune, pulmonary, renal, liver, mitochondrial,  
CC endocrine or reproductive diseases; and (b) for diagnosis, target  
CC validation, genomic discovery, genetic engineering, pharmacogenomics and  
CC analysis of gene function. Chemical modification of siNA molecules  
CC improves interfering activity; stability; cellular uptake; binding  
CC affinity and/or mediates increased polymerase activity. siNA may be  
CC designed to target many related genes containing a conserved sequence.  
CC The present sequence represents a siNA oligonucleotide sequence, which is  
CC used in the exemplification of the present invention.  
XX  
SQ Sequence 21 BP; 3 A; 3 C; 8 G; 0 T; 7 U; 0 Other;  
  
Query Match 75.0%; Score 21; DB 9; Length 21;  
Best Local Similarity 66.7%; Pred. No. 3.4;  
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;  
  
QY 7 TGGGATAGTCCGTCATGGTGT 27  
Db 1 UGGGAUAGUCCGCAUGGUGU 21  
  
RESULT 4  
ADAL13873  
ID ADAL13873 standard; RNA; 21 BP.  
XX  
AC ADAL13873;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Short interfering nucleic acid (siNA) oligonucleotide SEQ ID NO:210.  
XX  
KW double-stranded short interfering nucleic acid;  
KW short interfering nucleic acid; siNA; expression; replication;  
KW inhibition; RNA interference; virucide; anti-HIV; hepatotropic;  
KW anti-inflammatory; plant; antiviral; vasotropic; neuroprotective;  
KW cytostatic; cardiovascular; immunosuppressive; respiratory; nephrotropic;  
KW endocrine; viral infection; hepatitis B; hepatitis C; HIV;  
KW herpes simplex; cytomegalovirus; human papillomavirus;  
KW respiratory syncytial virus; influenza virus; restenosis;  
KW neurodegeneration; cancer; neurological; prion; inflammatory; autoimmune;  
KW pulmonary; renal; liver; mitochondrial; reproductive disease;  
KW chemical modification; ss.  
XX  
OS Synthetic.  
XX  
PN WO2003070918-A2.  
XX  
PD 28-AUG-2003.  
XX  
PF 20-FEB-2003; 2003WO-US005346.  
XX  
PR 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 06-JUN-2002; 2002US-0386782P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI Mcswiggen J, Beigelman L, Macejak D, Zinnen S, Pavco P;  
PI Morrissey D, Fosnaugh K, Mokier V, Jamison S;  
PI WPI; 2003-689785/65.  
XX  
XX New short interfering nucleic acid containing no ribonucleotides, useful  
XX e.g. for treating viral infection, downregulates expression of target  
XX gene or RNA.  
XX .PT

XX  
PS Example 4; Page 138; 204pp; English.  
XX  
CC The present invention describes a double-stranded short interfering  
CC nucleic acid (siNA) that downregulates expression of a target gene, where  
CC the siNA molecule comprises no ribonucleotides and each strand of the  
CC double-stranded siNA comprises about 21 nucleotides. Also described: (1)  
CC a siNA molecule that inhibits expression of target RNA; (2) a siNA  
CC molecule that inhibits replication of a virus and optionally does not  
CC require presence of a ribonucleotide for inhibition; (3) a siNA molecule  
CC that inhibits expression of a target gene and does not require presence  
CC of a ribonucleotide for inhibition; (4) a siNA molecule that inhibits  
CC expression of a target gene by mediating RNA interference; and (5) a  
CC method for modulating expression of a gene in a cell using siNA  
CC molecules. siNA's can have virucide, anti-HIV, hepatotropic,  
CC antiinflammatory, plant antiviral, vasotropic, neuroprotective,  
CC cytostatic, cardiovascular, immunosuppressive, respiratory, nephrotropic  
CC and endocrine activities. The siNA's are useful for downregulating  
CC expression of target genes, inhibiting expression of target RNA, and  
CC inhibiting replication of a virus. siNA molecules can be used: (a) for  
CC therapy of any disorder that responds to modulation of gene expression,  
CC especially animal and plant viral infections, specifically hepatitis B or  
CC C; HIV; herpes simplex; cytomegalovirus; human papilloma; respiratory  
CC syncytial or influenza viruses, and also many other diseases such as  
CC restenosis, neurodegeneration, cancers, and cardiovascular, neurological,  
CC prion, inflammatory, autoimmune, pulmonary, renal, liver, mitochondrial,  
CC endocrine or reproductive diseases; and (b) for diagnosis, target  
CC validation, genomic discovery, genetic engineering, pharmacogenomics and  
CC analysis of gene function. Chemical modification of siNA molecules  
CC improves interfering activity; stability; cellular uptake; binding  
CC affinity and/or mediates increased polymerase activity. siNA may be  
CC designed to target many related genes containing a conserved sequence.  
CC The present sequence represents a siNA oligonucleotide sequence, which is  
CC used in the exemplification of the present invention.  
XX  
SQ Sequence 21 BP; 3 A; 3 C; 9 G; 0 T; 6 U; 0 Other;  
  
Query Match 75.0%; Score 21; DB 9; Length 21;  
Best Local Similarity 71.4%; Pred. No. 3.4;  
Matches 15; Conservative 6; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 GTGGGATAGTCCGTCATGGTGT 26  
Db 1 GUGGAUAGUCCGCAUGGUGU 21  
  
RESULT 5  
ADFS2874  
ID ADFS2874 standard; RNA; 21 BP.  
XX  
AC ADFS2874;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Hepatitis C virus modified siNA sense strand SeqID1465.  
XX  
KW short interfering nucleic acid; siNA; virus replication inhibition;  
KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;  
KW hepatocellular cancer; cirrhosis; ss.  
XX  
OS Synthetic.  
OS Hepatitis C virus.  
XX  
PN WO2003070750-A2.  
XX  
PD 28-AUG-2003.  
XX  
PF 20-FEB-2003; 2003WO-US005043.  
XX  
PR 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 26-MAR-2002; 2002WO-US009187.  
XX



KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;  
KW hepatocellular cancer; cirrhosis; ss.

XX Synthetic.  
OS Hepatitis C virus.

XX WO2003070750-A2.

XX 28-AUG-2003.

XX 20-FEB-2003; 2003WO-US005043.

XX 20-FEB-2002; 2002US-0358580P.

XX 11-MAR-2002; 2002US-0363124P.

XX 26-MAR-2002; 2002WO-US009187.

XX 06-JUN-2002; 2002US-0386782P.

XX 05-AUG-2002; 2002US-0401104P.

XX 29-AUG-2002; 2002US-0406784P.

XX 05-SEP-2002; 2002US-0408378P.

XX 09-SEP-2002; 2002US-0409293P.

XX 15-JAN-2003; 2003US-0440129P.

XX (SIRN-) SIRNA THERAPEUTICS INC.

XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;

XX WPI; 2003-689778/65.

XX New double-stranded short interfering nucleic acid comprises sugar-  
PT modified pyrimidine bases useful for treating infection with hepatitis C  
PT virus.

XX Example 3; SEQ ID NO 1474; 183pp; English.

XX This invention relates to novel double-stranded short interfering nucleic  
CC acids (siRNA) that inhibits replication of hepatitis C virus (HCV), where  
CC one strand is an antisense strand (ASS) that is complementary to (part  
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
CC modification. The invention may allow development of compounds with  
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by  
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
CC interference. The siRNA's of the invention may be used to inhibit  
CC replication of HCV, in cells, tissue explants or organisms, for treating  
CC HCV infection and its consequences (liver failure, diagnosis, target  
CC and cirrhosis), and also for drug screening, genetic engineering, pharmacogenomics,  
CC identification and validation, gene mapping (for example of single-nucleotide  
CC studying gene function and gene mapping) improves stability, activity,  
CC polymorphisms). The chemical modification improves stability, activity,  
CC cellular uptake and/or binding affinity. The siRNA can be directed to  
CC conserved regions of HCV genes, so are active against many different  
CC strains. NOTE: This sequence may contain one or more of several  
CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine  
CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal  
CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These  
CC modifications are specified in table 3 of the specification (pages 150-  
CC 158).

XX Sequence 21 BP; 7 A; 8 C; 3 G; 0 T; 3 U; 0 Other;

XX Query Match 75.0%; Score 21; DB 10; Length 21;

XX Best Local Similarity 100.0%; Pred. No. 3.4;

XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GCGATAGTCGTCATGGTGT 28

Db 21 GCGATAGTCGTCATGGTGT 1

RESULT 8

ADF52875

.ID ADF52875 standard; RNA; 21 BP.

XX ADF52875;

XX 12-FEB-2004 (first entry)

XX Hepatitis C virus modified siNA sense strand SeqID1466.

XX short interfering nucleic acid; siNA; virus replication inhibition;  
KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;  
KW hepatocellular cancer; cirrhosis; ss.

XX Synthetic.

OS Hepatitis C virus.

XX WO2003070750-A2.

XX 28-AUG-2003.

XX 20-FEB-2003; 2003WO-US005043.

XX 20-FEB-2002; 2002US-0358580P.

XX 11-MAR-2002; 2002US-0363124P.

XX 26-MAR-2002; 2002WO-US009187.

XX 06-JUN-2002; 2002US-0386782P.

XX 05-AUG-2002; 2002US-0401104P.

XX 29-AUG-2002; 2002US-0406784P.

XX 05-SEP-2002; 2002US-0408378P.

XX 09-SEP-2002; 2002US-0409293P.

XX 15-JAN-2003; 2003US-0440129P.

XX (SIRN-) SIRNA THERAPEUTICS INC.

XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;

XX WPI; 2003-689778/65.

XX New double-stranded short interfering nucleic acid comprises sugar-  
PT modified pyrimidine bases useful for treating infection with hepatitis C  
PT virus.

XX Example 3; SEQ ID NO 1466; 183pp; English.

XX This invention relates to novel double-stranded short interfering nucleic  
CC acids (siRNA) that inhibits replication of hepatitis C virus (HCV), where  
CC one strand is an antisense strand (ASS) that is complementary to (part  
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
CC modification. The invention may allow development of compounds with  
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by  
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
CC interference. The siRNA's of the invention may be used to inhibit  
CC replication of HCV, in cells, tissue explants or organisms, for treating  
CC HCV infection and its consequences (liver failure, diagnosis, target  
CC and cirrhosis), and also for drug screening, genetic engineering, pharmacogenomics,  
CC identification and validation, gene mapping (for example of single-nucleotide  
CC studying gene function and gene mapping) improves stability, activity,  
CC polymorphisms). The chemical modification improves stability, activity,  
CC cellular uptake and/or binding affinity. The siRNA can be directed to  
CC conserved regions of HCV genes, so are active against many different  
CC strains. NOTE: This sequence may contain one or more of several  
CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine  
CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal  
CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These  
CC modifications are specified in table 3 of the specification (pages 150-  
CC 158).

XX Sequence 21 BP; 3 A; 3 C; 8 G; 0 T; 7 U; 0 Other;

XX Query Match 75.0%; Score 21; DB 10; Length 21;

XX Best Local Similarity 66.7%; Pred. No. 3.4;

XX Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TGGGATAGTCCGTCATGGTGT 27  
:||||:||||:||||:|  
Db 1 UGGGAUAGUCCGCAUGGUGU 21

RESULT 9  
ID ADA13879 standard; RNA; 21 BP.  
XX  
AC ADA13879;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
XX Short interfering nucleic acid (siNA) oligonucleotide SEQ ID NO:216.  
XX  
KW double-stranded short interfering nucleic acid; siNA; expression; replication;  
KW short interfering nucleic acid; siNA; expression; replication;  
KW inhibition; RNA interference; virucide; anti-HIV; hepatotropic;  
KW antiinflammatory; plant; antiviral; vasotropic; neuroprotective;  
KW cytosolic; cardiovascular; immunosuppressive; respiratory; nephrotropic;  
KW endocrine; viral infection; hepatitis B; hepatitis C; HIV;  
KW herpes simplex; cytomegalovirus; human papillomavirus;  
KW respiratory syncytial virus; influenza virus; restenosis;  
KW neurodegeneration; cancer; neurological; prion; inflammatory; autoimmune;  
KW pulmonary; renal; liver; mitochondrial; reproductive disease;  
KW chemical modification; ss.  
XX  
OS Synthetic.  
XX  
XX WO2003070918-A2.  
XX  
XX 28-AUG-2003.  
XX  
XX 20-FEB-2003; 2003WO-US005346.  
XX  
XX 20-FEB-2002; 2002US-0358580P.  
XX  
XX 11-MAR-2002; 2002US-0363124P.  
XX  
XX 06-JUN-2002; 2002US-0386782P.  
XX  
XX 29-AUG-2002; 2002US-0406784P.  
XX  
XX 05-SEP-2002; 2002US-0408378P.  
XX  
XX 09-SEP-2002; 2002US-0409293P.  
XX  
XX 15-JAN-2003; 2003US-0440129P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX  
XX Mcswiggen J, Beigelman L, Macejak D, Zinnen S, Pavco P;  
XX Morrissey D, Fosnaugh K, Mokler V, Jamison S;  
XX  
XX WPI; 2003-689785/65.  
XX  
XX New short interfering nucleic acid containing no ribonucleotides, useful  
XX e.g. for treating viral infection, downregulates expression of target  
XX gene or RNA.  
XX  
XX Example 4; Page 139; 204pp; English.  
XX  
XX The present invention describes a double-stranded short interfering  
XX nucleic acid (siNA) that downregulates expression of a target gene, where  
XX the siNA molecule comprises no ribonucleotides and each strand of the  
XX double-stranded siNA comprises about 21 nucleotides. Also described: (1)  
XX a siNA molecule that inhibits expression of target RNA; (2) a siNA  
XX molecule that inhibits replication of a virus and optionally does not  
XX require presence of a ribonucleotide for inhibition; (3) a siNA molecule  
XX that inhibits expression of a target gene and does not require presence  
XX of a ribonucleotide for inhibition; (4) a siNA molecule that inhibits  
XX expression of a target gene by mediating RNA interference; and (5) a  
XX method for modulating expression of a gene in a cell using siNA  
XX molecules. siNA's can have virucide, anti-HIV, hepatotropic,  
XX antiinflammatory, plant antiviral, vasotropic, neuroprotective,  
XX cytosolic, cardiovascular, immunosuppressive, respiratory, nephrotropic  
XX and endocrine activities. The siNA's are useful for downregulating  
XX expression of target genes, inhibiting expression of target RNA, and  
XX inhibiting replication of a virus. siNA molecules can be used: (a) for

CC therapy of any disorder that responds to modulation of gene expression,  
CC especially animal and plant viral infections, specifically hepatitis B or  
CC C; HIV; herpes simplex; cytomegalovirus; human papilloma; respiratory  
CC syncytial or influenza viruses, and also many other diseases such as  
CC restenosis, neurodegeneration, cancers, and cardiovascular, neurological,  
CC prion, inflammatory, autoimmune, pulmonary, renal, liver, mitochondrial,  
CC endocrine or reproductive diseases; and (b) for diagnosis, target  
CC validation, genomic discovery, genetic engineering, pharmacogenomics and  
CC analysis of gene function. Chemical modification of siNA molecules  
CC improves interfering activity; stability; cellular uptake; binding  
CC affinity and/or mediates increased polymerase activity. siNA may be  
CC designed to target many related genes containing a conserved sequence.  
CC The present sequence represents a siNA oligonucleotide sequence, which is  
XX used in the exemplification of the present invention.  
XX  
SQ Sequence 21 BP; 7 A; 7 C; 4 G; 0 T; 3 U; 0 Other;  
Query Match 71.4%; Score 20; DB 9; Length 21;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 9 GGATAGTCCGTCATGGTGT 28  
|||||  
Db 21 GGATAGTCCGTCATGGTGT 2  
|||||

RESULT 10  
ADA13824  
ID ADA13824 standard; RNA; 21 BP.  
XX  
XX ADA13824;  
XX  
XX 20-NOV-2003 (first entry)  
XX  
XX Short interfering nucleic acid (siNA) oligonucleotide SEQ ID NO:161.  
XX  
XX double-stranded short interfering nucleic acid;  
KW short interfering nucleic acid; siNA; expression; replication;  
KW inhibition; RNA interference; virucide; anti-HIV; hepatotropic;  
KW antiinflammatory; plant; antiviral; vasotropic; neuroprotective;  
KW cytosolic; cardiovascular; immunosuppressive; respiratory; nephrotropic;  
KW endocrine; viral infection; hepatitis B; hepatitis C; HIV;  
KW herpes simplex; cytomegalovirus; human papillomavirus;  
KW respiratory syncytial virus; influenza virus; restenosis;  
KW neurodegeneration; cancer; neurological; prion; inflammatory; autoimmune;  
KW pulmonary; renal; liver; mitochondrial; reproductive disease;  
KW chemical modification; ss.  
XX  
OS Synthetic.  
XX  
XX WO2003070918-A2.  
XX  
XX 28-AUG-2003.  
XX  
XX 20-FEB-2003; 2003WO-US005346.  
XX  
XX 20-FEB-2002; 2002US-0358580P.  
XX  
XX 11-MAR-2002; 2002US-0363124P.  
XX  
XX 06-JUN-2002; 2002US-0386782P.  
XX  
XX 29-AUG-2002; 2002US-0406784P.  
XX  
XX 05-SEP-2002; 2002US-0408378P.  
XX  
XX 09-SEP-2002; 2002US-0409293P.  
XX  
XX 15-JAN-2003; 2003US-0440129P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX  
XX Mcswiggen J, Beigelman L, Macejak D, Zinnen S, Pavco P;  
XX Morrissey D, Fosnaugh K, Mokler V, Jamison S;  
XX  
XX WPI; 2003-689785/65.  
XX  
XX New short interfering nucleic acid containing no ribonucleotides, useful  
XX e.g. for treating viral infection, downregulates expression of target  
XX gene or RNA.  
XX  
XX Example 4; Page 139; 204pp; English.  
XX  
XX The present invention describes a double-stranded short interfering  
XX nucleic acid (siNA) that downregulates expression of a target gene, where  
XX the siNA molecule comprises no ribonucleotides and each strand of the  
XX double-stranded siNA comprises about 21 nucleotides. Also described: (1)  
XX a siNA molecule that inhibits expression of target RNA; (2) a siNA  
XX molecule that inhibits replication of a virus and optionally does not  
XX require presence of a ribonucleotide for inhibition; (3) a siNA molecule  
XX that inhibits expression of a target gene and does not require presence  
XX of a ribonucleotide for inhibition; (4) a siNA molecule that inhibits  
XX expression of a target gene by mediating RNA interference; and (5) a  
XX method for modulating expression of a gene in a cell using siNA  
XX molecules. siNA's can have virucide, anti-HIV, hepatotropic,  
XX antiinflammatory, plant antiviral, vasotropic, neuroprotective,  
XX cytosolic, cardiovascular, immunosuppressive, respiratory, nephrotropic  
XX and endocrine activities. The siNA's are useful for downregulating  
XX expression of target genes, inhibiting expression of target RNA, and  
XX inhibiting replication of a virus. siNA molecules can be used: (a) for



PN WO2003070750-A2.  
 XX 28-AUG-2003.  
 XX 20-FEB-2003; 2003WO-US005043.  
 XX 20-FEB-2002; 2002US-0358580P.  
 PR 11-MAR-2002; 2002US-0363124P.  
 PR 26-MAR-2002; 2002WO-US009187.  
 PR 06-JUN-2002; 2002US-0386782P.  
 PR 05-AUG-2002; 2002US-0401104P.  
 PR 29-AUG-2002; 2002US-0406784P.  
 PR 03-SEP-2002; 2002US-0408378P.  
 PR 09-SEP-2002; 2002US-0409293P.  
 PR 15-JAN-2003; 2003US-0440129P.  
 XX (SIRN-) SIRNA THERAPEUTICS INC.  
 XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;  
 PI WPI; 2003-689778/65.  
 XX New double-stranded short interfering nucleic acid comprises sugar-  
 PT modified pyrimidine bases useful for treating infection with hepatitis C  
 PT virus.  
 XX Example 3; SEQ ID NO 1439; 183pp; English.  
 XX This invention relates to novel double-stranded short interfering nucleic  
 CC acids (siRNA) that inhibits replication of hepatitis C virus (HCV), where  
 CC one strand is an antisense strand (ASS) that is complementary to (part  
 CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
 CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
 CC modification. The invention may allow development of compounds with  
 CC virucide, antiinflammatory, hepatotropic or cytostatic activities by  
 CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
 CC interference. The siRNA's of the invention may be used to inhibit  
 CC replication of HCV, in cells, tissue explants or organisms, for treating  
 CC HCV infection and its consequences (liver failure; hepatocellular cancer  
 CC and cirrhosis), and also for drug screening, diagnosis, target  
 CC studying gene function and gene mapping (for example of single-nucleotide  
 CC polymorphisms). The chemical modification improves stability, activity,  
 CC cellular uptake and/or binding affinity. The siRNA can be directed to  
 CC conserved regions of HCV genes, so are active against many different  
 CC strains. NOTE: This sequence may contain one or more of several  
 CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine  
 CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal  
 CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These  
 CC modifications are specified in table 3 of the specification (pages 150-  
 CC 158).  
 XX Sequence 21 BP; 3 A; 3 C; 8 G; 2 T; 5 U; 0 Other;  
 SQ Query Match 71.4%; Score 20; DB 10; Length 21;  
 Best Local Similarity 75.0%; Pred. No. 10;  
 Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 TGGGATAGTCGTCATGGT 26  
 |||||:||||:||||:||||:  
 Db 2 TGGGAUAGUCCGCAUGGUG 21  
 RESULT 13  
 ADF52996  
 ID ADF52996 standard; RNA; 23 BP.  
 XX ADF52996;  
 AC ADF52996;  
 XX 12-FEB-2004 (first entry)  
 DT Hepatitis C virus modified siRNA sense strand SeqID1587.  
 DE  
 XX

KW short interfering nucleic acid; siRNA; virus replication inhibition;  
 KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
 KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;  
 KW hepatocellular cancer; cirrhosis; ss.  
 XX Synthetic.  
 OS Hepatitis C virus.  
 XX WO2003070750-A2.  
 XX 28-AUG-2003.  
 XX 20-FEB-2003; 2003WO-US005043.  
 XX 20-FEB-2002; 2002US-0358580P.  
 PR 11-MAR-2002; 2002US-0363124P.  
 PR 26-MAR-2002; 2002WO-US009187.  
 PR 06-JUN-2002; 2002US-0386782P.  
 PR 05-AUG-2002; 2002US-0401104P.  
 PR 29-AUG-2002; 2002US-0406784P.  
 PR 03-SEP-2002; 2002US-0408378P.  
 PR 09-SEP-2002; 2002US-0409293P.  
 PR 15-JAN-2003; 2003US-0440129P.  
 XX (SIRN-) SIRNA THERAPEUTICS INC.  
 XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;  
 PI WPI; 2003-689778/65.  
 XX New double-stranded short interfering nucleic acid comprises sugar-  
 PT modified pyrimidine bases useful for treating infection with hepatitis C  
 PT virus.  
 XX Example 3; SEQ ID NO 1587; 183pp; English.  
 XX This invention relates to novel double-stranded short interfering nucleic  
 CC acids (siRNA) that inhibits replication of hepatitis C virus (HCV), where  
 CC one strand is an antisense strand (ASS) that is complementary to (part  
 CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
 CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
 CC modification. The invention may allow development of compounds with  
 CC virucide, antiinflammatory, hepatotropic or cytostatic activities by  
 CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
 CC interference. The siRNA's of the invention may be used to inhibit  
 CC replication of HCV, in cells, tissue explants or organisms, for treating  
 CC HCV infection and its consequences (liver failure; hepatocellular cancer  
 CC and cirrhosis), and also for drug screening, diagnosis, target  
 CC studying gene function and gene mapping (for example of single-nucleotide  
 CC polymorphisms). The chemical modification improves stability, activity,  
 CC cellular uptake and/or binding affinity. The siRNA can be directed to  
 CC conserved regions of HCV genes, so are active against many different  
 CC strains. NOTE: This sequence may contain one or more of several  
 CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine  
 CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal  
 CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These  
 CC modifications are specified in table 3 of the specification (pages 150-  
 CC 158).  
 XX Sequence 23 BP; 3 A; 3 C; 8 G; 2 T; 5 U; 2 Other;  
 SQ Query Match 71.4%; Score 20; DB 10; Length 23;  
 Best Local Similarity 75.0%; Pred. No. 10;  
 Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 GTGGATAGTCGTCATGGT 25  
 |||||:||||:||||:||||:  
 Db 2 GUGGAUAGUCCGCAUGGUG 21  
 RESULT 14  
 ADF52938

ID ADF52938 standard; RNA; 23 BP.  
AC ADF52938;  
XX 12-FEB-2004 (first entry)  
DT  
XX Hepatitis C virus modified siNA sense strand SeqID1529.  
DE  
XX short interfering nucleic acid; siNA; virus replication inhibition;  
KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;  
KW hepatocellular cancer; cirrhosis; ss.  
XX  
OS Synthetic.  
OS Hepatitis C virus.  
XX WO2003070750-A2.  
PN  
XX  
XX 28-AUG-2003.  
PD  
XX 20-FEB-2003; 2003WO-US005043.  
PF  
XX 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 06-MAR-2002; 2002WO-US009187.  
PR 06-JUN-2002; 2002US-0386782P.  
PR 05-AUG-2002; 2002US-0401104P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX  
XX (SIRN-) SIRNA THERAPEUTICS INC.  
PA  
XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;  
PI WPI; 2003-689778/65.  
XX New double-stranded short interfering nucleic acid comprises sugar-  
PT modified pyrimidine bases useful for treating infection with hepatitis C  
PT virus.  
PT  
PS Example 3; SEQ ID NO 1529; 183pp; English.  
XX  
XX This invention relates to novel double-stranded short interfering nucleic  
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where  
CC one strand is an antisense strand (ASS) that is complementary to (part  
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
CC modification. The invention may allow development of compounds with  
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by  
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
CC interference. The siNA's of the invention may be used to inhibit  
CC replication of HCV, in cells, tissue explants or organisms, for treating  
CC HCV infection and its consequences (liver failure; hepatocellular cancer  
CC and cirrhosis), and also for drug screening, diagnosis, target  
CC identification and validation, genetic engineering, pharmacogenomics,  
CC studying gene function and gene mapping (for example of single-nucleotide  
CC polymorphisms). The chemical modification improves stability, activity,  
CC cellular uptake and/or binding affinity. The siNA can be directed to  
CC conserved regions of HCV genes, so are active against many different  
CC strains. NOTE: This sequence may contain one or more of several  
CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine  
CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal  
CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These  
CC modifications are specified in table 3 of the specification (pages 150-  
CC 158).  
XX  
SQ Sequence 23 BP; 3 A; 3 C; 8 G; 2 T; 5 U; 2 Other;  
Query Match 71.4%; Score 20; DB 10; Length 23;  
Best Local Similarity 75.0%; Pred. No. 10;  
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 6 GTGGGATAGTCGTCATGCT 25  
Db 1-:|||||:|||||:|||||  
2 GUGGGAUGUCCGUCAUGGT 21  
RESULT 15  
ID ADAL3825  
XX ADAL3825 standard; RNA; 21 BP.  
AC ADAL3825;  
XX 20-NOV-2003 (first entry)  
DT  
XX Short interfering nucleic acid (siNA) oligonucleotide SEQ ID NO:162.  
DE  
XX double-stranded short interfering nucleic acid;  
KW short interfering nucleic acid; siNA; expression; replication;  
KW inhibition; RNA interference; virucide; anti-HIV; hepatotropic;  
KW antiinflammatory; plant; antiviral; vasotrophic; neuroprotective;  
KW cytostatic; cardiovascular; immunosuppressive; respiratory; nephrotropic;  
KW endocrine; viral infection; hepatitis B; hepatitis C; HIV;  
KW herpes simplex; cytomegalovirus; human papillomavirus;  
KW respiratory syncytial virus; influenza virus; restenosis;  
KW neurodegeneration; cancer; neurological; prion; inflammatory; autoimmune;  
KW pulmonary; renal; liver; mitochondrial; reproductive disease;  
KW chemical modification; ss.  
XX Synthetic.  
OS WO2003070918-A2.  
XX 28-AUG-2003.  
PD  
XX 20-FEB-2003; 2003WO-US005346.  
PF  
XX 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 06-JUN-2002; 2002US-0386782P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA  
XX Mcswiggen J, Beigelman L, Macejak D, Zinnen S, Pavco P;  
PI Morrissey D, Fosnaugh K, Mokler V, Jamison S;  
XX WPI; 2003-689785/65.  
XX New short interfering nucleic acid containing no ribonucleotides, useful  
PT e.g. for treating viral infection, downregulates expression of target  
PT gene or RNA.  
PS Example 4; Page 136; 204pp; English.  
XX The present invention describes a double-stranded short interfering  
CC nucleic acid (siNA) that downregulates expression of a target gene, where  
CC the siNA molecule comprises no ribonucleotides and each strand of the  
CC double-stranded siNA comprises about 21 nucleotides. Also described: (1)  
CC a siNA molecule that inhibits expression of target RNA; (2) a siNA  
CC molecule that inhibits replication of a virus and optionally does not  
CC require presence of a ribonucleotide for inhibition; (3) a siNA molecule  
CC that inhibits expression of a target gene and does not require presence  
CC of a ribonucleotide for inhibition; (4) a siNA molecule that inhibits  
CC expression of a target gene by mediating RNA interference; and (5) a  
CC method for modulating expression of a gene in a cell using siNA  
CC molecules. siNA's can have virucide, anti-HIV, hepatotropic,  
CC antiinflammatory, plant antiviral, vasotrophic, neuroprotective,  
CC cytostatic, cardiovascular, immunosuppressive, respiratory, nephrotropic  
CC and endocrine activities. The siNA's are useful for downregulating  
CC expression of target genes, inhibiting expression of target RNA, and



CC inhibiting replication of a virus. siNA molecules can be used: (a) for  
 CC therapy of any disorder that responds to modulation of gene expression,  
 CC especially animal and plant viral infections, specifically hepatitis B or  
 CC C; HIV; herpes simplex; cytomegalovirus; human papilloma; respiratory  
 CC syncytial or influenza viruses, and also many other diseases such as  
 CC reasthenosis, neurodegeneration, cancers, and cardiovascular, neurological,  
 CC prion, inflammatory, autoimmune, pulmonary, renal, liver, mitochondrial,  
 CC endocrine or reproductive diseases; and (b) for diagnosis, target  
 CC validation, genomic discovery, genetic engineering, pharmacogenomics and  
 CC analysis of gene function. Chemical modification of siNA molecules  
 CC improves interfering activity; stability; cellular uptake; binding  
 CC affinity and/or mediates increased polymerase activity. siNA may be  
 CC designed to target many related genes containing a conserved sequence.  
 CC The present sequence represents a siNA oligonucleotide sequence, which is  
 CC used in the exemplification of the present invention.

XX Sequence 21 BP; 3 A; 3 C; 7 G; 2 T; 6 U; 0 Other;

Query Match 69.3%; Score 19.4; DB 9; Length 21;  
 Best Local Similarity 66.7%; Pred. No. 20;  
 Matches 14; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 7 TGGGATAGTCGTCATCGTGT 27  
 Db 1 TTGGAUAGUCCGCAUGGUGU 21

RESULT 16

ADFS2849

ID ADF52849 standard; RNA; 21 BP.

XX ADF52849;

AC ADF52849;

XX 12-FEB-2004 (first entry)

XX Hepatitis C virus modified siNA sense strand SeqID1440.

XX short interfering nucleic acid; siNA; virus replication inhibition;  
 KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
 KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;  
 KW hepatocellular cancer; cirrhosis; ss.

XX Synthetic.

OS Hepatitis C virus.

XX WO2003070750-A2.

XX 28-AUG-2003.

XX 20-FEB-2003; 2003WO-US005043.

XX 20-FEB-2002; 2002US-0358580P.

XX 11-MAR-2002; 2002US-0363124P.

XX 26-MAR-2002; 2002WO-US009187.

XX 06-JUN-2002; 2002US-0386782P.

XX 05-AUG-2002; 2002US-0401104P.

XX 29-AUG-2002; 2002US-0406784P.

XX 05-SEP-2002; 2002US-0408378P.

XX 09-SEP-2002; 2002US-0409293P.

XX 15-JAN-2003; 2003US-0440129P.

XX (SIRN-) SIRNA THERAPEUTICS INC.

XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;

XX WPI; 2003-689778/65.

XX New double-stranded short interfering nucleic acid comprises sugar-  
 FT modified pyrimidine bases useful for treating infection with hepatitis C  
 PT virus.

XX Example 3; SEQ ID NO 1440; 183pp; English.

XX

CC This invention relates to novel double-stranded short interfering nucleic  
 CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where  
 CC one strand is an antisense strand (ASS) that is complementary to (part  
 CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
 CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
 CC modification. The invention may allow development of compounds with  
 CC virucide, antiinflammatory, hepatotropic or cytostatic activities by  
 CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
 CC interference. The siNA's of the invention may be used to inhibit  
 CC replication of HCV, in cells, tissue explants or organisms, for treating  
 CC HCV infection and its consequences (liver failure; hepatocellular cancer  
 CC and cirrhosis), and also for drug screening, diagnosis, target  
 CC identification and validation, genetic engineering, pharmacogenomics,  
 CC studying gene function and gene mapping (for example of single-nucleotide  
 CC polymorphisms). The chemical modification improves stability, activity,  
 CC cellular uptake and/or binding affinity. The siNA can be directed to  
 CC conserved regions of HCV genes, so are active against many different  
 CC strains. NOTE: This sequence may contain one or more of several  
 CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine  
 CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal  
 CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These  
 CC modifications are specified in table 3 of the specification (pages 150-  
 CC 158).

SQ Sequence 21 BP; 3 A; 3 C; 7 G; 2 T; 6 U; 0 Other;

Query Match 69.3%; Score 19.4; DB 10; Length 21;

Best Local Similarity 66.7%; Pred. No. 20;

Matches 14; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 7 TGGGATAGTCGTCATCGTGT 27

Db 1 TTGGAUAGUCCGCAUGGUGU 21

RESULT 17

ADFS2995

ID ADF52995 standard; RNA; 23 BP.

XX ADF52995;

XX 12-FEB-2004 (first entry)

XX Hepatitis C virus modified siNA sense strand SeqID1586.

XX short interfering nucleic acid; siNA; virus replication inhibition;  
 KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
 KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;  
 KW hepatocellular cancer; cirrhosis; ss.

XX Synthetic.

OS Hepatitis C virus.

XX WO2003070750-A2.

XX 28-AUG-2003.

XX 20-FEB-2003; 2003WO-US005043.

XX 20-FEB-2002; 2002US-0358580P.

XX 11-MAR-2002; 2002US-0363124P.

XX 26-MAR-2002; 2002WO-US009187.

XX 06-JUN-2002; 2002US-0386782P.

XX 05-AUG-2002; 2002US-0401104P.

XX 29-AUG-2002; 2002US-0406784P.

XX 05-SEP-2002; 2002US-0408378P.

XX 09-SEP-2002; 2002US-0409293P.

XX 15-JAN-2003; 2003US-0440129P.

XX (SIRN-) SIRNA THERAPEUTICS INC.

XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;

DR WPI; 2003-689778/65.  
XX New double-stranded short interfering nucleic acid comprises sugar-  
PT modified pyrimidine bases useful for treating infection with hepatitis C  
PT virus.  
XX  
XX Example 3; SEQ ID NO 1586; 183pp; English.  
XX  
XX This invention relates to novel double-stranded short interfering nucleic  
CC acids (siRNA) that inhibits replication of hepatitis C virus (HCV), where  
CC one strand is an antisense strand (ASS) that is complementary to (part  
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
CC modification. The invention may allow development of compounds with  
CC virucide, anti-inflammatory, hepatotropic or cytostatic activities by  
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
CC interference. The siRNA's of the invention may be used to inhibit  
CC replication of HCV, in cells, tissue explants or organisms, for treating  
CC HCV infection and its consequences (liver failure; hepatocellular cancer  
CC and cirrhosis), and also for drug screening, diagnosis, target  
CC identification and validation, genetic engineering, pharmacogenomics,  
CC studying gene function and gene mapping (for example of single-nucleotide  
CC polymorphisms). The chemical modification improves stability, activity,  
CC cellular uptake and/or binding affinity. The siRNA can be directed to  
CC conserved regions of HCV genes, so are active against many different  
CC strains. NOTE: This sequence may contain one or more of several  
CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine  
CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal  
CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These  
CC modifications are specified in table 3 of the specification (pages 150-  
CC 158).  
XX  
XX Sequence 23 BP; 3 A; 3 C; 7 G; 2 T; 6 U; 2 Other;  
SQ  
Query Match 69.3%; Score 19.4; DB 10; Length 23;  
Best Local Similarity 66.7%; Pred. No. 20;  
Matches 14; Conservative 6; Mismatches 1; Indels 0; Gaps 0;  
QY 7 TGGGATAGTCGTCATCGTGT 27  
:||||:||||:||||:|  
Db 2 UGGGAUAGUCGCGUAGGUTT 22  
RESULT 18  
ADF52937  
ID ADF52937 standard; RNA; 23 BP.  
XX  
XX ADF52937;  
XX  
XX 12-FEB-2004 (first entry)  
XX  
XX Hepatitis C virus modified siRNA sense strand SeqID1528.  
DE  
XX short interfering nucleic acid; siRNA; virus replication inhibition;  
XX hepatitis C virus; HCV; sugar modification; virucide; anti-inflammatory;  
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;  
KW hepatocellular cancer; cirrhosis; ss.  
XX  
XX Synthetic.  
OS  
OS Hepatitis C virus.  
XX  
XX WO2003070750-A2.  
PN  
XX 28-AUG-2003.  
XX  
XX 20-FEB-2003; 2003WO-US005043.  
XX  
XX 20-FEB-2002; 2002US-0359580P.  
PR  
XX 11-MAR-2002; 2002US-0363124P.  
PR  
XX 26-MAR-2002; 2002WO-US009187.  
PR  
XX 06-JUN-2002; 2002US-0386782P.  
PR  
XX 05-AUG-2002; 2002US-0401104P.  
PR  
XX 29-AUG-2002; 2002US-0406784P.  
PR

PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;  
PI  
XX WPI; 2003-689778/65.  
XX  
XX New double-stranded short interfering nucleic acid comprises sugar-  
PT modified pyrimidine bases useful for treating infection with hepatitis C  
PT virus.  
XX  
XX Example 3; SEQ ID NO 1528; 183pp; English.  
PS  
XX This invention relates to novel double-stranded short interfering nucleic  
CC acids (siRNA) that inhibits replication of hepatitis C virus (HCV), where  
CC one strand is an antisense strand (ASS) that is complementary to (part  
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
CC modification. The invention may allow development of compounds with  
CC virucide, anti-inflammatory, hepatotropic or cytostatic activities by  
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
CC interference. The siRNA's of the invention may be used to inhibit  
CC replication of HCV, in cells, tissue explants or organisms, for treating  
CC HCV infection and its consequences (liver failure; hepatocellular cancer  
CC and cirrhosis), and also for drug screening, diagnosis, target  
CC identification and validation, genetic engineering, pharmacogenomics,  
CC studying gene function and gene mapping (for example of single-nucleotide  
CC polymorphisms). The chemical modification improves stability, activity,  
CC cellular uptake and/or binding affinity. The siRNA can be directed to  
CC conserved regions of HCV genes, so are active against many different  
CC strains. NOTE: This sequence may contain one or more of several  
CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine  
CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal  
CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These  
CC modifications are specified in table 3 of the specification (pages 150-  
CC 158).  
XX  
XX Sequence 23 BP; 3 A; 3 C; 7 G; 2 T; 6 U; 2 Other;  
SQ  
Query Match 69.3%; Score 19.4; DB 10; Length 23;  
Best Local Similarity 66.7%; Pred. No. 20;  
Matches 14; Conservative 6; Mismatches 1; Indels 0; Gaps 0;  
QY 7 TGGGATAGTCGTCATCGTGT 27  
:||||:||||:||||:|  
Db 2 UGGGAUAGUCGCGUAGGUTT 22  
RESULT 19  
ADF52997  
ID ADF52997 standard; RNA; 23 BP.  
XX  
XX ADF52997;  
XX  
XX 12-FEB-2004 (first entry)  
XX  
XX Hepatitis C virus modified siRNA sense strand SeqID1588.  
DE  
XX short interfering nucleic acid; siRNA; virus replication inhibition;  
XX hepatitis C virus; HCV; sugar modification; virucide; anti-inflammatory;  
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;  
KW hepatocellular cancer; cirrhosis; ss.  
XX  
XX Synthetic.  
OS  
OS Hepatitis C virus.  
XX  
XX WO2003070750-A2.  
PN  
XX 28-AUG-2003.  
XX

PF 20-FEB-2003; 2003WO-US005043.  
 XX 20-FEB-2002; 2002US-0358580P.  
 PR 11-MAR-2002; 2002US-0363124P.  
 PR 26-MAR-2002; 2002WO-US009187.  
 PR 06-JUN-2002; 2002US-0386782P.  
 PR 05-AUG-2002; 2002US-0401104P.  
 PR 29-AUG-2002; 2002US-0406784P.  
 PR 05-SEP-2002; 2002US-0408378P.  
 PR 09-SEP-2002; 2002US-0409293P.  
 PR 15-JAN-2003; 2003US-0440129P.  
 XX (SIRN-) SIRNA THERAPEUTICS INC.  
 XX  
 PI Mcswiggen J, Beigelman L, Macejak D, Morrissey D;  
 XX WPI; 2003-689778/65.  
 DR  
 XX New double-stranded short interfering nucleic acid comprises sugar-  
 PT modified pyrimidine bases useful for treating infection with hepatitis C  
 PT virus.  
 XX  
 PS Example 3; SEQ ID NO 1588; 183pp; English.  
 XX  
 CC This invention relates to novel double-stranded short interfering nucleic  
 CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where  
 CC one strand is an antisense strand (ASS) that is complementary to (part  
 CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
 CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
 CC modification. The invention may allow development of compounds with  
 CC virucide, antiinflammatory, hepatotropic or cytostatic activities by  
 CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
 CC replication of HCV, in cells, tissue explants or organisms, for treating  
 CC HCV infection and its consequences (liver failure; hepatocellular cancer  
 CC and cirrhosis), and also for drug screening, diagnosis, target  
 CC identification and validation, genetic engineering, pharmacogenomics,  
 CC studying gene function and gene mapping (for example of single-nucleotide  
 CC polymorphisms). The chemical modification improves stability, activity,  
 CC cellular uptake and/or binding affinity. The siNA can be directed to  
 CC conserved regions of HCV genes, so are active against many different  
 CC strains. NOTE: This sequence may contain one or more of several  
 CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine  
 CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal  
 CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These  
 CC modifications are specified in table 3 of the specification (pages 150-  
 CC 158).  
 XX  
 SQ Sequence 23 BP; 3 A; 4 C; 7 G; 2 T; 5 U; 2 Other;  
 Query Match 69.3%; Score 19.4; DB 10; Length 23;  
 Best Local Similarity 71.4%; Pred. No. 20;  
 Matches 15; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
 Qy 5 CGTGGGATGTCGTCATGGT 25  
 ||:||||:||||:||||:  
 Db 2 CGUGGGAUAGUCCGCAUGTT 22  
 RESULT 20  
 ADF52999  
 ID ADF52999 standard; RNA; 23 BP.  
 XX ADF52999;  
 AC  
 XX 12-FEB-2004 (first entry)  
 DT  
 XX Hepatitis C virus modified siNA sense strand SeqID1590.  
 DE  
 XX short interfering nucleic acid; siNA; virus replication inhibition;  
 KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
 KW hepatotropic; cytosstatic; RNA interference; HCV infection; liver failure;  
 KW hepatocellular cancer; cirrhosis; ss.

XX Synthetic...  
 OS Hepatitis C virus.  
 XX WO2003070750-A2.  
 XX 28-AUG-2003.  
 PD  
 XX 20-FEB-2003; 2003WO-US005043.  
 XX 20-FEB-2002; 2002US-0358580P.  
 PR 11-MAR-2002; 2002US-0363124P.  
 PR 26-MAR-2002; 2002WO-US009187.  
 PR 06-JUN-2002; 2002US-0386782P.  
 PR 05-AUG-2002; 2002US-0401104P.  
 PR 29-AUG-2002; 2002US-0406784P.  
 PR 05-SEP-2002; 2002US-0408378P.  
 PR 09-SEP-2002; 2002US-0409293P.  
 PR 15-JAN-2003; 2003US-0440129P.  
 XX (SIRN-) SIRNA THERAPEUTICS INC.  
 XX  
 PI Mcswiggen J, Beigelman L, Macejak D, Morrissey D;  
 XX WPI; 2003-689778/65.  
 DR  
 XX New double-stranded short interfering nucleic acid comprises sugar-  
 PT modified pyrimidine bases useful for treating infection with hepatitis C  
 PT virus.  
 XX  
 PS Example 3; SEQ ID NO 1590; 183pp; English.  
 XX  
 CC This invention relates to novel double-stranded short interfering nucleic  
 CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where  
 CC one strand is an antisense strand (ASS) that is complementary to (part  
 CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
 CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
 CC modification. The invention may allow development of compounds with  
 CC virucide, antiinflammatory, hepatotropic or cytostatic activities by  
 CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
 CC replication of HCV, in cells, tissue explants or organisms, for treating  
 CC HCV infection and its consequences (liver failure; hepatocellular cancer  
 CC and cirrhosis), and also for drug screening, diagnosis, target  
 CC identification and validation, genetic engineering, pharmacogenomics,  
 CC studying gene function and gene mapping (for example of single-nucleotide  
 CC polymorphisms). The chemical modification improves stability, activity,  
 CC cellular uptake and/or binding affinity. The siNA can be directed to  
 CC conserved regions of HCV genes, so are active against many different  
 CC strains. NOTE: This sequence may contain one or more of several  
 CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine  
 CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal  
 CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These  
 CC modifications are specified in table 3 of the specification (pages 150-  
 CC 158).  
 XX  
 SQ Sequence 23 BP; 2 A; 4 C; 7 G; 2 T; 6 U; 2 Other;  
 Query Match 69.3%; Score 19.4; DB 10; Length 23;  
 Best Local Similarity 66.7%; Pred. No. 20;  
 Matches 14; Conservative 6; Mismatches 1; Indels 0; Gaps 0;  
 Qy 2 GTTCGTCGGGATGTCGTCAT 22  
 ||:||||:||||:||||:  
 Db 2 GUUCGUGGAUAGUCCGCTT 22  
 RESULT 21  
 ADF52939  
 ID ADF52939 standard; RNA; 23 BP.  
 XX ADF52939;  
 AC  
 XX

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DT 12-FEB-2004 (first entry)
DE Hepatitis C virus modified siNA sense strand SeqID1530.
XX short interfering nucleic acid; siNA; virus replication inhibition;
XX Hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
KW hepatocellular cancer; cirrhosis; ss.
XX Synthetic.
OS Hepatitis C virus.
XX WO2003070750-A2.
XX 28-AUG-2003.
XX 20-FEB-2003; 2003WO-US005043.
XX 20-FEB-2002; 2002US-0358580P.
XX 11-MAR-2002; 2002US-0363124P.
XX 26-MAR-2002; 2002WO-US009187.
XX 06-JUN-2002; 2002US-0386782P.
XX 05-AUG-2002; 2002US-0401104P.
XX 29-AUG-2002; 2002US-0406784P.
XX 05-SEP-2002; 2002US-0408378P.
XX 09-SEP-2002; 2002US-0409293P.
XX 15-JAN-2003; 2003US-0440129P.
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX WPI; 2003-689778/65.
XX New double-stranded short interfering nucleic acid comprises sugar-
XX modified pyrimidine bases useful for treating infection with hepatitis C
XX virus.
XX Example 3; SEQ ID NO 1530; 183pp; English.
XX This invention relates to novel double-stranded short interfering nucleic
XX acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
XX one strand is an antisense strand (ASS) that is complementary to (part
XX of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
XX ASS, and where most of the pyrimidine nucleotides comprise a sugar
XX modification. The invention may allow development of compounds with
XX virucide, antiinflammatory, hepatotropic or cytostatic activities by
XX modulation (inhibition) of expression or activity of HCV RNA, by RNA
XX interference. The siNA's of the invention may be used to inhibit
XX replication of HCV, in cells, tissue explants or organisms, for treating
XX HCV infection and its consequences (liver failure; hepatocellular cancer
XX and cirrhosis), and also for drug screening, diagnosis, target
XX identification and validation, genetic engineering, pharmacogenomics,
XX studying gene function and gene mapping (for example of single-nucleotide
XX polymorphisms). The chemical modification improves stability, activity,
XX cellular uptake and/or binding affinity. The siNA can be directed to
XX conserved regions of HCV genes, so are active against many different
XX strains. NOTE: This sequence may contain one or more of several
XX modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
XX (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
XX base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These
XX modifications are specified in table 3 of the specification (pages 150-
XX 158).
XX Sequence 23 BP; 3 A; 4 C; 7 G; 2 T; 5 U; 2 Other;
XX Query Match 69.3%; Score 19.4; DB 10; Length 23;
XX Best Local Similarity 71.4%; Pred. NO. 20;
XX Matches 15; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 5 CGTGGGATGTCGTCATGGT 25
DB 2 CGUGGAGUAGUCCGUGAUGTT 22
```

Query Match 69.3%; Score 19.4; DB 10; Length 23;  
Best Local Similarity 66.7%; Pred. No. 20;  
Matches 14; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTTCTGGGATAGTCGTCAT 22  
Db 2 GUUCGUGGUAUAGCCGUCTT 22

RESULT 23  
ID ADA13832/C standard; RNA; 21 BP.  
XX  
AC ADA13832;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Short interfering nucleic acid (siNA) oligonucleotide SEQ ID NO:169.  
XX  
KW double-stranded short interfering nucleic acid;  
KW short interfering nucleic acid; siNA; expression; replication;  
KW inhibition; RNA interference; virucide; anti-HIV; hepatotropic;  
KW antiinflammatory; plant; antiviral; vasotropic; neuroprotective;  
KW cytosolic; cardiovascular; immunosuppressive; respiratory; nephrotropic;  
KW endocrine; viral infection; hepatitis B; hepatitis C; HIV;  
KW herpes simplex; cytomegalovirus; human papillomavirus;  
KW respiratory syncytial virus; influenza virus; restenosis;  
KW neurodegeneration; cancer; neurological; prion; inflammatory; autoimmune;  
KW pulmonary; renal; liver; mitochondrial; reproductive disease;  
KW chemical modification; ss.  
XX  
OS Synthetic.  
XX  
PN WO2003070918-A2.  
XX  
PD 28-AUG-2003.  
XX  
PF 20-FEB-2003; 2003WO-US005346.  
XX  
PR 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 06-JUN-2002; 2002US-0386782P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
XX Mcswiggen J, Beigelman L, Macejak D, Zinnen S, Pavco P;  
PI Morrissey D, Fosnaugh K, Mokler V, Jamison S;  
XX  
DR WPI; 2003-689785/65.  
XX  
PT New short interfering nucleic acid containing no ribonucleotides, useful  
PT e.g. for treating viral infection, downregulates expression of target  
PT gene or RNA.  
XX  
PS Example 4; Page 137; 204pp; English.  
XX

The present invention describes a double-stranded short interfering nucleic acid (siNA) that downregulates expression of a target gene, where the siNA molecule comprises no ribonucleotides and each strand of the double-stranded siNA comprises about 21 nucleotides. Also described: (1) a siNA molecule that inhibits expression of target RNA; (2) a siNA molecule that inhibits replication of a virus and optionally does not require presence of a ribonucleotide for inhibition; (3) a siNA molecule that inhibits expression of a target gene and does not require presence of a ribonucleotide for inhibition; (4) a siNA molecule that inhibits expression of a target gene by mediating RNA interference; and (5) a method for modulating expression of a gene in a cell using siNA molecules. siNA's can have virucide, anti-HIV, hepatotropic,

antiinflammatory, plant antiviral, vasotropic, neuroprotective, cytosolic, cardiovascular, immunosuppressive, respiratory, nephrotropic and endocrine activities. The siNA's are useful for downregulating expression of target genes, inhibiting expression of target RNA, and inhibiting replication of a virus. siNA molecules can be used: (a) for therapy of any disorder that responds to modulation of gene expression, especially animal and plant viral infections, specifically hepatitis B or C; HIV; herpes simplex; cytomegalovirus; human papilloma; respiratory syncytial or influenza viruses, and also many other diseases such as restenosis, neurodegeneration, cancers, and cardiovascular, neurological, prion, inflammatory, autoimmune, pulmonary, renal, liver, mitochondrial, endocrine or reproductive diseases; and (b) for diagnosis, target validation, genomic discovery, genetic engineering, pharmacogenomics and analysis of gene function. Chemical modification of siNA molecules improves interfering activity; stability; cellular uptake; binding affinity and/or mediates increased polymerase activity. siNA may be designed to target many related genes containing a conserved sequence. The present sequence represents a siNA oligonucleotide sequence, which is used in the exemplification of the present invention.

XX SQ Sequence 21 BP; 6 A; 7 C; 3 G; 2 T; 3 U; 0 Other;

Query Match 67.9%; Score 19; DB 9; Length 21;

Best Local Similarity 100.0%; Pred. No. 30;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGATAGTCCGTCATGGTGT 27

Db 21 GGATAGTCCGTCATGGTGT 3

RESULT 24

ADA13878/C

ID ADA13878 standard; RNA; 21 BP.

XX AC ADA13878;

XX DT 20-NOV-2003 (first entry)

XX DE Short interfering nucleic acid (siNA) oligonucleotide SEQ ID NO:215.

XX KW double-stranded short interfering nucleic acid;

XX KW short interfering nucleic acid; siNA; expression; replication;

XX KW inhibition; RNA interference; virucide; anti-HIV; hepatotropic;

XX KW antiinflammatory; plant; antiviral; vasotropic; neuroprotective;

XX KW cytosolic; cardiovascular; immunosuppressive; respiratory; nephrotropic;

XX KW endocrine; viral infection; hepatitis B; hepatitis C; HIV;

XX KW herpes simplex; cytomegalovirus; human papillomavirus;

XX KW respiratory syncytial virus; influenza virus; restenosis;

XX KW neurodegeneration; cancer; neurological; prion; inflammatory; autoimmune;

XX KW pulmonary; renal; liver; mitochondrial; reproductive disease;

XX KW chemical modification; ss.

XX OS Synthetic.

XX PN WO2003070918-A2.

XX PD 28-AUG-2003.

XX PF 20-FEB-2003; 2003WO-US005346.

XX PR 20-FEB-2002; 2002US-0358580P.

XX PR 11-MAR-2002; 2002US-0363124P.

XX PR 06-JUN-2002; 2002US-0386782P.

XX PR 29-AUG-2002; 2002US-0406784P.

XX PR 05-SEP-2002; 2002US-0408378P.

XX PR 09-SEP-2002; 2002US-0409293P.

XX PR 15-JAN-2003; 2003US-0440129P.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX XX Mcswiggen J, Beigelman L, Macejak D, Zinnen S, Pavco P;

PI Morrissey D, Fosnaugh K, Mokler V, Jamison S;

XX OS Synthetic.

XX PN WO2003070918-A2.

XX PD 28-AUG-2003.

XX PF 20-FEB-2003; 2003WO-US005346.

XX PR 20-FEB-2002; 2002US-0358580P.

XX PR 11-MAR-2002; 2002US-0363124P.

XX PR 06-JUN-2002; 2002US-0386782P.

XX PR 29-AUG-2002; 2002US-0406784P.

XX PR 05-SEP-2002; 2002US-0408378P.

XX PR 09-SEP-2002; 2002US-0409293P.

XX PR 15-JAN-2003; 2003US-0440129P.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PI McSwiggen J, Beigelman L, Macejak D, Zinnen S, Pavco P;

XX PI Morrissey D, Fosnaugh K, Mokler V, Jamison S;

XX WPI; 2003-689785/65.

XX New short interfering nucleic acid containing no ribonucleotides, useful e.g. for treating viral infection, downregulates expression of target gene or RNA.

XX Example 4; Page 137; 204pp; English.

XX The present invention describes a double-stranded short interfering nucleic acid (siRNA) that downregulates expression of a target gene, where the siRNA molecule comprises no ribonucleotides and each strand of the double-stranded siRNA comprises about 21 nucleotides. Also described: (1) a siRNA molecule that inhibits expression of a virus and optionally does not require presence of a ribonucleotide for inhibition; (3) a siRNA molecule that inhibits expression of a target gene and does not require presence of a ribonucleotide for inhibition; (4) a siRNA molecule that inhibits expression of a target gene by mediating RNA interference; and (5) a method for modulating expression of a gene in a cell using siRNA molecules. siRNA's can have virucide, anti-HIV, hepatotropic, antiinflammatory, plant antiviral, vasotrophic, neuroprotective, cytostatic, cardiovascular, immunosuppressive, respiratory, nephrotropic and endocrine activities. The siRNA's are useful for downregulating expression of target genes, inhibiting expression of target RNA, and inhibiting replication of a virus. siRNA molecules can be used: (a) for therapy of any disorder that responds to modulation of gene expression, especially animal and plant viral infections, specifically hepatitis B or C; HIV; herpes simplex; cytomegalo; human papilloma; respiratory syncytial or influenza viruses, and also many other diseases such as restenosis, neurodegeneration, cancers, and cardiovascular, neurological, prion, inflammatory, autoimmune, pulmonary, renal, liver, mitochondrial, endocrine or reproductive diseases; and (b) for diagnosis, target validation, genomic discovery, genetic engineering, pharmacogenomics and analysis of gene function. Chemical modification of siRNA molecules improves interfering activity; stability; cellular uptake; binding affinity and/or mediates increased polymerase activity. siRNA may be designed to target many related genes containing a conserved sequence. The present sequence represents a siRNA oligonucleotide sequence, which is used in the exemplification of the present invention.

XX Sequence 21 BP; 7 A; 6 C; 5 G; 0 T; 3 U; 0 Other;

XX Query Match 67.9%; Score 19; DB 9; Length 21;

XX Best Local Similarity 100.0%; Pred. No. 30;

XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GATAGTCCGTCATGGTGT 28

DB 21 GATAGTCCGTCATGGTGT 3

RESULT 25

ADA13833/c

ID ADA13833 standard; RNA; 21 BP.

XX ADA13833;

XX 20-NOV-2003 (first entry)

XX Short interfering nucleic acid (siRNA) oligonucleotide SEQ ID NO:170.

XX double-stranded short interfering nucleic acid;

XX short interfering nucleic acid; siRNA; expression; replication;

XX inhibition; RNA interference; virucide; anti-HIV; hepatotropic;

XX antiinflammatory; plant; antiviral; vasotrophic; neuroprotective;

XX cytostatic; cardiovascular; immunosuppressive; respiratory; nephrotropic;

XX endocrine; viral infection; hepatitis B; hepatitis C; HIV;

XX herpes simplex; cytomegalovirus; human papillomavirus;

XX respiratory syncytial virus; influenza virus; restenosis;

XX neurodegeneration; cancer; neurological; prion; inflammatory; autoimmune;

XX pulmonary; renal; liver; mitochondrial; reproductive disease;

XX chemical modification; ss.

RESULT 26  
 ADA13831/c  
 ID ADA13831 standard; RNA; 21 BP.  
 XX  
 AC ADA13831;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Short interfering nucleic acid (siNA) oligonucleotide SEQ ID NO:168.  
 XX  
 KW double-stranded short interfering nucleic acid;  
 KW short interfering nucleic acid; siNA; expression; replication;  
 KW inhibition; RNA interference; virucide; anti-HIV; hepatotropic;  
 KW antiinflammatory; plant; antiviral; vasotropic; neuroprotective;  
 KW cytostatic; cardiovascular; immunosuppressive; respiratory; nephrotropic;  
 KW endocrine; viral infection; hepatitis B; hepatitis C; HIV;  
 KW herpes simplex; cytomegalovirus; human papillomavirus;  
 KW respiratory syncytial virus; influenza virus; restenosis;  
 KW neurodegeneration; cancer; neurological; prion; inflammatory; autoimmune;  
 KW pulmonary; renal; liver; mitochondrial; reproductive disease;  
 KW chemical modification; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX WO2003070918-A2.  
 PN  
 XX  
 XX 28-AUG-2003.  
 PD  
 XX  
 XX 20-FEB-2003; 2003WO-US005346.  
 PF  
 XX  
 XX 20-FEB-2002; 2002US-0358580P.  
 PR  
 PR 11-MAR-2002; 2002US-0363124P.  
 PR  
 PR 06-JUN-2002; 2002US-0386782P.  
 PR  
 PR 29-AUG-2002; 2002US-0406784P.  
 PR  
 PR 05-SEP-2002; 2002US-0408378P.  
 PR  
 PR 09-SEP-2002; 2002US-0409293P.  
 PR  
 PR 15-JAN-2003; 2003US-0440129P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 XX Mcswiggen J, Beigelman L, Macejak D, Zinnen S, Pavco P;  
 PI Morrissey D, Fosnaugh K, Mokler V, Jamison S;  
 XX  
 XX WPI; 2003-689785/65.  
 DR  
 XX  
 XX New short interfering nucleic acid containing no ribonucleotides, useful  
 PT e.g. for treating viral infection, down-regulates expression of target  
 PT gene or RNA.  
 XX  
 XX Example 4; Page 137; 204pp; English.  
 PS  
 XX  
 CC The present invention describes a double-stranded short interfering  
 CC nucleic acid (siNA) that down-regulates expression of a target gene, where  
 CC the siNA molecule comprises no ribonucleotides and each strand of the  
 CC double-stranded siNA comprises about 21 nucleotides. Also described: (1)  
 CC a siNA molecule that inhibits expression of target RNA; (2) a siNA  
 CC molecule that inhibits replication of a virus and optionally does not  
 CC require presence of a ribonucleotide for inhibition; (3) a siNA molecule  
 CC that inhibits expression of a target gene and does not require presence  
 CC of a ribonucleotide for inhibition; (4) a siNA molecule that inhibits  
 CC expression of a target gene by mediating RNA interference; and (5) a  
 CC method for modulating expression of a gene in a cell using siNA  
 CC molecules. siNA's can have virucide, anti-HIV, hepatotropic,  
 CC antiinflammatory, plant antiviral, vasotropic, neuroprotective,  
 CC cytostatic, cardiovascular, immunosuppressive, respiratory, nephrotropic  
 CC and endocrine activities. The siNA's are useful for down-regulating  
 CC expression of target genes, inhibiting expression of target RNA, and  
 CC inhibiting replication of a virus. siNA molecules can be used: (a) for  
 CC therapy of any disorder that responds to modulation of gene expression,  
 CC especially animal and plant viral infections, specifically hepatitis B or  
 CC C; HIV; herpes simplex; cytomegalovirus; human papilloma; respiratory  
 CC syncytial or influenza viruses, and also many other diseases such as  
 CC restenosis, neurodegeneration, cancers, and cardiovascular, neurological,

CC prion, inflammatory, autoimmune, pulmonary, renal, liver, mitochondrial,  
 CC endocrine or reproductive diseases; and (b) for diagnosis, target  
 CC validation, genomic discovery, genetic engineering, pharmacogenomics and  
 CC analysis of gene function. Chemical modification of siNA molecules  
 CC improves interfering activity; stability; cellular uptake; binding  
 CC affinity and/or mediates increased polymerase activity. siNA may be  
 CC designed to target many related genes containing a conserved sequence.  
 CC The present sequence represents a siNA oligonucleotide sequence, which is  
 CC used in the exemplification of the present invention.  
 XX  
 SQ Sequence 21 BP; 5 A; 8 C; 3 G; 2 T; 3 U; 0 Other;  
 XX  
 Query Match 67.9%; Score 19; DB 9; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 30;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 8 GGGATAGTCCGTCATGGTG 26  
 |||||  
 DB 21 GGGATAGTCCGTCATGGTG 3  
 |||||  
 RESULT 27  
 ADA13826  
 ID ADA13826 standard; RNA; 21 BP.  
 XX  
 AC ADA13826;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Short interfering nucleic acid (siNA) oligonucleotide SEQ ID NO:163.  
 XX  
 KW double-stranded short interfering nucleic acid;  
 KW short interfering nucleic acid; siNA; expression; replication;  
 KW inhibition; RNA interference; virucide; anti-HIV; hepatotropic;  
 KW antiinflammatory; plant; antiviral; vasotropic; neuroprotective;  
 KW cytostatic; cardiovascular; immunosuppressive; respiratory; nephrotropic;  
 KW endocrine; viral infection; hepatitis B; hepatitis C; HIV;  
 KW herpes simplex; cytomegalovirus; human papillomavirus;  
 KW respiratory syncytial virus; influenza virus; restenosis;  
 KW neurodegeneration; cancer; neurological; prion; inflammatory; autoimmune;  
 KW pulmonary; renal; liver; mitochondrial; reproductive disease;  
 KW chemical modification; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX WO2003070918-A2.  
 PN  
 XX  
 XX 28-AUG-2003.  
 PD  
 XX  
 XX 20-FEB-2003; 2003WO-US005346.  
 PF  
 XX  
 XX 20-FEB-2002; 2002US-0358580P.  
 PR  
 PR 11-MAR-2002; 2002US-0363124P.  
 PR  
 PR 06-JUN-2002; 2002US-0386782P.  
 PR  
 PR 29-AUG-2002; 2002US-0406784P.  
 PR  
 PR 05-SEP-2002; 2002US-0408378P.  
 PR  
 PR 09-SEP-2002; 2002US-0409293P.  
 PR  
 PR 15-JAN-2003; 2003US-0440129P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 XX Mcswiggen J, Beigelman L, Macejak D, Zinnen S, Pavco P;  
 PI Morrissey D, Fosnaugh K, Mokler V, Jamison S;  
 XX  
 XX WPI; 2003-689785/65.  
 DR  
 XX  
 XX New short interfering nucleic acid containing no ribonucleotides, useful  
 PT e.g. for treating viral infection, down-regulates expression of target  
 PT gene or RNA.  
 XX  
 XX Example 4; Page 136; 204pp; English.  
 PS  
 XX  
 CC The present invention describes a double-stranded short interfering



CC nucleic acid (siRNA) that downregulates expression of a target gene, where  
 CC the siRNA molecule comprises no ribonucleotides and each strand of the  
 CC double-stranded siRNA comprises about 21 nucleotides. Also described: (1)  
 CC a siRNA molecule that inhibits expression of target RNA; (2) a siRNA  
 CC molecule that inhibits replication of a virus and optionally does not  
 CC require presence of a ribonucleotide for inhibition; (3) a siRNA molecule  
 CC that inhibits expression of a target gene and does not require presence  
 CC of a ribonucleotide for inhibition; (4) a siRNA molecule that inhibits  
 CC expression of a target gene by mediating RNA interference; and (5) a  
 CC method for modulating expression of a gene in a cell using siRNA  
 CC molecules. siRNA's can have virucide, anti-HIV, hepatotropic,  
 CC antiinflammatory, plant antiviral, vasotrophic, neuroprotective,  
 CC cytostatic, cardiovascular, immunosuppressive, respiratory, nephrotropic  
 CC and endocrine activities. The siRNA's are useful for downregulating  
 CC expression of target genes, inhibiting expression of target RNA, and  
 CC inhibiting replication of a virus. siRNA molecules can be used: (a) for  
 CC therapy of any disorder that responds to modulation of gene expression,  
 CC especially animal and plant viral infections, specifically hepatitis B or  
 CC C; HIV; herpes simplex; cytomegalovirus; human papilloma; respiratory  
 CC syncytial or influenza viruses, and also many other diseases such as  
 CC restenosis, neurodegeneration, cancers, and cardiovascular, neurological,  
 CC prion, inflammatory, autoimmune, pulmonary, renal, liver, mitochondrial,  
 CC endocrine or reproductive diseases; and (b) for diagnosis, target  
 CC validation, genomic discovery, genetic engineering, pharmacogenomics and  
 CC analysis of gene function. Chemical modification of siRNA molecules  
 CC improves interfering activity; stability; cellular uptake; binding  
 CC affinity and/or mediates increased polymerase activity. siRNA may be  
 CC designed to target many related genes containing a conserved sequence.  
 CC The present sequence represents a siRNA oligonucleotide sequence, which is  
 CC used in the exemplification of the present invention.

XX Sequence 21 BP; 3 A; 3 C; 6 G; 2 T; 7 U; 0 Other;  
 XX Query Match 67.9%; Score 19; DB 9; Length 21;  
 XX Best Local Similarity 63.2%; Pred. No. 30;  
 XX Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

OY 10 GATAGTCCGTCATGGTGT 28  
 DB 3 GAUAGUCCGUAUGGUU 21

RESULT 28  
 ADF52954/c  
 ID ADF52954 standard; RNA; 21 BP.

XX ADF52954;

XX 12-FEB-2004 (first entry)

XX Hepatitis C virus modified siRNA antisense strand SeqID1545.

XX short interfering nucleic acid; siRNA; virus replication inhibition;  
 KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
 KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;  
 KW hepatocellular cancer; cirrhosis; ss.

XX Synthetic.  
 OS Hepatitis C virus.

XX WO2003070750-A2.

XX 28-AUG-2003.

XX 20-FEB-2003; 2003WO-US005043.

XX 20-FEB-2002; 2002US-0358580P.

PR 11-MAR-2002; 2002US-0363124P.

PR 26-MAR-2002; 2002WO-US009187.

PR 06-JUN-2002; 2002US-0386782P.

PR 05-AUG-2002; 2002US-0401104P.

PR 29-AUG-2002; 2002US-0406784P.

PR 05-SEP-2002; 2002US-0408378P.

PR 09-SEP-2002; 2002US-0409293P.  
 PR 15-JAN-2003; 2003US-0440129P.  
 XX (STRN-) SIRNA THERAPEUTICS INC.  
 XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;  
 XX WPI; 2003-689778/65.

XX New double-stranded short interfering nucleic acid comprises sugar-  
 PT modified pyrimidine bases useful for treating infection with hepatitis C  
 PT virus.

XX Example 3; SEQ ID NO 1545; 183pp; English.

XX This invention relates to novel double-stranded short interfering nucleic  
 CC acids (siRNA) that inhibits replication of hepatitis C virus (HCV), where  
 CC one strand is an antisense strand (ASS) that is complementary to (part  
 CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary  
 CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
 CC modification. The invention may allow development of compounds with  
 CC virucide, antiinflammatory, hepatotropic or cytostatic activities by  
 CC modulation (inhibition) of expression or activity of HCV RNA by RNA  
 CC interference. The siRNA's of the invention may be used to inhibit  
 CC replication of HCV, in cells, tissue explants or organisms, for treating  
 CC HCV infection and its consequences (liver failure; hepatocellular cancer  
 CC and cirrhosis), and also for drug screening, diagnosis, target  
 CC identification and validation, genetic engineering, pharmacogenomics,  
 CC studying gene function and gene mapping (for example of single-nucleotide  
 CC polymorphisms). The chemical modification improves stability, activity,  
 CC cellular uptake and/or binding affinity. The siRNA can be directed to  
 CC conserved regions of HCV genes, so are active against many different  
 CC strains. NOTE: This sequence may contain one or more of several  
 CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine  
 CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal  
 CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These  
 CC modifications are specified in table 3 of the specification (pages 150-  
 CC 158).

XX Sequence 21 BP; 6 A; 7 C; 4 G; 2 T; 2 U; 0 Other;

XX Query Match 67.9%; Score 19; DB 10; Length 21;  
 XX Best Local Similarity 100.0%; Pred. No. 30;  
 XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTTCGTGGGATAGTCCGT 19

DB 19 CTTTCGTGGGATAGTCCGT 1

RESULT 29

ADP53008/c

ID ADF53008 standard; RNA; 21 BP.

XX ADF53008;

XX 12-FEB-2004 (first entry)

XX Hepatitis C virus modified siRNA antisense strand SeqID1599.

XX short interfering nucleic acid; siRNA; virus replication inhibition;  
 KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
 KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;  
 KW hepatocellular cancer; cirrhosis; ss.

XX Synthetic.

OS Hepatitis C virus.

XX WO2003070750-A2.

XX 28-AUG-2003.

XX 20-FEB-2003; 2003WO-US005043.

```

XX 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 26-MAR-2002; 2002WO-US009187.
PR 06-JUN-2002; 2002US-0386782P.
PR 05-AUG-2002; 2002US-0401104P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX
XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX WPI; 2003-689778/65.
XX
XX New double-stranded short interfering nucleic acid comprises sugar-
XX modified pyrimidine bases useful for treating infection with hepatitis C
XX virus.
XX
XX Example 3; SEQ ID NO 1599; 183pp; English.
XX
XX This invention relates to novel double-stranded short interfering nucleic
XX acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
XX one strand is an antisense strand (ASS) that is complementary to (part
XX of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
XX ASS, and where most of the pyrimidine nucleotides comprise a sugar
XX modification. The invention may allow development of compounds with
XX virucide, antiinflammatory, hepatotropic or cytostatic activities by
XX modulation (inhibition) of expression or activity of HCV RNA, by RNA
XX interference. The siNA's of the invention may be used to inhibit
XX replication of HCV, in cells, tissue explants or organisms, for treating
XX HCV infection and its consequences (liver failure; hepatocellular cancer
XX and cirrhosis), and also for drug screening, diagnosis, target
XX identification and validation, genetic engineering, pharmacogenomics,
XX studying gene function and gene mapping (for example of single-nucleotide
XX polymorphisms). The chemical modification improves stability, activity,
XX cellular uptake and/or binding affinity. The siNA can be directed to
XX conserved regions of HCV genes, so are active against many different
XX strains. NOTE: This sequence may contain one or more of several
XX modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
XX (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
XX base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These
XX modifications are specified in table 3 of the specification (pages 150-
XX 158).
XX
XX Sequence 21 BP; 5 A; 8 C; 3 G; 2 T; 3 U; 0 Other;
XX
XX Query Match 67.9%; Score 19; DB 10; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 30;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 6 GTGGGATAGTCGTCATCG 24
XX |||||
XX Db 19 GTGGGATAGTCGTCATCG 1
XX
XX RESULT 30
XX ADF52857/c
XX ID ADF52857 standard; RNA; 21 BP.
XX
XX AC ADF52857;
XX
XX DT 12-FEB-2004 (first entry)
XX
XX DE Hepatitis C virus modified siNA sense strand SeqID1448.
XX
XX KW short interfering nucleic acid; siNA; virus replication inhibition;
XX hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
XX hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
XX hepatocellular cancer; cirrhosis; ss.
XX

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OS Synthetic.
OS Hepatitis C virus.
XX WO2003070750-A2.
XX
XX 28-AUG-2003.
XX
XX 20-FEB-2003; 2003WO-US005043.
XX
XX 20-FEB-2002; 2002US-0358580P.
XX 11-MAR-2002; 2002US-0363124P.
XX 26-MAR-2002; 2002WO-US009187.
XX 06-JUN-2002; 2002US-0386782P.
XX 05-AUG-2002; 2002US-0401104P.
XX 29-AUG-2002; 2002US-0406784P.
XX 05-SEP-2002; 2002US-0408378P.
XX 09-SEP-2002; 2002US-0409293P.
XX 15-JAN-2003; 2003US-0440129P.
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX
XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX WPI; 2003-689778/65.
XX
XX New double-stranded short interfering nucleic acid comprises sugar-
XX modified pyrimidine bases useful for treating infection with hepatitis C
XX virus.
XX
XX Example 3; SEQ ID NO 1448; 183pp; English.
XX
XX This invention relates to novel double-stranded short interfering nucleic
XX acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
XX one strand is an antisense strand (ASS) that is complementary to (part
XX of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
XX ASS, and where most of the pyrimidine nucleotides comprise a sugar
XX modification. The invention may allow development of compounds with
XX virucide, antiinflammatory, hepatotropic or cytostatic activities by
XX modulation (inhibition) of expression or activity of HCV RNA, by RNA
XX interference. The siNA's of the invention may be used to inhibit
XX replication of HCV, in cells, tissue explants or organisms, for treating
XX HCV infection and its consequences (liver failure; hepatocellular cancer
XX and cirrhosis), and also for drug screening, diagnosis, target
XX identification and validation, genetic engineering, pharmacogenomics,
XX studying gene function and gene mapping (for example of single-nucleotide
XX polymorphisms). The chemical modification improves stability, activity,
XX cellular uptake and/or binding affinity. The siNA can be directed to
XX conserved regions of HCV genes, so are active against many different
XX strains. NOTE: This sequence may contain one or more of several
XX modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
XX (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
XX base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These
XX modifications are specified in table 3 of the specification (pages 150-
XX 158).
XX
XX Sequence 21 BP; 7 A; 6 C; 3 G; 2 T; 3 U; 0 Other;
XX
XX Query Match 67.9%; Score 19; DB 10; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 30;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 10 GATAGTCGTCATCGTGTT 28
XX |||||
XX Db 21 GATAGTCGTCATCGTGTT 3
XX
XX RESULT 31
XX ADF53007/c
XX ID ADF53007 standard; RNA; 21 BP.
XX
XX AC ADF53007;
XX
XX DT 12-FEB-2004 (first entry)
XX

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XX Hepatitis C virus modified siNA antisense strand SeqID1598.  
DE  
XX short interfering nucleic acid; siNA; virus replication inhibition;  
KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;  
KW hepatocellular cancer; cirrhosis; ss.  
XX  
OS Synthetic.  
OS Hepatitis C virus.  
XX  
XX WO2003070750-A2.  
XX  
XX 28-AUG-2003.  
XX  
XX 20-FEB-2003; 2003WO-US005043.  
XX  
XX 20-FEB-2002; 2002US-0358580P.  
XX  
XX 11-MAR-2002; 2002US-0363124P.  
XX  
XX 26-MAR-2002; 2002WO-US009187.  
XX  
XX 06-JUN-2002; 2002US-0386782P.  
XX  
XX 05-AUG-2002; 2002US-0401104P.  
XX  
XX 29-AUG-2002; 2002US-0406784P.  
XX  
XX 05-SEP-2002; 2002US-0408378P.  
XX  
XX 09-SEP-2002; 2002US-0409293P.  
XX  
XX 15-JAN-2003; 2003US-0440129P.  
XX  
XX (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;  
XX WPI; 2003-689778/65.  
XX  
XX New double-stranded short interfering nucleic acid comprises sugar-  
PT modified pyrimidine bases useful for treating infection with hepatitis C  
PT virus.  
XX  
XX Example 3; SEQ ID NO 1598; 183pp; English.  
XX  
XX This invention relates to novel double-stranded short interfering nucleic  
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where  
CC one strand is an antisense strand (ASS) that is complementary to (part  
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
CC modification. The invention may allow development of compounds with  
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by  
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
CC interference. The siNA's of the invention may be used to inhibit  
CC replication of HCV, in cells, tissue explants or organisms, for treating  
CC HCV infection and its consequences (liver failure; hepatocellular cancer  
CC and cirrhosis), and also for drug screening, diagnosis, target  
CC identification and validation, genetic engineering, pharmacogenomics,  
CC studying gene function and gene mapping (for example of single-nucleotide  
CC polymorphisms). The chemical modification improves stability, activity,  
CC cellular uptake and/or binding affinity. The siNA can be directed to  
CC conserved regions of HCV genes, so are active against many different  
CC strains. NOTE: This sequence may contain one or more of several  
CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine  
CC (?); inverted deoxy abasic (B); phosphorothioate linkage (s); universal  
CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These  
CC modifications are specified in table 3 of the specification (pages 150-  
CC 158).  
XX  
XX Sequence 21 BP; 6 A; 7 C; 3 G; 2 T; 3 U; 0 Other;  
SQ  
Query Match 67.9%; Score 19; DB 10; Length 21;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 TGGGATAGTCGGTCATGGT 25  
Db 19 TGGGATAGTCGGTCATGGT 1

RESULT 32  
ADF52850  
ID ADF52850 standard; RNA; 21 BP.  
XX  
XX ADF52850;  
XX  
XX 12-FEB-2004 (first entry)  
XX  
XX Hepatitis C virus modified siNA sense strand SeqID1441.  
DE  
XX short interfering nucleic acid; siNA; virus replication inhibition;  
KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;  
KW hepatocellular cancer; cirrhosis; ss.  
XX  
OS Synthetic.  
OS Hepatitis C virus.  
XX  
XX WO2003070750-A2.  
XX  
XX 28-AUG-2003.  
XX  
XX 20-FEB-2003; 2003WO-US005043.  
XX  
XX 20-FEB-2002; 2002US-0358580P.  
XX  
XX 11-MAR-2002; 2002US-0363124P.  
XX  
XX 26-MAR-2002; 2002WO-US009187.  
XX  
XX 06-JUN-2002; 2002US-0386782P.  
XX  
XX 05-AUG-2002; 2002US-0401104P.  
XX  
XX 29-AUG-2002; 2002US-0406784P.  
XX  
XX 05-SEP-2002; 2002US-0408378P.  
XX  
XX 09-SEP-2002; 2002US-0409293P.  
XX  
XX 15-JAN-2003; 2003US-0440129P.  
XX  
XX (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;  
XX WPI; 2003-689778/65.  
XX  
XX New double-stranded short interfering nucleic acid comprises sugar-  
PT modified pyrimidine bases useful for treating infection with hepatitis C  
PT virus.  
XX  
XX Example 3; SEQ ID NO 1441; 183pp; English.  
XX  
XX This invention relates to novel double-stranded short interfering nucleic  
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where  
CC one strand is an antisense strand (ASS) that is complementary to (part  
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
CC modification. The invention may allow development of compounds with  
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by  
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
CC interference. The siNA's of the invention may be used to inhibit  
CC replication of HCV, in cells, tissue explants or organisms, for treating  
CC HCV infection and its consequences (liver failure; hepatocellular cancer  
CC and cirrhosis), and also for drug screening, diagnosis, target  
CC identification and validation, genetic engineering, pharmacogenomics,  
CC studying gene function and gene mapping (for example of single-nucleotide  
CC polymorphisms). The chemical modification improves stability, activity,  
CC cellular uptake and/or binding affinity. The siNA can be directed to  
CC conserved regions of HCV genes, so are active against many different  
CC strains. NOTE: This sequence may contain one or more of several  
CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine  
CC (?); inverted deoxy abasic (B); phosphorothioate linkage (s); universal  
CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These  
CC modifications are specified in table 3 of the specification (pages 150-  
CC 158).  
XX  
XX Sequence 21 BP; 3 A; 3 C; 6 G; 2 T; 7 U; 0 Other;  
SQ

Query Match 67.9%; Score 19; DB 10; Length 21;  
Best Local Similarity 63.2%; Pred. No. 30;  
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

OY 10 GATAGTCGTCATGCTGTT 28  
||:||||:||||:|:|:|:  
DB 3 GAUAGUCGCUAUGGUGUU 21

RESULT 33  
ID ADF52949/c  
XX ADF52949 standard; RNA; 21 BP.  
AC ADF52949;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Hepatitis C virus modified siRNA antisense strand SeqID1540.  
XX  
KW short interfering nucleic acid; siRNA; virus replication inhibition;  
KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;  
KW hepatocellular cancer; cirrhosis; ss.  
XX  
OS Synthetic.  
OS Hepatitis C virus.  
XX  
FN WO2003070750-A2.  
PD 28-AUG-2003.  
XX  
PF 20-FEB-2003; 2003WO-US005043.  
XX  
PR 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 26-MAR-2002; 2002WO-US009187.  
PR 06-JUN-2002; 2002US-0386782P.  
PR 05-AUG-2002; 2002US-0401104P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX  
PA (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
PI Mcswiggen J, Beigelman L, Macejak D, Morrissey D;  
XX  
DR WPI; 2003-689778/65.  
XX  
PT New double-stranded short interfering nucleic acid comprises sugar-  
PT modified pyrimidine bases useful for treating infection with hepatitis C  
PT virus.  
XX  
PS Example 3; SEQ ID NO 1540; 183pp; English.  
XX  
CC This invention relates to novel double-stranded short interfering nucleic  
CC acids (siRNA) that inhibits replication of hepatitis C virus (HCV), where  
CC one strand is an antisense strand (ASS) that is complementary to (part  
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
CC modification. The invention may allow development of compounds with  
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by  
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
CC interference. The siRNA's of the invention may be used to inhibit  
CC replication of HCV, in cells, tissue explants or organisms, for treating  
CC cirrhosis), and also for drug screening, diagnosis, target  
CC identification and validation, genetic engineering, pharmacogenomics,  
CC studying gene function and gene mapping (for example of single-nucleotide  
CC polymorphisms). The chemical modification improves stability, activity,  
CC cellular uptake and/or binding affinity. The siRNA can be directed to  
CC conserved regions of HCV genes, so are active against many different  
CC strains. NOTE: This sequence may contain one or more of several

CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine  
CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal  
CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These  
CC modifications are specified in table 3 of the specification (pages 150-  
CC 158).  
XX  
SQ Sequence 21 BP; 6 A; 7 C; 3 G; 2 T; 3 U; 0 Other;

Query Match 67.9%; Score 19; DB 10; Length 21;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 TGGGATAGTCGTCATGCT 25  
|||||||:|||||:  
DB 19 TGGGATAGTCGTCATGCT 1

RESULT 34  
ID ADF52951/c  
XX ADF52951 standard; RNA; 21 BP.  
AC ADF52951;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Hepatitis C virus modified siRNA antisense strand SeqID1542.  
XX  
KW short interfering nucleic acid; siRNA; virus replication inhibition;  
KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;  
KW hepatocellular cancer; cirrhosis; ss.  
XX  
OS Synthetic.  
OS Hepatitis C virus.  
XX  
FN WO2003070750-A2.  
PD 28-AUG-2003.  
XX  
PF 20-FEB-2003; 2003WO-US005043.  
XX  
PR 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 26-MAR-2002; 2002WO-US009187.  
PR 06-JUN-2002; 2002US-0386782P.  
PR 05-AUG-2002; 2002US-0401104P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX  
PA (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
PI Mcswiggen J, Beigelman L, Macejak D, Morrissey D;  
XX  
DR WPI; 2003-689778/65.  
XX  
PT New double-stranded short interfering nucleic acid comprises sugar-  
PT modified pyrimidine bases useful for treating infection with hepatitis C  
PT virus.  
XX  
PS Example 3; SEQ ID NO 1542; 183pp; English.  
XX  
CC This invention relates to novel double-stranded short interfering nucleic  
CC acids (siRNA) that inhibits replication of hepatitis C virus (HCV), where  
CC one strand is an antisense strand (ASS) that is complementary to (part  
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
CC modification. The invention may allow development of compounds with  
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by  
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
CC interference. The siRNA's of the invention may be used to inhibit  
CC replication of HCV, in cells, tissue explants or organisms, for treating

CC HCV infection and its consequences (liver failure; hepatocellular cancer  
CC and cirrhosis), and also for drug screening, diagnosis, target  
CC identification and validation, genetic engineering, pharmacogenomics,  
CC studying gene function and gene mapping (for example of single-nucleotide  
CC polymorphisms). The chemical modification improves stability, activity,  
CC cellular uptake and/or binding affinity. The siNA can be directed to  
CC conserved regions of HCV genes, so are active against many different  
CC strains. NOTE: This sequence may contain one or more of several  
CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine  
CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal  
CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These  
CC modifications are specified in table 3 of the specification (pages 150-  
CC 158).

XX SQ Sequence 21 BP; 5 A; 7 C; 4 G; 2 T; 3 U; 0 Other;  
Query Match 67.9%; Score 19; DB 10; Length 21;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGTGGGATAGTCGGTCATG 23  
DB 19 CGTGGGATAGTCGGTCATG 1

RESULT 35  
ADFS2952/c  
ID ADFS2952 standard; RNA; 21 BP.  
XX AC ADFS2952;  
XX DT 12-FEB-2004 (first entry)  
XX DE Hepatitis C virus modified siNA antisense strand SeqID1543.  
XX KW short interfering nucleic acid; siNA; virus replication inhibition;  
XX KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
XX KW hepatotropic; cytosolic; RNA interference; HCV infection; liver failure;  
XX KW hepatocellular cancer; cirrhosis; ss.  
XX OS Synthetic.  
XX OS Hepatitis C virus.  
XX PN WO2003070750-A2.  
XX PD 28-AUG-2003.  
XX PF 20-FEB-2003; 2003WO-US005043.  
XX PR 20-FEB-2002; 2002US-0358580P.  
XX PR 11-MAR-2002; 2002US-0363124P.  
XX PR 26-MAR-2002; 2002WO-US009187.  
XX PR 06-JUN-2002; 2002US-0386782P.  
XX PR 05-AUG-2002; 2002US-0401104P.  
XX PR 29-AUG-2002; 2002US-0406784P.  
XX PR 05-SEP-2002; 2002US-0408378P.  
XX PR 09-SEP-2002; 2002US-0409293P.  
XX PR 15-JAN-2003; 2003US-0440129P.  
XX PA (SIRN-) SIRNA THERAPEUTICS INC.  
XX PI Mcswiggen J, Beigelman L, Macejak D, Morrissey D;  
XX WPI; 2003-689778/65.  
XX DR New double-stranded short interfering nucleic acid comprises sugar-  
XX modified pyrimidine bases useful for treating infection with hepatitis C  
XX virus.  
XX FS Example 3; SEQ ID NO 1543; 183pp; English.  
XX KW This invention relates to novel double-stranded short interfering nucleic  
XX acids (siNA) that inhibits replication of hepatitis C virus (HCV), where

CC one strand is an antisense strand (ASS) that is complementary to (part  
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
CC modification. The invention may allow development of compounds with  
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by  
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
CC interference. The siNA's of the invention may be used to inhibit  
CC replication of HCV, in cells, tissue explants or organisms, for treating  
CC HCV infection and its consequences (liver failure; hepatocellular cancer  
CC and cirrhosis), and also for drug screening, diagnosis, target  
CC identification and validation, genetic engineering, pharmacogenomics,  
CC studying gene function and gene mapping (for example of single-nucleotide  
CC polymorphisms). The chemical modification improves stability, activity,  
CC cellular uptake and/or binding affinity. The siNA can be directed to  
CC conserved regions of HCV genes, so are active against many different  
CC strains. NOTE: This sequence may contain one or more of several  
CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine  
CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal  
CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These  
CC modifications are specified in table 3 of the specification (pages 150-  
CC 158).

XX SQ Sequence 21 BP; 6 A; 6 C; 4 G; 2 T; 3 U; 0 Other;  
Query Match 67.9%; Score 19; DB 10; Length 21;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCGTGGGATAGTCGGTCAT 22  
DB 19 TCGTGGGATAGTCGGTCAT 1

RESULT 36  
ADFS3011/c  
ID ADFS3011 standard; RNA; 21 BP.  
XX AC ADFS3011;  
XX DT 12-FEB-2004 (first entry)  
XX DE Hepatitis C virus modified siNA antisense strand SeqID1602.  
XX KW short interfering nucleic acid; siNA; virus replication inhibition;  
XX KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
XX KW hepatotropic; cytosolic; RNA interference; HCV infection; liver failure;  
XX KW hepatocellular cancer; cirrhosis; ss.  
XX OS Synthetic.  
XX OS Hepatitis C virus.  
XX PN WO2003070750-A2.  
XX PD 28-AUG-2003.  
XX PF 20-FEB-2003; 2003WO-US005043.  
XX PR 20-FEB-2002; 2002US-0358580P.  
XX PR 11-MAR-2002; 2002US-0363124P.  
XX PR 26-MAR-2002; 2002WO-US009187.  
XX PR 06-JUN-2002; 2002US-0386782P.  
XX PR 05-AUG-2002; 2002US-0401104P.  
XX PR 29-AUG-2002; 2002US-0406784P.  
XX PR 05-SEP-2002; 2002US-0408378P.  
XX PR 09-SEP-2002; 2002US-0409293P.  
XX PR 15-JAN-2003; 2003US-0440129P.  
XX PA (SIRN-) SIRNA THERAPEUTICS INC.  
XX PI Mcswiggen J, Beigelman L, Macejak D, Morrissey D;  
XX WPI; 2003-689778/65.  
XX DR

PT New double-stranded short interfering nucleic acid comprises sugar-  
PT modified pyrimidine bases useful for treating infection with hepatitis C  
XX virus.  
XX  
PS Example 3; SEQ ID NO 1602; 183pp; English.  
XX  
CC This invention relates to novel double-stranded short interfering nucleic  
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where  
CC one strand is an antisense strand (ASS) that is complementary to (part  
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
CC modification. The invention may allow development of compounds with  
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by  
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
CC replication of HCV, in cells, tissue explants or organisms, for treating  
CC HCV infection and its consequences (liver failure; hepatocellular cancer  
CC and cirrhosis), and also for drug screening, diagnosis, target  
CC identification and validation, genetic engineering, pharmacogenomics,  
CC studying gene function and gene mapping (for example of single-nucleotide  
CC polymorphisms). The chemical modification improves stability, activity,  
CC cellular uptake and/or binding affinity. The siNA can be directed to  
CC conserved regions of HCV genes, so are active against many different  
CC strains. NOTE: This sequence may contain one or more of several  
CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine  
CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal  
CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These  
CC modifications are specified in table 3 of the specification (pages 150-  
XX 158).  
XX  
SQ Sequence 21 BP; 6 A; 7 C; 4 G; 2 T; 2 U; 0 Other;  
Query Match 67.9%; Score 19; DB 10; Length 21;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GTTCGTGGGATAGTCGTC 20  
DB 19 GTTCGTGGGATAGTCGTC 1  
RESULT 37  
ADFS2950/c  
ID ADFS2950 standard; RNA; 21 BP.  
XX  
AC ADFS2950;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Hepatitis C virus modified siNA antisense strand SeqID1541.  
XX  
KW short interfering nucleic acid; siNA; virus replication inhibition;  
KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;  
KW hepatocellular cancer; cirrhosis; ss.  
XX  
OS Synthetic.  
OS Hepatitis C virus.  
XX  
PN WO2003070750-A2.  
XX  
PD 28-AUG-2003.  
XX  
PF 20-FEB-2003; 2003WO-US005043.  
XX  
PR 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 26-MAR-2002; 2002WO-US009187.  
PR 06-JUN-2002; 2002US-0386782P.  
PR 05-AUG-2002; 2002US-0401104P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.

PR 15-JAN-2003; 2003US-0440129P.  
XX  
PA (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
PI Mcswiggen J, Beigelman L, Macejak D, Morrissey D;  
XX  
XX WPI; 2003-689778/65.  
DR  
XX New double-stranded short interfering nucleic acid comprises sugar-  
PT modified pyrimidine bases useful for treating infection with hepatitis C  
PT virus.  
XX  
PS Example 3; SEQ ID NO 1541; 183pp; English.  
XX  
CC This invention relates to novel double-stranded short interfering nucleic  
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where  
CC one strand is an antisense strand (ASS) that is complementary to (part  
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
CC modification. The invention may allow development of compounds with  
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by  
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
CC interference. The siNA's of the invention may be used to inhibit  
CC replication of HCV, in cells, tissue explants or organisms, for treating  
CC HCV infection and its consequences (liver failure; hepatocellular cancer  
CC and cirrhosis), and also for drug screening, diagnosis, target  
CC identification and validation, genetic engineering, pharmacogenomics,  
CC studying gene function and gene mapping (for example of single-nucleotide  
CC polymorphisms). The chemical modification improves stability, activity,  
CC cellular uptake and/or binding affinity. The siNA can be directed to  
CC conserved regions of HCV genes, so are active against many different  
CC strains. NOTE: This sequence may contain one or more of several  
CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine  
CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal  
CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These  
CC modifications are specified in table 3 of the specification (pages 150-  
XX 158).  
XX  
SQ Sequence 21 BP; 5 A; 8 C; 3 G; 2 T; 3 U; 0 Other;  
Query Match 67.9%; Score 19; DB 10; Length 21;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 GTGGGATAGTCGTCATGG 24  
DB 19 GTGGGATAGTCGTCATGG 1  
RESULT 38  
ADFS3009/c  
ID ADFS3009 standard; RNA; 21 BP.  
XX  
AC ADFS3009;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Hepatitis C virus modified siNA antisense strand SeqID1600.  
XX  
KW short interfering nucleic acid; siNA; virus replication inhibition;  
KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;  
KW hepatocellular cancer; cirrhosis; ss.  
XX  
OS Synthetic.  
OS Hepatitis C virus.  
XX  
PN WO2003070750-A2.  
XX  
PD 28-AUG-2003.  
XX  
PF 20-FEB-2003; 2003WO-US005043.  
XX

```
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 26-MAR-2002; 2002WO-US009187.
PR 06-JUN-2002; 2002US-0386782P.
PR 05-AUG-2002; 2002US-0401104P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
XX (SIRN-) SIRNA THERAPEUTICS INC.
PA
XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX WPI; 2003-689778/65.
XX
XX New double-stranded short interfering nucleic acid comprises sugar-
PT modified pyrimidine bases useful for treating infection with hepatitis C
PT virus.
XX
XX Example 3; SEQ ID NO 1600; 183pp; English.
XX
XX This invention relates to novel double-stranded short interfering nucleic
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
CC one strand is an antisense strand (ASS) that is complementary to (part
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
CC modification. The invention may allow development of compounds with
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
CC interference. The siNA's of the invention may be used to inhibit
CC replication of HCV, in cells, tissue explants or organisms, for treating
CC HCV infection and its consequences (liver failure; hepatocellular cancer
CC and cirrhosis), and also for drug screening, diagnosis, target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function and gene mapping (for example of single-nucleotide
CC polymorphisms). The chemical modification improves stability, activity,
CC cellular uptake and/or binding affinity. The siNA can be directed to
CC conserved regions of HCV genes, so are active against many different
CC strains. NOTE: This sequence may contain one or more of several
CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These
CC modifications are specified in table 3 of the specification (pages 150-
CC 158).
XX
XX Sequence 21 BP; 5 A; 7 C; 4 G; 2 T; 3 U; 0 Other;
SQ
Query Match 67.9%; Score 19; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 CGTGGGATAGTCGGTCATG 23
DB 19 CGTGGGATAGTCGGTCATG 1
RESULT 39
ADF53010/c
ID ADF53010 standard; RNA; 21 BP.
XX
XX ADF53010;
XX
XX 12-FEB-2004 (first entry)
DT
XX Hepatitis C virus modified siNA antisense strand SeqID1601.
DE
XX short interfering nucleic acid; siNA; virus replication inhibition;
XX hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
XX hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
XX hepatocellular cancer; cirrhosis; ss.
XX
XX Synthetic.
OS
```

```
OS Hepatitis C virus.
XX
XX WO2003070750-A2.
XX
XX 28-AUG-2003.
XX
XX 20-FEB-2003; 2003WO-US005043.
XX
XX 20-FEB-2002; 2002US-0358580P.
XX 11-MAR-2002; 2002US-0363124P.
XX 26-MAR-2002; 2002WO-US009187.
XX 06-JUN-2002; 2002US-0386782P.
XX 05-AUG-2002; 2002US-0401104P.
XX 29-AUG-2002; 2002US-0406784P.
XX 05-SEP-2002; 2002US-0408378P.
XX 09-SEP-2002; 2002US-0409293P.
XX 15-JAN-2003; 2003US-0440129P.
XX
XX (SIRN-) SIRNA THERAPEUTICS INC.
PA
XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX WPI; 2003-689778/65.
XX
XX New double-stranded short interfering nucleic acid comprises sugar-
PT modified pyrimidine bases useful for treating infection with hepatitis C
PT virus.
XX
XX Example 3; SEQ ID NO 1601; 183pp; English.
XX
XX This invention relates to novel double-stranded short interfering nucleic
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
CC one strand is an antisense strand (ASS) that is complementary to (part
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
CC modification. The invention may allow development of compounds with
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
CC interference. The siNA's of the invention may be used to inhibit
CC replication of HCV, in cells, tissue explants or organisms, for treating
CC HCV infection and its consequences (liver failure; hepatocellular cancer
CC and cirrhosis), and also for drug screening, diagnosis, target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function and gene mapping (for example of single-nucleotide
CC polymorphisms). The chemical modification improves stability, activity,
CC cellular uptake and/or binding affinity. The siNA can be directed to
CC conserved regions of HCV genes, so are active against many different
CC strains. NOTE: This sequence may contain one or more of several
CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These
CC modifications are specified in table 3 of the specification (pages 150-
CC 158).
XX
XX Sequence 21 BP; 6 A; 6 C; 4 G; 2 T; 3 U; 0 Other;
SQ
Query Match 67.9%; Score 19; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 TCGTGGGATAGTCGGTCAT 22
DB 19 TCGTGGGATAGTCGGTCAT 1
RESULT 40
ADF52855/c
ID ADF52855 standard; RNA; 21 BP.
XX
XX ADF52855;
XX
XX 12-FEB-2004 (first entry)
DT
XX
```



Search completed: November 23, 2004, 17:30:09  
Job time : 168.277 secs

DE Hepatitis C virus modified siNA sense strand SeqID1446.  
XX short interfering nucleic acid; siNA; virus replication inhibition;  
KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;  
KW hepatocellular cancer; cirrhosis; ss.

OS Synthetic.  
OS Hepatitis C virus.

PN WO2003070750-A2.

XX 28-AUG-2003.

PD 20-FEB-2003; 2003WO-US005043.

XX 20-FEB-2002; 2002US-0358580P.

PR 11-MAR-2002; 2002US-0363124P.

PR 26-MAR-2002; 2002WO-US009187.

PR 06-JUN-2002; 2002US-0386782P.

PR 05-AUG-2002; 2002US-0401104P.

PR 29-AUG-2002; 2002US-0406784P.

PR 05-SEP-2002; 2002US-0408378P.

PR 09-SEP-2002; 2002US-0409293P.

PR 15-JAN-2003; 2003US-0440129P.

XX (SIRN-) SIRNA THERAPEUTICS INC.

PA Mcswiggen J, Beigelman L, Macejak D, Morrissey D;

XX WPI; 2003-689778/65.

DR New double-stranded short interfering nucleic acid comprises sugar-

XX modified pyrimidine bases useful for treating infection with hepatitis C

PT virus.

PT Example 3; SEQ ID NO 1446; 183pp; English.

XX This invention relates to novel double-stranded short interfering nucleic  
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where  
CC one strand is an antisense strand (ASS) that is complementary to (part  
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
CC modification. The invention may allow development of compounds with  
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by  
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
CC interference. The siNA's of the invention may be used to inhibit  
CC replication of HCV, in cells, tissue explants or organisms, for treating  
CC HCV infection and its consequences (liver failure; hepatocellular cancer  
CC and cirrhosis), and also for drug screening, diagnosis, target  
CC identification and validation, genetic engineering, pharmacogenomics,  
CC studying gene function and gene mapping (for example of single-nucleotide  
CC polymorphisms). The chemical modification improves stability, activity,  
CC cellular uptake and/or binding affinity. The siNA can be directed to  
CC conserved regions of HCV genes, so are active against many different  
CC strains. NOTE: This sequence may contain one or more of several  
CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine  
CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal  
CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These  
CC modifications are specified in table 3 of the specification (pages 150-  
CC 158).

XX Sequence 21 BP; 5 A; 8 C; 3 G; 2 T; 3 U; 0 Other;

Query Match 67.9%; Score 19; DB 10; Length 21;

Best Local Similarity 100.0%; Pred. No. 30;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GGGATAGTCCGTCATGGTG 26

|||||

21 GGGATAGTCCGTCATGGTG 3

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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:59:48 ; Search time 32.4045 Seconds  
(without alignments)  
614.177 Million cell updates/sec

Title: US-10-087-631B-9

Perfect score: 28

Sequence: 1 cgttcgtggatgcgcgtcatgtgtt 28

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 905748

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Issued\_Patents\_NA.\*

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2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*

3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*

4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*

5: /cgn2\_6/ptodata/1/ina/PTCUS\_COMB.seq.\*

6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	15	53.6	15	4	US-09-153-242-37
3	14.6	52.1	21	4	US-09-657-472-2496
4	14.6	52.1	38	3	US-08-821-827C-25
5	14.6	52.1	38	3	US-09-290-202B-25
6	14.6	52.1	50	4	US-09-469-211A-14
7	14.4	51.4	32	3	US-08-833-167-78
8	14.4	51.4	32	3	US-09-344-837A-78
9	14.4	51.4	38	2	US-08-985-337A-6
10	14.4	51.4	38	2	US-08-985-124A-6
11	14.4	51.4	38	2	US-08-985-320A-6
12	14.4	51.4	38	3	US-08-984-732A-6
13	14.4	51.4	38	3	US-09-195-578-18
14	14.4	51.4	38	3	US-09-170-951-18
15	14.4	51.4	38	3	US-09-164-482-18
16	14.4	51.4	38	3	US-09-332-769-13
17	14.4	51.4	38	3	US-09-456-153-13
18	14.4	51.4	38	3	US-09-167-180-18
19	14.4	51.4	38	3	US-09-455-627-13
20	14.4	51.4	38	3	US-09-426-533-13
21	14.4	51.4	38	3	US-09-609-205-14
22	14.4	51.4	38	3	US-09-516-945-13
23	14.4	51.4	38	3	US-09-757-218-14
24	14.4	51.4	38	3	US-09-516-757-13
25	14.4	51.4	38	3	US-09-516-750-13
26	14.4	51.4	38	3	US-09-342-577-14
27	14.4	51.4	38	3	US-09-516-756-13

14.4	51.4	38	3	US-09-828-061A-14	Sequence 14, Appl
14.4	51.4	38	3	US-09-463-917-13	Sequence 13, Appl
14.4	51.4	38	4	US-09-347-673-14	Sequence 14, Appl
14.4	51.4	38	4	US-09-757-213-14	Sequence 14, Appl
14.4	51.4	38	4	US-09-656-653-13	Sequence 13, Appl
14.4	51.4	38	4	US-09-757-251-14	Sequence 14, Appl
14.4	51.4	38	4	US-09-828-259A-14	Sequence 14, Appl
14.4	51.4	38	4	US-09-719-878-14	Sequence 14, Appl
14.4	51.4	38	4	US-09-757-217A-14	Sequence 14, Appl
14.4	51.4	38	4	US-09-828-325A-14	Sequence 14, Appl
14.4	51.4	38	4	US-09-756-248-13	Sequence 13, Appl
14.2	50.7	20	1	US-08-333-555-58	Sequence 58, Appl
14.2	50.7	20	2	US-08-661-479-58	Sequence 58, Appl
14.2	50.7	46	4	US-09-486-241-20	Sequence 20, Appl
14.2	50.7	48	4	US-09-556-877-215	Sequence 215, Appl
14.2	50.7	48	4	US-09-620-412C-215	Sequence 215, Appl
14.2	50.7	48	4	US-09-598-419-215	Sequence 215, Appl
13.8	49.3	40	1	US-08-474-542A-235	Sequence 235, Appl
13.6	49.3	40	1	US-08-457-648-235	Sequence 235, Appl
13.6	48.6	20	3	US-09-358-972-182	Sequence 182, Appl
13.6	48.6	20	3	US-09-406-147-44	Sequence 44, Appl
13.6	48.6	20	4	US-09-790-417-182	Sequence 182, Appl
13.6	48.6	26	2	US-08-632-434-10	Sequence 10, Appl
13.6	48.6	35	2	US-08-333-372A-29	Sequence 29, Appl
13.6	48.6	35	3	US-08-057-430A-20	Sequence 20, Appl
13.6	48.6	36	3	US-09-331-362-9	Sequence 9, Appl
13.6	48.6	42	3	US-08-974-549A-505	Sequence 505, Appl
13.6	48.6	42	3	US-09-311-362-7	Sequence 7, Appl
13.6	48.6	42	4	US-08-912-951-272	Sequence 272, Appl
13.6	48.6	42	4	US-09-402-181B-505	Sequence 505, Appl
13.6	48.6	42	4	US-09-721-456-505	Sequence 505, Appl
13.6	48.6	50	4	US-09-554-929-184	Sequence 184, Appl
13.4	47.9	48	3	US-09-486-356-20	Sequence 20, Appl
13.4	47.9	48	4	US-09-577-528B-20	Sequence 20, Appl
13.2	47.1	18	1	US-08-328-592-13	Sequence 13, Appl
13.2	47.1	18	1	US-08-328-592-14	Sequence 14, Appl
13.2	47.1	18	1	US-08-328-592-14	Sequence 14, Appl
13.2	47.1	20	4	US-09-332-522E-36	Sequence 36, Appl
13.2	47.1	29	3	US-08-713-569-7	Sequence 7, Appl
13.2	47.1	29	3	US-09-304-232-11	Sequence 11, Appl
13.2	47.1	43	1	US-08-640-378-1	Sequence 1, Appl
13.2	47.1	45	4	US-09-561-490E-37	Sequence 37, Appl
13	46.4	30	1	US-08-381-572-24	Sequence 24, Appl
13	46.4	30	1	US-08-592-820-24	Sequence 24, Appl
13	46.4	36	3	US-09-411-977-13	Sequence 13, Appl
13	46.4	36	3	US-09-411-977-13	Sequence 13, Appl
13	46.4	36	3	US-08-846-338-16	Sequence 16, Appl
13	46.4	43	2	US-08-846-338-16	Sequence 16, Appl
13	46.4	45	2	US-08-882-756-6	Sequence 6, Appl
12.8	45.7	20	3	US-09-344-001-37	Sequence 37, Appl
12.8	45.7	34	3	US-09-609-205-23	Sequence 23, Appl
12.8	45.7	38	2	US-08-985-337A-12	Sequence 12, Appl
12.8	45.7	38	2	US-08-985-124A-12	Sequence 12, Appl
12.8	45.7	38	2	US-08-985-320A-12	Sequence 12, Appl
12.8	45.7	38	3	US-08-984-732A-12	Sequence 12, Appl
12.8	45.7	38	3	US-08-195-578-24	Sequence 24, Appl
12.8	45.7	38	3	US-09-170-951-24	Sequence 24, Appl
12.8	45.7	38	3	US-09-164-482-24	Sequence 24, Appl
12.8	45.7	38	3	US-09-332-769-19	Sequence 19, Appl
12.8	45.7	38	3	US-09-456-153-19	Sequence 19, Appl
12.8	45.7	38	3	US-09-167-180-24	Sequence 24, Appl
12.8	45.7	38	3	US-09-455-627-19	Sequence 19, Appl
12.8	45.7	38	3	US-09-426-533-19	Sequence 19, Appl
12.8	45.7	38	3	US-09-609-205-20	Sequence 20, Appl
12.8	45.7	38	3	US-09-516-945-19	Sequence 19, Appl
12.8	45.7	38	3	US-09-757-218-20	Sequence 20, Appl
12.8	45.7	38	3	US-08-757-218-23	Sequence 23, Appl
12.8	45.7	38	3	US-09-516-757-19	Sequence 19, Appl
12.8	45.7	38	3	US-09-516-750-19	Sequence 19, Appl
12.8	45.7	38	3	US-09-342-577-20	Sequence 20, Appl
12.8	45.7	38	3	US-09-342-577-23	Sequence 23, Appl
12.8	45.7	38	3	US-09-516-756-19	Sequence 19, Appl
12.8	45.7	38	3	US-08-828-061A-20	Sequence 20, Appl
12.8	45.7	38	3	US-09-828-061A-23	Sequence 23, Appl
12.8	45.7	38	3	US-09-463-917-19	Sequence 19, Appl

c 101	12.8	45.7	38	4	US-09-347-673-20	Sequence 20, Appl	c 174	12.2	43.6	19	4	US-09-064-935-2	Sequence 2, Appl
c 102	12.8	45.7	38	4	US-09-347-673-23	Sequence 23, Appl	c 175	12.2	43.6	20	4	US-09-517-467B-131	Sequence 131, App
c 103	12.8	45.7	38	4	US-09-757-213-20	Sequence 20, Appl	c 176	12.2	43.6	20	4	US-09-305-856B-110	Sequence 110, App
c 104	12.8	45.7	38	4	US-09-757-213-23	Sequence 23, Appl	c 177	12.2	43.6	23	4	US-08-887-497A-52	Sequence 52, Appl
c 105	12.8	45.7	38	4	US-09-656-663-19	Sequence 19, Appl	c 178	12.2	43.6	25	3	US-09-155-427-12	Sequence 12, Appl
c 106	12.8	45.7	38	4	US-09-656-663-22	Sequence 22, Appl	c 179	12.2	43.6	26	3	US-08-859-998-374	Sequence 374, App
c 107	12.8	45.7	38	4	US-09-757-231-20	Sequence 20, Appl	c 180	12.2	43.6	28	3	US-09-225-928-374	Sequence 374, App
c 108	12.8	45.7	38	4	US-09-757-251-23	Sequence 23, Appl	c 181	12.2	43.6	28	3	US-09-225-201B-374	Sequence 374, App
c 109	12.8	45.7	38	4	US-09-828-259A-20	Sequence 20, Appl	c 182	12.2	43.6	28	3	US-09-304-232-642	Sequence 642, App
c 110	12.8	45.7	38	4	US-09-828-259A-23	Sequence 23, Appl	c 183	12.2	43.6	29	3	US-08-960-656B-5	Sequence 5, Appl
c 111	12.8	45.7	38	4	US-09-719-878-23	Sequence 23, Appl	c 184	12.2	43.6	30	3	US-08-173-510B-11	Sequence 11, Appl
c 112	12.8	45.7	38	4	US-09-757-217A-20	Sequence 20, Appl	c 185	12.2	43.6	33	1	US-08-458-218-11	Sequence 11, Appl
c 113	12.8	45.7	38	4	US-09-757-217A-23	Sequence 23, Appl	c 186	12.2	43.6	33	2	US-08-450-497-11	Sequence 11, Appl
c 114	12.8	45.7	38	4	US-09-828-325A-20	Sequence 20, Appl	c 187	12.2	43.6	33	3	US-09-167-796-5	Sequence 5, Appl
c 115	12.8	45.7	38	4	US-09-828-325A-23	Sequence 23, Appl	c 188	12.2	43.6	33	3	US-08-840-767-28	Sequence 28, Appl
c 116	12.8	45.7	38	4	US-09-756-248-19	Sequence 19, Appl	c 189	12.2	43.6	35	3	US-09-910-174B-25	Sequence 25, Appl
c 117	12.8	45.7	38	4	US-09-281-481A-13	Sequence 13, Appl	c 190	12.2	43.6	38	4	US-09-620-461-25	Sequence 25, App
c 118	12.8	45.7	43	3	US-09-281-481A-15	Sequence 15, Appl	c 191	12.2	43.6	38	4	US-07-931-473B-235	Sequence 235, App
c 119	12.8	45.7	43	3	US-08-406-855A-13	Sequence 13, Appl	c 192	12.2	43.6	41	1	US-07-714-131C-235	Sequence 235, App
c 120	12.8	45.7	45	3	US-09-206-899-13	Sequence 13, Appl	c 193	12.2	43.6	41	1	US-08-412-110-235	Sequence 235, App
c 121	12.8	45.7	45	3	US-09-688-415-18	Sequence 18, Appl	c 194	12.2	43.6	41	1	US-08-409-442A-235	Sequence 235, App
c 122	12.8	45.7	45	3	US-08-669-536-3	Sequence 3, Appl	c 195	12.2	43.6	41	2	US-08-469-609A-235	Sequence 235, App
c 123	12.6	45.0	20	2	US-09-600-848-3	Sequence 3, Appl	c 196	12.2	43.6	41	2	US-09-143-190-235	Sequence 235, App
c 124	12.6	45.0	22	4	US-09-359-301A-11	Sequence 11, Appl	c 197	12.2	43.6	41	3	US-09-502-344-235	Sequence 235, App
c 125	12.6	45.0	30	4	US-09-640-304-12	Sequence 12, Appl	c 198	12.2	43.6	41	3	US-07-931-473B-246	Sequence 246, App
c 126	12.6	45.0	38	1	US-08-190-103-12	Sequence 12, Appl	c 199	12.2	43.6	43	1	US-07-714-131C-246	Sequence 246, App
c 127	12.6	45.0	38	1	US-08-454-778-4	Sequence 4, Appl	c 200	12.2	43.6	43	1	US-08-412-110-246	Sequence 246, App
c 128	12.6	45.0	38	1	US-08-373-124A-501	Sequence 501, App	c 201	12.2	43.6	43	1	US-08-409-442A-246	Sequence 246, App
c 129	12.6	45.0	38	1	US-08-373-124A-2388	Sequence 2388, Ap	c 202	12.2	43.6	43	2	US-08-469-609A-246	Sequence 246, App
c 130	12.6	45.0	38	1	US-08-435-628-501	Sequence 501, App	c 203	12.2	43.6	43	3	US-09-143-190-246	Sequence 246, App
c 131	12.6	45.0	38	1	US-08-435-628-2388	Sequence 2388, Ap	c 204	12.2	43.6	43	3	US-09-502-344-246	Sequence 246, App
c 132	12.6	45.0	38	1	US-09-434-354-31	Sequence 31, Appl	c 205	12.2	43.6	43	3	US-08-446-822-11	Sequence 11, Appl
c 133	12.6	45.0	41	4	US-09-709-785-31	Sequence 31, Appl	c 206	12.2	43.6	45	1	US-09-328-314-11	Sequence 11, Appl
c 134	12.6	45.0	41	4	US-09-119-507B-63	Sequence 63, Appl	c 207	12.2	43.6	45	3	PCT-US93-12586-11	Sequence 11, Appl
c 135	12.6	45.0	42	4	US-09-434-354-28	Sequence 28, Appl	c 208	12.2	43.6	45	5	US-09-069-821-32	Sequence 32, Appl
c 136	12.6	45.0	42	4	US-08-897-556A-63	Sequence 63, Appl	c 209	12.2	43.6	48	3	US-09-956-086-32	Sequence 32, Appl
c 137	12.6	45.0	42	4	US-09-547-693-63	Sequence 63, Appl	c 210	12.2	43.6	48	4	US-09-288-461-45	Sequence 45, Appl
c 138	12.6	45.0	42	4	US-09-709-785-28	Sequence 28, Appl	c 211	12.2	42.9	20	3	US-09-380-662-13	Sequence 13, Appl
c 139	12.6	45.0	42	4	US-09-217-228-4	Sequence 4, Appl	c 212	12.2	42.9	20	3	US-08-758-881-45	Sequence 3, Appl
c 140	12.6	45.0	45	3	US-09-422-978-1173	Sequence 1173, Ap	c 213	12.2	42.9	20	4	US-08-465-615-3	Sequence 496, App
c 141	12.6	45.0	47	3	US-09-630-706-4	Sequence 4, Appl	c 214	12.2	42.9	20	4	US-08-411-796-496	Sequence 496, App
c 142	12.4	44.3	27	3	US-09-161-466-5	Sequence 5, Appl	c 215	12.2	42.9	32	1	US-08-471-039-496	Sequence 14, Appl
c 143	12.4	44.3	31	3	US-09-161-466-5	Sequence 18, Appl	c 216	12.2	42.9	32	3	US-08-535-057A-14	Sequence 496, App
c 144	12.4	44.3	31	3	US-08-454-028-18	Sequence 18, Appl	c 217	12.2	42.9	32	3	US-08-535-057A-14	Sequence 14, Appl
c 145	12.4	44.3	32	2	PCT-US94-05388-18	Sequence 18, Appl	c 218	12.2	42.9	32	4	US-08-559-390-496	Sequence 496, App
c 146	12.4	44.3	32	5	PCT-US94-05388-19	Sequence 19, Appl	c 219	12.2	42.9	32	4	US-09-503-252-14	Sequence 14, Appl
c 147	12.4	44.3	32	5	PCT-US96-07496-18	Sequence 18, Appl	c 220	12.2	42.9	32	5	PCT-US93-11198-496	Sequence 9, Appl
c 148	12.4	44.3	32	5	PCT-US96-07496-19	Sequence 19, Appl	c 221	12.2	42.9	33	3	US-08-468-846-9	Sequence 38, Appl
c 149	12.4	44.3	36	1	US-08-435-480-2	Sequence 11, Appl	c 222	12.2	42.9	33	3	US-09-110-517-38	Sequence 9, Appl
c 150	12.4	44.3	36	4	US-09-675-016-11	Sequence 3, Appl	c 223	12.2	42.9	33	3	US-08-915-056A-9	Sequence 5, Appl
c 151	12.4	44.3	36	4	US-09-277-016-3	Sequence 3, Appl	c 224	12.2	42.9	33	4	US-09-227-853A-11	Sequence 11, Appl
c 152	12.4	44.3	37	3	US-09-455-950-3	Sequence 58, Appl	c 225	12.2	42.9	33	4	PCT-US95-06385-11	Sequence 5, Appl
c 153	12.4	44.3	37	4	US-08-716-284-3	Sequence 2307, Ap	c 226	12.2	42.9	33	4	PCT-US95-06385-11	Sequence 11, Appl
c 154	12.4	44.3	42	2	US-09-578-634A-58	Sequence 5, Appl	c 227	12.2	42.9	33	5	US-09-343-634-12	Sequence 12, Appl
c 155	12.4	44.3	42	4	US-09-422-978-2307	Sequence 6, Appl	c 228	12.2	42.9	34	3	US-09-197-801-1	Sequence 1, Appl
c 156	12.4	44.3	42	4	US-09-613-263-5	Sequence 9, Appl	c 229	12.2	42.9	35	3	US-09-551-028-1	Sequence 23, Appl
c 157	12.4	44.3	47	4	US-09-613-263-6	Sequence 10, Appl	c 230	12.2	42.9	35	4	US-09-463-282D-23	Sequence 23, Appl
c 158	12.4	44.3	50	4	US-09-613-263-9	Sequence 2, Appl	c 231	12.2	42.9	35	4	US-09-664-595A-1	Sequence 1, Appl
c 159	12.4	44.3	50	4	US-09-613-263-9	Sequence 3, Appl	c 232	12.2	42.9	35	4	US-08-943-336A-13	Sequence 13, Appl
c 160	12.4	44.3	50	4	US-09-613-263-10	Sequence 3, Appl	c 233	12.2	42.9	36	3	US-09-635-899-13	Sequence 13, Appl
c 161	12.4	44.3	50	4	US-09-998-155B-2	Sequence 5, Appl	c 234	12.2	42.9	36	4	US-09-479-005A-950	Sequence 950, App
c 162	12.4	44.3	50	4	US-09-998-155B-2	Sequence 5, Appl	c 235	12.2	42.9	36	4	PCT-US95-01780-13	Sequence 13, Appl
c 163	12.4	44.3	50	4	US-09-909-496-5	Sequence 2, Appl	c 236	12.2	42.9	36	5	US-08-411-796-497	Sequence 497, App
c 164	12.4	44.3	50	4	US-09-909-496-7	Sequence 7, Appl	c 237	12.2	42.9	37	1	US-08-471-039-497	Sequence 497, App
c 165	12.4	44.3	50	4	US-09-909-496-11	Sequence 11, Appl	c 238	12.2	42.9	37	3	US-08-559-390-497	Sequence 497, App
c 166	12.4	44.3	50	4	US-08-152-313-90	Sequence 90, Appl	c 239	12.2	42.9	37	4	US-08-471-039-497	Sequence 1159, Ap
c 167	12.2	43.6	18	1	US-08-579-223-90	Sequence 90, Appl	c 240	12.2	42.9	37	4	PCT-US93-11198-497	Sequence 497, App
c 168	12.2	43.6	18	5	PCT-US94-12947A-90	Sequence 136, App	c 241	12.2	42.9	37	5	PCT-US93-11198-497	Sequence 48, Appl
c 169	12.2	43.6	19	1	US-08-379-081B-136	Sequence 137, App	c 242	12.2	42.9	38	3	US-09-476-299-48	Sequence 48, Appl
c 170	12.2	43.6	19	1	US-08-379-081B-137	Sequence 137, App	c 243	12.2	42.9	38	3	US-09-609-154-48	Sequence 28, Appl
c 171	12.2	43.6	19	1	US-08-379-078-136	Sequence 137, App	c 244	12.2	42.9	38	4	US-09-608-730B-28	Sequence 7157, Ap
c 172	12.2	43.6	19	1	US-08-379-078-137	Sequence 2, Appl	c 245	12.2	42.9	38	4	US-09-371-772B-7157	
c 173	12.2	43.6	19	2	US-08-741-327E-2		c 246	12.2	42.9	38	4		

247	12	42.9	45	1	US-08-078-683A-27	Sequence 27, Appl	c 320	11.8	42.1	38	4	US-09-656-653-16	Sequence 16, Appl
248	12	42.9	45	1	US-08-078-683A-28	Sequence 28, Appl	c 321	11.8	42.1	38	4	US-09-757-251-17	Sequence 17, Appl
249	12	42.9	45	1	US-08-233-009-44	Sequence 44, Appl	c 322	11.8	42.1	38	4	US-09-828-259A-17	Sequence 17, Appl
250	12	42.9	45	4	US-08-471-970A-27	Sequence 27, Appl	c 323	11.8	42.1	38	4	US-09-719-878-17	Sequence 17, Appl
251	12	42.9	45	4	US-08-471-970A-28	Sequence 28, Appl	c 324	11.8	42.1	38	4	US-09-757-217A-17	Sequence 17, Appl
252	12	42.9	45	4	US-09-723-677B-27	Sequence 27, Appl	c 325	11.8	42.1	38	4	US-09-828-325A-17	Sequence 17, Appl
253	12	42.9	45	4	US-09-723-677B-28	Sequence 28, Appl	c 326	11.8	42.1	38	4	US-09-756-248-16	Sequence 16, Appl
254	12	42.9	47	1	US-08-078-683A-29	Sequence 29, Appl	c 327	11.8	42.1	40	4	US-09-348-910A-28	Sequence 28, Appl
255	12	42.9	47	4	US-08-471-970A-27	Sequence 29, Appl	c 328	11.8	42.1	41	2	US-08-985-337A-4	Sequence 4, Appl
256	12	42.9	47	4	US-09-422-978-697	Sequence 697, App	c 329	11.8	42.1	41	2	US-08-761-277A-66	Sequence 66, Appl
257	12	42.9	47	4	US-09-422-978-697	Sequence 3251, Ap	c 330	11.8	42.1	41	2	US-08-985-124A-4	Sequence 4, Appl
258	12	42.9	47	4	US-09-723-677B-29	Sequence 29, Appl	c 331	11.8	42.1	41	2	US-08-985-124A-4	Sequence 4, Appl
259	12	42.9	48	1	US-08-078-683A-26	Sequence 26, Appl	c 332	11.8	42.1	41	3	US-08-984-732A-4	Sequence 4, Appl
260	12	42.9	48	4	US-08-471-970A-26	Sequence 26, Appl	c 333	11.8	42.1	41	3	US-09-135-578-16	Sequence 16, Appl
261	12	42.9	48	4	US-09-443-199C-1075	Sequence 1075, Ap	c 334	11.8	42.1	41	3	US-09-170-951-16	Sequence 16, Appl
262	12	42.9	48	4	US-09-723-677B-26	Sequence 26, Appl	c 335	11.8	42.1	41	3	US-09-164-482-16	Sequence 16, Appl
263	12	42.9	49	4	US-09-907-794A-238	Sequence 238, App	c 336	11.8	42.1	41	3	US-09-332-769-11	Sequence 11, Appl
264	12	42.9	49	4	US-09-907-794A-380	Sequence 380, App	c 337	11.8	42.1	41	3	US-09-456-153-11	Sequence 11, Appl
265	12	42.9	49	4	US-09-905-125A-238	Sequence 238, App	c 338	11.8	42.1	41	3	US-09-167-180-16	Sequence 16, Appl
266	12	42.9	49	4	US-09-905-125A-380	Sequence 380, App	c 339	11.8	42.1	41	3	US-09-455-627-11	Sequence 11, Appl
267	12	42.9	49	4	US-09-902-775A-238	Sequence 238, App	c 340	11.8	42.1	41	3	US-09-426-533-11	Sequence 11, Appl
268	12	42.9	49	4	US-09-902-775A-380	Sequence 380, App	c 341	11.8	42.1	41	3	US-09-609-205-12	Sequence 12, Appl
269	12	42.9	49	4	US-09-906-700-238	Sequence 238, App	c 342	11.8	42.1	41	3	US-09-516-945-11	Sequence 11, Appl
270	12	42.9	49	4	US-09-906-700-380	Sequence 380, App	c 343	11.8	42.1	41	3	US-09-757-218-12	Sequence 12, Appl
271	12	42.9	49	4	US-09-903-603A-238	Sequence 238, App	c 344	11.8	42.1	41	3	US-09-516-757-11	Sequence 11, Appl
272	12	42.9	49	4	US-09-903-603A-380	Sequence 380, App	c 345	11.8	42.1	41	3	US-09-516-750-11	Sequence 11, Appl
273	11.8	42.1	18	2	US-09-205-922-10	Sequence 10, Appl	c 346	11.8	42.1	41	3	US-09-342-577-12	Sequence 12, Appl
274	11.8	42.1	19	4	US-09-627-122-1	Sequence 1, Appl	c 347	11.8	42.1	41	3	US-09-516-756-11	Sequence 11, Appl
275	11.8	42.1	19	4	US-09-627-122-10	Sequence 10, Appl	c 348	11.8	42.1	41	3	US-09-828-061A-12	Sequence 12, Appl
276	11.8	42.1	20	2	US-08-193-039B-10	Sequence 10, Appl	c 349	11.8	42.1	41	3	US-09-463-917-11	Sequence 11, Appl
277	11.8	42.1	20	3	US-09-476-239-51	Sequence 51, Appl	c 350	11.8	42.1	41	4	US-09-347-673-12	Sequence 12, Appl
278	11.8	42.1	20	3	US-09-609-154-51	Sequence 51, Appl	c 351	11.8	42.1	41	4	US-09-757-213-12	Sequence 12, Appl
279	11.8	42.1	20	4	US-09-608-730B-3	Sequence 3, Appl	c 352	11.8	42.1	41	4	US-09-656-653-11	Sequence 11, Appl
280	11.8	42.1	20	4	US-09-860-761-10	Sequence 10, Appl	c 353	11.8	42.1	41	4	US-09-757-251-12	Sequence 12, Appl
281	11.8	42.1	22	1	US-08-148-117A-5	Sequence 5, Appl	c 354	11.8	42.1	41	4	US-09-828-259A-12	Sequence 12, Appl
282	11.8	42.1	22	2	US-08-608-163-2	Sequence 2, Appl	c 355	11.8	42.1	41	4	US-09-719-878-12	Sequence 12, Appl
283	11.8	42.1	24	1	US-08-323-910-9	Sequence 9, Appl	c 356	11.8	42.1	41	4	US-09-757-217A-12	Sequence 12, Appl
284	11.8	42.1	25	4	US-09-866-108A-13626	Sequence 13626, A	c 357	11.8	42.1	41	4	US-09-828-245A-12	Sequence 12, Appl
285	11.8	42.1	25	4	US-09-866-108A-13627	Sequence 13627, A	c 358	11.8	42.1	41	4	US-09-756-248-11	Sequence 11, Appl
286	11.8	42.1	25	4	US-09-866-108A-13628	Sequence 13628, A	c 359	11.8	42.1	44	4	US-10-001-051B-8	Sequence 8, Appl
287	11.8	42.1	27	5	PCT-US93-05224-1	Sequence 1, Appl	c 360	11.8	42.1	47	3	US-09-306-405-14	Sequence 14, Appl
288	11.8	42.1	37	1	US-08-049-264C-36	Sequence 36, Appl	c 361	11.8	42.1	47	3	US-09-306-405-30	Sequence 30, Appl
289	11.8	42.1	37	1	US-08-476-562-36	Sequence 36, Appl	c 362	11.8	42.1	47	4	US-09-671-317-804	Sequence 804, App
290	11.8	42.1	37	1	US-08-476-723A-36	Sequence 36, Appl	c 363	11.8	42.1	47	4	US-09-422-978-786	Sequence 786, App
291	11.8	42.1	37	3	US-09-476-299-49	Sequence 49, Appl	c 364	11.8	42.1	50	4	US-09-613-263-7	Sequence 7, Appl
292	11.8	42.1	37	3	US-09-609-154-49	Sequence 49, Appl	c 365	11.8	42.1	50	4	US-09-613-263-8	Sequence 8, Appl
293	11.8	42.1	37	3	US-09-210-748A-16	Sequence 16, Appl	c 366	11.8	42.1	50	4	US-09-613-263-11	Sequence 11, Appl
294	11.8	42.1	37	4	US-09-608-730B-29	Sequence 29, Appl	c 367	11.8	42.1	50	4	US-09-909-496-6	Sequence 6, Appl
295	11.8	42.1	37	4	US-09-593-581A-16	Sequence 16, Appl	c 368	11.8	42.1	50	4	US-09-909-496-8	Sequence 8, Appl
296	11.8	42.1	37	5	PCT-US94-04310-36	Sequence 36, Appl	c 369	11.8	42.1	50	4	US-09-909-496-10	Sequence 10, Appl
297	11.8	42.1	38	2	US-08-985-337A-9	Sequence 9, Appl	c 370	11.8	42.1	18	4	US-09-527-058-12	Sequence 12, Appl
298	11.8	42.1	38	2	US-08-985-124A-9	Sequence 9, Appl	c 371	11.6	41.4	18	4	US-09-527-058-14	Sequence 14, Appl
299	11.8	42.1	38	2	US-08-985-320A-9	Sequence 9, Appl	c 372	11.6	41.4	19	3	US-08-803-346-51	Sequence 51, Appl
300	11.8	42.1	38	3	US-08-984-732A-9	Sequence 9, Appl	c 373	11.6	41.4	19	4	US-09-725-752A-11	Sequence 11, Appl
301	11.8	42.1	38	3	US-09-193-578-21	Sequence 21, Appl	c 374	11.6	41.4	20	4	US-09-138-452A-1394	Sequence 1394, Ap
302	11.8	42.1	38	3	US-09-170-951-21	Sequence 21, Appl	c 375	11.6	41.4	21	4	US-09-676-610B-14	Sequence 14, Appl
303	11.8	42.1	38	3	US-09-164-482-21	Sequence 21, Appl	c 376	11.6	41.4	21	4	US-09-657-472-1914	Sequence 1914, Ap
304	11.8	42.1	38	3	US-09-332-769-16	Sequence 16, Appl	c 377	11.6	41.4	22	4	US-08-192-943-27	Sequence 27, Appl
305	11.8	42.1	38	3	US-09-456-153-16	Sequence 16, Appl	c 378	11.6	41.4	23	3	US-09-266-409-4	Sequence 4, Appl
306	11.8	42.1	38	3	US-09-167-180-21	Sequence 21, Appl	c 379	11.6	41.4	23	3	US-09-172-045-10	Sequence 10, Appl
307	11.8	42.1	38	3	US-09-455-627-16	Sequence 16, Appl	c 380	11.6	41.4	23	3	US-09-304-452-4	Sequence 4, Appl
308	11.8	42.1	38	3	US-09-426-533-16	Sequence 16, Appl	c 381	11.6	41.4	23	4	US-09-636-735A-18	Sequence 18, Appl
309	11.8	42.1	38	3	US-09-609-205-17	Sequence 17, Appl	c 382	11.6	41.4	23	4	US-09-678-620-4	Sequence 4, Appl
310	11.8	42.1	38	3	US-09-516-945-16	Sequence 16, Appl	c 383	11.6	41.4	23	4	US-09-342-325C-10	Sequence 10, Appl
311	11.8	42.1	38	3	US-09-757-218-17	Sequence 17, Appl	c 384	11.6	41.4	23	4	US-09-688-188B-48	Sequence 48, Appl
312	11.8	42.1	38	3	US-09-516-757-16	Sequence 16, Appl	c 385	11.6	41.4	23	4	US-09-291-417D-48	Sequence 48, Appl
313	11.8	42.1	38	3	US-09-516-750-16	Sequence 16, Appl	c 386	11.6	41.4	24	2	US-08-442-010-9	Sequence 9, Appl
314	11.8	42.1	38	3	US-09-342-577-17	Sequence 17, Appl	c 387	11.6	41.4	24	3	US-08-680-116-11	Sequence 11, Appl
315	11.8	42.1	38	3	US-09-516-756-16	Sequence 16, Appl	c 388	11.6	41.4	25	4	US-09-866-108A-4555	Sequence 4555, Ap
316	11.8	42.1	38	3	US-09-828-061A-17	Sequence 17, Appl	c 389	11.6	41.4	25	4	US-09-866-108A-4557	Sequence 4557, Ap
317	11.8	42.1	38	3	US-09-463-917-15	Sequence 16, Appl	c 390	11.6	41.4	25	4	US-09-866-108A-4558	Sequence 4558, Ap
318	11.8	42.1	38	4	US-09-347-673-17	Sequence 17, Appl	c 391	11.6	41.4	25	4	US-09-866-108A-4559	Sequence 4559, Ap
319	11.8	42.1	38	4	US-09-757-213-17	Sequence 17, Appl	c 392	11.6	41.4	25	4		

C 393	11.6	41.4	25	4	US-09-866-108A-4560	Sequence 4560, Ap	C 466	11.4	40.7	32	1	US-08-591-070A-30	Sequence 30, Appl
C 394	11.6	41.4	25	4	US-09-866-108A-4561	Sequence 4561, Ap	C 467	11.4	40.7	32	2	US-08-927-855-30	Sequence 30, Appl
C 395	11.6	41.4	25	4	US-09-866-108A-4562	Sequence 4562, Ap	C 468	11.4	40.7	33	3	US-09-477-392-23	Sequence 23, Appl
C 396	11.6	41.4	28	4	US-09-559-306-12	Sequence 12, Appl	C 469	11.4	40.7	35	3	US-09-023-173-15	Sequence 15, Appl
C 397	11.6	41.4	28	4	US-09-877-476-46	Sequence 46, Appl	C 470	11.4	40.7	35	3	US-09-023-339-12	Sequence 12, Appl
C 398	11.6	41.4	30	3	US-09-092-317-3	Sequence 3, Appl	C 471	11.4	40.7	36	3	US-09-013-895A-9	Sequence 9, Appl
C 399	11.6	41.4	30	3	US-09-433-621-1	Sequence 1, Appl	C 472	11.4	40.7	36	4	US-09-565-918-10	Sequence 10, Appl
C 400	11.6	41.4	35	1	US-08-361-337-75	Sequence 75, Appl	C 473	11.4	40.7	36	4	US-09-448-868-9	Sequence 9, Appl
C 401	11.6	41.4	35	4	US-09-568-051-1	Sequence 1, Appl	C 474	11.4	40.7	36	4	US-09-371-772B-14190	Sequence 14190, A
C 402	11.6	41.4	36	1	US-08-373-124A-113	Sequence 113, App	C 475	11.4	40.7	38	3	US-09-266-596-41	Sequence 41, Appl
C 403	11.6	41.4	36	1	US-08-334-847-257	Sequence 257, App	C 476	11.4	40.7	38	4	US-09-944-411-41	Sequence 41, Appl
C 404	11.6	41.4	36	1	US-08-334-847-681	Sequence 681, App	C 477	11.4	40.7	39	3	US-08-675-568-120	Sequence 120, App
C 405	11.6	41.4	36	1	US-08-334-847-715	Sequence 715, App	C 478	11.4	40.7	39	4	US-09-223-139-4	Sequence 4, Appl
C 406	11.6	41.4	36	1	US-08-363-240A-872	Sequence 872, App	C 479	11.4	40.7	41	4	US-09-666-890-5	Sequence 5, Appl
C 407	11.6	41.4	36	1	US-08-311-486C-332	Sequence 332, App	C 480	11.4	40.7	42	4	US-09-674-677-32	Sequence 32, Appl
C 408	11.6	41.4	36	1	US-08-435-628-113	Sequence 113, App	C 481	11.4	40.7	42	4	US-08-467-816-3	Sequence 3, Appl
C 409	11.6	41.4	36	2	US-08-585-684B-1111	Sequence 1111, App	C 482	11.4	40.7	45	2	US-08-983-035A-47	Sequence 47, Appl
C 410	11.6	41.4	36	2	US-08-585-684B-1112	Sequence 1112, App	C 483	11.4	40.7	45	4	US-09-641-638-1251	Sequence 1251, Ap
C 411	11.6	41.4	36	2	US-08-585-684B-2187	Sequence 2187, Ap	C 484	11.4	40.7	47	4	US-09-422-978-164	Sequence 164, App
C 412	11.6	41.4	36	2	US-08-833-167-75	Sequence 75, Appl	C 485	11.4	40.7	47	4	US-09-422-978-2714	Sequence 2714, Ap
C 413	11.6	41.4	36	3	US-09-038-073-1111	Sequence 1111, Ap	C 486	11.4	40.7	47	4	US-09-422-978-3731	Sequence 3731, Ap
C 414	11.6	41.4	36	3	US-09-038-073-2187	Sequence 2187, Ap	C 487	11.4	40.7	47	4	US-10-170-097-1251	Sequence 1251, Ap
C 415	11.6	41.4	36	3	US-09-344-837A-75	Sequence 75, Appl	C 488	11.4	40.7	48	3	US-08-817-787-26	Sequence 26, Appl
C 416	11.6	41.4	36	3	US-08-373-124A-1578	Sequence 1578, Ap	C 489	11.4	40.7	48	4	US-09-583-808-26	Sequence 26, Appl
C 417	11.6	41.4	38	1	US-08-373-124A-2446	Sequence 2446, Ap	C 490	11.4	40.7	49	1	US-08-384-708A-121	Sequence 121, App
C 418	11.6	41.4	38	1	US-08-373-124A-2580	Sequence 2580, Ap	C 491	11.4	40.7	49	3	US-08-687-421-121	Sequence 121, App
C 419	11.6	41.4	38	1	US-08-435-628-1578	Sequence 1578, Ap	C 492	11.4	40.7	49	4	US-08-442-423-121	Sequence 121, App
C 420	11.6	41.4	38	1	US-08-435-628-2446	Sequence 2446, Ap	C 493	11.4	40.7	50	3	US-09-298-886-19	Sequence 19, App
C 421	11.6	41.4	38	1	US-08-435-628-2580	Sequence 2580, Ap	C 494	11.4	40.7	50	3	US-09-298-886-25	Sequence 25, Appl
C 422	11.6	41.4	38	1	US-09-247-890-13	Sequence 13, Appl	C 495	11.4	40.7	50	3	US-09-298-886-28	Sequence 28, Appl
C 423	11.6	41.4	40	4	US-09-724-969-13	Sequence 13, Appl	C 496	11.4	40.7	50	4	US-09-218-089A-10	Sequence 10, Appl
C 424	11.6	41.4	40	4	US-09-724-969-13	Sequence 13, Appl	C 497	11.4	40.7	50	4	US-09-999-672-19	Sequence 19, Appl
C 425	11.6	41.4	40	4	US-09-434-354-16	Sequence 16, Appl	C 498	11.4	40.7	50	4	US-09-999-672-25	Sequence 25, Appl
C 426	11.6	41.4	41	4	US-09-568-051-2	Sequence 2, Appl	C 499	11.4	40.7	50	4	US-09-888-413-10	Sequence 10, Appl
C 427	11.6	41.4	41	4	US-09-709-785-16	Sequence 16, Appl	C 500	11.4	40.7	50	4	US-08-758-306-1237	Sequence 1237, Ap
C 428	11.6	41.4	41	4	US-08-679-645-23	Sequence 23, Appl	C 501	11.2	40.0	17	1	US-09-339-993-32	Sequence 32, Appl
C 429	11.6	41.4	41	4	US-09-671-317-584	Sequence 584, App	C 502	11.2	40.0	18	3	US-09-723-534-25	Sequence 25, Appl
C 430	11.6	41.4	41	4	US-09-671-317-749	Sequence 749, App	C 503	11.2	40.0	18	3	US-08-820-479-6	Sequence 6, Appl
C 431	11.6	41.4	42	3	US-09-422-978-2883	Sequence 2883, Ap	C 504	11.2	40.0	19	4	US-09-166-186-81	Sequence 81, Appl
C 432	11.6	41.4	47	4	US-09-422-978-3782	Sequence 3782, Ap	C 505	11.2	40.0	20	3	US-09-313-932-81	Sequence 81, Appl
C 433	11.6	41.4	47	4	US-08-243-870-10	Sequence 10, Appl	C 506	11.2	40.0	20	3	US-09-659-791A-78	Sequence 78, Appl
C 434	11.6	41.4	50	1	US-08-409-439A-10	Sequence 10, Appl	C 507	11.2	40.0	20	3	US-08-110-161A-1	Sequence 1, Appl
C 435	11.6	41.4	50	1	US-09-470-661A-36	Sequence 36, Appl	C 508	11.2	40.0	21	4	US-08-110-161A-5	Sequence 5, Appl
C 436	11.6	41.4	50	1	US-09-621-976-18753	Sequence 18753, A	C 509	11.2	40.0	21	5	PCT-US94-09350-1	Sequence 1, Appl
C 437	11.6	41.4	50	4	US-08-621-976-18753	Sequence 6346, Ap	C 510	11.2	40.0	21	5	PCT-US94-09350-5	Sequence 5, Appl
C 438	11.6	41.4	50	4	US-08-070-328A-9	Sequence 9, Appl	C 511	11.2	40.0	21	5	US-08-887-497A-50	Sequence 50, Appl
C 439	11.6	41.4	50	4	US-08-455-116-9	Sequence 15, Appl	C 512	11.2	40.0	23	4	US-09-328-174A-58	Sequence 58, Appl
C 440	11.6	41.4	50	4	US-08-455-116-15	Sequence 15, Appl	C 513	11.2	40.0	24	4	US-08-887-497A-48	Sequence 48, Appl
C 441	11.6	41.4	50	4	US-08-455-116-9	Sequence 9, Appl	C 514	11.2	40.0	24	4	US-08-327-832-13	Sequence 13, Appl
C 442	11.4	40.7	22	1	US-08-070-328A-15	Sequence 15, Appl	C 515	11.2	40.0	25	2	US-08-454-549-7	Sequence 7, Appl
C 443	11.4	40.7	22	1	US-08-455-116-9	Sequence 9, Appl	C 516	11.2	40.0	25	2	US-08-828-584-13	Sequence 13, Appl
C 444	11.4	40.7	22	1	US-08-455-116-15	Sequence 15, Appl	C 517	11.2	40.0	25	2	US-08-454-552-7	Sequence 7, Appl
C 445	11.4	40.7	22	1	US-08-455-116-9	Sequence 9, Appl	C 518	11.2	40.0	25	3	US-08-887-497A-48	Sequence 48, Appl
C 446	11.4	40.7	22	3	US-08-594-452-70	Sequence 70, Appl	C 519	11.2	40.0	26	4	US-08-447-702-3	Sequence 3, Appl
C 447	11.4	40.7	22	3	US-09-258-408-70	Sequence 70, Appl	C 520	11.2	40.0	26	4	US-08-612-973-104	Sequence 104, App
C 448	11.4	40.7	23	5	PCT-US92-02377-7	Sequence 7, Appl	C 521	11.2	40.0	26	3	US-08-927-597-104	Sequence 104, App
C 449	11.4	40.7	23	5	PCT-US92-02377-7	Sequence 7, Appl	C 522	11.2	40.0	26	3	US-08-927-597-104	Sequence 10, Appl
C 450	11.4	40.7	23	5	PCT-US95-03032-8	Sequence 8, Appl	C 523	11.2	40.0	29	1	US-08-349-696-13	Sequence 13, Appl
C 451	11.4	40.7	23	6	5310649-2	Patent No. 5310649	C 524	11.2	40.0	29	1	US-08-233-009-13	Sequence 13, Appl
C 452	11.4	40.7	23	6	US-09-049-698-25	Sequence 25, Appl	C 525	11.2	40.0	29	1	US-08-233-009-13	Sequence 13, Appl
C 453	11.4	40.7	25	3	US-08-465-590-77	Sequence 77, Appl	C 526	11.2	40.0	29	2	US-08-560-231-13	Sequence 13, Appl
C 454	11.4	40.7	25	3	US-09-721-417C-77	Sequence 77, Appl	C 527	11.2	40.0	29	2	US-08-244-122-18	Sequence 18, Appl
C 455	11.4	40.7	25	3	US-08-723-909-77	Sequence 77, Appl	C 528	11.2	40.0	29	2	US-09-080-704A-13	Sequence 13, Appl
C 456	11.4	40.7	25	5	PCT-US93-08743-19	Sequence 19, Appl	C 529	11.2	40.0	30	3	US-08-217-210B-9	Sequence 9, Appl
C 457	11.4	40.7	26	4	US-09-437-568A-17	Sequence 17, Appl	C 530	11.2	40.0	30	1	US-08-232-015-54	Sequence 54, Appl
C 458	11.4	40.7	27	2	US-08-706-322-4	Sequence 4, Appl	C 531	11.2	40.0	30	1	US-08-480-784-46	Sequence 46, Appl
C 459	11.4	40.7	28	2	US-08-859-998-1123	Sequence 1123, Ap	C 532	11.2	40.0	30	1	US-08-483-553-46	Sequence 46, Appl
C 460	11.4	40.7	28	3	US-09-225-928-1123	Sequence 1123, Ap	C 533	11.2	40.0	30	1	US-08-487-002-46	Sequence 46, Appl
C 461	11.4	40.7	28	4	US-09-225-201B-1123	Sequence 1123, Ap	C 534	11.2	40.0	30	1	US-08-483-554B-46	Sequence 46, Appl
C 462	11.4	40.7	28	4	US-09-857-716-23	Sequence 23, Appl	C 535	11.2	40.0	30	1	US-08-488-011B-46	Sequence 46, Appl
C 463	11.4	40.7	29	3	US-09-189-653-7	Sequence 7, Appl	C 536	11.2	40.0	30	3	US-08-115-753-20	Sequence 20, Appl
C 464	11.4	40.7	29	4	US-09-485-539-94	Sequence 94, Appl	C 537	11.2	40.0	30	3	US-08-850-727-46	Sequence 46, Appl
C 465	11.4	40.7	29	4	US-09-574-779B-112	Sequence 112, App	C 538	11.2	40.0	30	4	US-08-887-497A-85	Sequence 85, Appl

539	11.2	40.0	30	4	US-08-887-497A-86	Sequence 86, Appl	612	11	39.3	20	4	US-09-501-612A-29	Sequence 29, Appl
540	11.2	40.0	30	5	PCT-US95-10202-46	Sequence 46, Appl	613	11	39.3	20	4	US-09-835-370-15	Sequence 15, Appl
541	11.2	40.0	30	5	PCT-US95-10203-46	Sequence 46, Appl	614	11	39.3	20	3	US-08-594-452-69	Sequence 69, Appl
542	11.2	40.0	30	5	PCT-US95-10220-46	Sequence 46, Appl	615	11	39.3	21	3	US-09-258-408-69	Sequence 69, Appl
543	11.2	40.0	33	3	US-09-476-299-6	Sequence 6, Appl	616	11	39.3	21	3	US-09-262-773-80	Sequence 80, Appl
544	11.2	40.0	33	3	US-09-609-154-6	Sequence 6, Appl	617	11	39.3	21	4	US-09-657-472-1455	Sequence 1455, Ap
545	11.2	40.0	34	1	US-08-741-881-75	Sequence 75, Appl	618	11	39.3	21	4	US-09-657-472-1622	Sequence 1622, Ap
546	11.2	40.0	34	1	US-08-739-158-75	Sequence 75, Appl	619	11	39.3	21	4	US-09-696-791-4476	Sequence 4476, Ap
547	11.2	40.0	34	2	US-08-739-167-75	Sequence 75, Appl	620	11	39.3	22	3	US-09-262-773-82	Sequence 82, Appl
548	11.2	40.0	34	3	US-08-404-796-75	Sequence 75, Appl	621	11	39.3	22	4	US-09-972-115A-37	Sequence 37, Appl
549	11.2	40.0	34	3	US-08-931-869-75	Sequence 75, Appl	622	11	39.3	23	3	US-08-666-221B-15	Sequence 15, Appl
550	11.2	40.0	34	3	US-09-011-745-13	Sequence 13, Appl	623	11	39.3	24	3	US-08-343-398-3	Sequence 3, Appl
551	11.2	40.0	34	3	US-09-350-399-75	Sequence 75, Appl	624	11	39.3	24	3	US-09-135-021-43	Sequence 43, Appl
552	11.2	40.0	34	3	US-09-236-140A-75	Sequence 75, Appl	625	11	39.3	24	3	US-09-135-020-45	Sequence 45, Appl
553	11.2	40.0	35	3	US-09-164-023-20	Sequence 20, Appl	626	11	39.3	24	3	US-09-135-010A-45	Sequence 45, Appl
554	11.2	40.0	36	3	US-09-204-208A-5	Sequence 5, Appl	627	11	39.3	24	3	US-09-444-871-45	Sequence 45, Appl
555	11.2	40.0	36	4	US-09-269-861A-5	Sequence 5, Appl	628	11	39.3	24	4	US-09-597-735-45	Sequence 45, Appl
556	11.2	40.0	36	4	US-10-072-436-5	Sequence 5, Appl	629	11	39.3	24	4	US-09-444-295-45	Sequence 45, Appl
557	11.2	40.0	37	2	US-08-291-074-4	Sequence 4, Appl	630	11	39.3	24	4	US-09-597-732-45	Sequence 45, Appl
558	11.2	40.0	37	4	US-09-470-661A-31	Sequence 31, Appl	631	11	39.3	24	4	US-09-597-731-45	Sequence 45, Appl
559	11.2	40.0	38	3	US-08-931-608A-10	Sequence 10, Appl	632	11	39.3	25	4	US-09-367-007C-29	Sequence 29, Appl
560	11.2	40.0	38	4	US-08-983-397-10	Sequence 10, Appl	633	11	39.3	25	4	US-08-887-497A-75	Sequence 75, Appl
561	11.2	40.0	38	4	US-09-851-847-10	Sequence 10, Appl	634	11	39.3	25	4	US-09-888-413-93	Sequence 93, Appl
562	11.2	40.0	39	3	US-09-213-053-28	Sequence 28, Appl	635	11	39.3	26	3	US-09-382-256-24	Sequence 24, Appl
563	11.2	40.0	39	3	US-09-476-239-12	Sequence 12, Appl	636	11	39.3	26	3	US-09-395-115-24	Sequence 24, Appl
564	11.2	40.0	39	3	US-09-609-154-12	Sequence 12, Appl	637	11	39.3	26	3	US-08-436-265-24	Sequence 24, Appl
565	11.2	40.0	39	3	US-09-415-784-71	Sequence 71, Appl	638	11	39.3	26	3	US-09-679-187-24	Sequence 24, Appl
566	11.2	40.0	39	4	US-09-415-785A-71	Sequence 71, Appl	639	11	39.3	26	4	US-09-267-963D-24	Sequence 24, Appl
567	11.2	40.0	39	4	US-08-944-465-71	Sequence 71, Appl	640	11	39.3	26	4	US-09-792-616-14	Sequence 14, Appl
568	11.2	40.0	39	4	US-09-415-868-71	Sequence 71, Appl	641	11	39.3	27	1	US-08-306-870-1	Sequence 1, Appl
569	11.2	40.0	39	4	US-09-415-900-71	Sequence 71, Appl	642	11	39.3	27	1	US-08-305-769A-1	Sequence 1, Appl
570	11.2	40.0	39	4	US-09-254-547A-2	Sequence 2, Appl	643	11	39.3	27	1	US-08-495-743-38	Sequence 38, Appl
571	11.2	40.0	39	4	US-09-507-362-71	Sequence 71, Appl	644	11	39.3	27	1	US-08-495-739-38	Sequence 38, Appl
572	11.2	40.0	40	3	US-09-254-352B-71	Sequence 2, Appl	645	11	39.3	27	1	US-08-495-741-38	Sequence 38, Appl
573	11.2	40.0	40	4	US-09-538-709-1225	Sequence 1225, Ap	646	11	39.3	27	1	US-08-555-678-62	Sequence 62, Appl
574	11.2	40.0	45	3	US-09-091-814-105	Sequence 105, Ap	647	11	39.3	27	2	US-08-643-282-1	Sequence 1, Appl
575	11.2	40.0	46	2	US-08-406-855A-18	Sequence 18, Appl	648	11	39.3	27	3	US-08-642-023-38	Sequence 38, Appl
576	11.2	40.0	46	3	US-09-208-899-18	Sequence 18, Appl	649	11	39.3	27	4	US-09-305-681-19	Sequence 19, Appl
577	11.2	40.0	46	4	US-09-688-415-23	Sequence 23, Appl	650	11	39.3	27	4	US-08-062-021A-16	Sequence 16, Appl
578	11.2	40.0	47	3	US-09-263-904-3	Sequence 3, Appl	651	11	39.3	28	1	US-08-554-659-6	Sequence 6, Appl
579	11.2	40.0	47	4	US-09-641-638-1272	Sequence 1272, Ap	652	11	39.3	30	1	US-08-160-670A-40	Sequence 40, Appl
580	11.2	40.0	47	4	US-09-422-978-3203	Sequence 3203, Ap	653	11	39.3	30	1	US-08-488-702-14	Sequence 14, Appl
581	11.2	40.0	47	4	US-10-170-097-1272	Sequence 1272, Ap	654	11	39.3	30	2	US-08-859-998-446	Sequence 446, App
582	11.2	40.0	48	1	US-08-116-389-16	Sequence 16, Appl	655	11	39.3	30	3	US-08-463-903-72	Sequence 72, Appl
583	11.2	40.0	48	1	US-08-708-431-16	Sequence 16, Appl	656	11	39.3	30	3	US-07-935-695-72	Sequence 72, Appl
584	11.2	40.0	48	2	US-08-800-830-16	Sequence 16, Appl	657	11	39.3	30	3	US-09-235-928-446	Sequence 446, App
585	11.2	40.0	48	3	US-08-864-473-58	Sequence 58, Appl	658	11	39.3	30	4	US-08-225-201B-446	Sequence 446, App
586	11.2	40.0	48	3	US-09-440-523-58	Sequence 58, Appl	659	11	39.3	31	1	US-08-086-428B-116	Sequence 116, App
587	11.2	40.0	48	4	US-09-918-156-58	Sequence 58, Appl	660	11	39.3	31	2	US-08-468-570-116	Sequence 116, App
588	11.2	40.0	48	5	PCT-US94-13895-16	Sequence 16, Appl	661	11	39.3	31	2	US-08-290-665A-220	Sequence 220, App
589	11.2	40.0	50	3	US-09-208-966-14	Sequence 14, Appl	662	11	39.3	31	4	US-08-466-601A-116	Sequence 116, App
590	11.2	40.0	50	4	US-09-775-052A-14	Sequence 14, Appl	663	11	39.3	31	4	US-09-854-549A-3	Sequence 3, Appl
591	11.2	40.0	50	4	US-09-422-978-7202	Sequence 7202, Ap	664	11	39.3	31	5	PCT-US95-10398-220	Sequence 220, App
592	11	39.3	19	4	US-09-015-876-18	Sequence 18, Appl	665	11	39.3	32	2	US-08-747-536-9	Sequence 9, Appl
593	11	39.3	20	1	US-08-462-305-14	Sequence 14, Appl	666	11	39.3	32	2	US-08-815-718-4	Sequence 4, Appl
594	11	39.3	20	1	US-08-613-417A-14	Sequence 14, Appl	667	11	39.3	32	4	PCT-US95-05616-11	Sequence 11, Appl
595	11	39.3	20	2	US-08-594-452-14	Sequence 14, Appl	668	11	39.3	32	4	US-08-394-177-9	Sequence 9, Appl
596	11	39.3	20	3	US-08-578-686C-13	Sequence 13, Appl	669	11	39.3	33	2	US-08-333-636-9	Sequence 9, Appl
597	11	39.3	20	3	US-08-281-203-16	Sequence 16, Appl	670	11	39.3	33	4	US-08-464-340A-7	Sequence 7, Appl
598	11	39.3	20	3	US-09-094-405-16	Sequence 16, Appl	671	11	39.3	34	1	US-09-334-181-1	Sequence 1, Appl
599	11	39.3	20	3	US-09-258-408-14	Sequence 14, Appl	672	11	39.3	34	3	US-08-442-497C-7	Sequence 7, Appl
600	11	39.3	20	3	US-09-418-641-22	Sequence 22, Appl	673	11	39.3	35	2	US-09-333-033-7	Sequence 7, Appl
601	11	39.3	20	3	US-09-196-132-14	Sequence 14, Appl	674	11	39.3	35	3	US-10-004-832-7	Sequence 7, Appl
602	11	39.3	20	3	US-09-287-796-157	Sequence 157, App	675	11	39.3	35	4	US-08-556-877-211	Sequence 211, App
603	11	39.3	20	3	US-09-144-112-13	Sequence 13, Appl	676	11	39.3	36	4	US-09-620-412C-211	Sequence 211, App
604	11	39.3	20	3	US-09-130-616-157	Sequence 157, App	677	11	39.3	36	4	US-09-598-419-211	Sequence 211, App
605	11	39.3	20	3	US-09-657-481A-79	Sequence 79, Appl	678	11	39.3	36	4	US-08-373-124A-401	Sequence 401, App
606	11	39.3	20	3	US-09-471-016-5	Sequence 5, Appl	680	11	39.3	38	1	US-08-435-628-401	Sequence 401, App
607	11	39.3	20	3	US-08-895-981-14	Sequence 14, Appl	681	11	39.3	38	1	US-08-537-811-13	Sequence 13, Appl
608	11	39.3	20	3	US-08-337-120A-16	Sequence 16, Appl	682	11	39.3	38	2	US-09-371-772B-8259	Sequence 8259, Ap
609	11	39.3	20	3	US-09-495-797-10	Sequence 10, Appl	683	11	39.3	38	4		
610	11	39.3	20	4	US-09-643-233-13	Sequence 13, Appl	684	11	39.3	38	4		



685	11	39.3	38	4	US-09-371-772B-9444	Sequence 9444, Ap	758	10.8	38.6	20	4	US-08-802-331-2	Sequence 2, Appli
686	11	39.3	38	4	US-09-371-772B-9572	Sequence 9572, Ap	759	10.8	38.6	20	4	US-09-389-283-2	Sequence 2, Appli
687	11	39.3	38	4	US-09-371-772B-9748	Sequence 9748, Ap	760	10.8	38.6	20	4	US-09-575-554-1	Sequence 1, Appli
688	11	39.3	38	4	US-09-371-772B-11035	Sequence 11035, A	C 761	10.8	38.6	21	3	US-08-817-913-27	Sequence 27, Appl
689	11	39.3	40	2	US-08-423-684-126	Sequence 126, App	C 762	10.8	38.6	21	3	US-09-002-361-38	Sequence 38, Appl
690	11	39.3	40	2	US-08-675-502-126	Sequence 126, App	C 763	10.8	38.6	21	3	US-09-422-978-9594	Sequence 9594, Ap
691	11	39.3	40	3	US-08-964-877-1	Sequence 1, Appli	C 764	10.8	38.6	21	4	US-09-269-939A-31	Sequence 31, Appl
692	11	39.3	40	3	US-09-546-483-1	Sequence 1, Appli	C 765	10.8	38.6	22	4	US-08-821-994-32	Sequence 47, Appl
693	11	39.3	40	4	US-09-823-177-1	Sequence 126, App	C 766	10.8	38.6	23	4	US-09-523-263B-47	Sequence 22, Appl
694	11	39.3	42	4	US-09-245-802-126	Sequence 13, Appli	C 767	10.8	38.6	24	1	US-08-261-822A-22	Sequence 49, Appl
695	11	39.3	42	1	US-08-250-859-13	Sequence 3, Appli	C 768	10.8	38.6	24	1	US-08-465-590-49	Sequence 53, Appl
696	11	39.3	42	1	US-08-381-572-3	Sequence 13, Appli	C 769	10.8	38.6	24	2	US-08-465-590-53	Sequence 5, Appli
697	11	39.3	42	1	US-08-490-803-13	Sequence 3, Appli	C 770	10.8	38.6	24	2	US-08-819-288-5	Sequence 49, Appl
698	11	39.3	42	1	US-08-592-820-3	Sequence 24, Appl	C 771	10.8	38.6	24	3	US-08-711-417C-49	Sequence 53, Appl
699	11	39.3	42	2	US-08-457-254-24	Sequence 13, Appl	C 772	10.8	38.6	24	3	US-08-711-417C-53	Sequence 5, Appli
700	11	39.3	42	2	US-08-484-257-13	Sequence 13, Appl	C 773	10.8	38.6	24	3	US-09-400-348-5	Sequence 18, Appl
701	11	39.3	42	3	US-09-230-199-13	Sequence 14, Appl	C 774	10.8	38.6	24	3	US-09-284-627-18	Sequence 676, App
702	11	39.3	42	3	US-09-230-199-13	Sequence 14, Appl	C 775	10.8	38.6	24	4	US-08-469-260A-676	Sequence 676, App
703	11	39.3	42	3	US-08-230-199-13	Sequence 14, Appl	C 776	10.8	38.6	24	4	US-08-469-260A-676	Sequence 676, App
704	11	39.3	42	4	US-08-944-410-80	Sequence 80, Appl	C 777	10.8	38.6	24	4	US-08-467-344A-676	Sequence 676, App
705	11	39.3	42	5	PCT-US94-08806-13	Sequence 13, Appl	C 778	10.8	38.6	24	4	US-09-723-909-49	Sequence 49, Appl
706	11	39.3	42	5	PCT-US95-16626-24	Sequence 24, Appl	C 779	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
707	11	39.3	43	1	US-07-531-473B-241	Sequence 241, App	C 780	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
708	11	39.3	43	1	US-07-714-131C-241	Sequence 241, App	C 781	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
709	11	39.3	43	1	US-08-412-110-241	Sequence 241, App	C 782	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
710	11	39.3	43	2	US-08-409-442A-241	Sequence 241, App	C 783	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
711	11	39.3	43	2	US-08-469-609A-241	Sequence 241, App	C 784	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
712	11	39.3	43	3	US-09-143-190-241	Sequence 241, App	C 785	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
713	11	39.3	43	3	US-09-502-344-241	Sequence 241, App	C 786	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
714	11	39.3	44	2	US-08-749-852-21	Sequence 21, Appl	C 787	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
715	11	39.3	44	3	US-08-434-099A-13	Sequence 13, Appl	C 788	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
716	11	39.3	47	4	US-09-641-638-895	Sequence 895, App	C 789	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
717	11	39.3	47	4	US-09-422-978-196	Sequence 196, App	C 790	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
718	11	39.3	47	4	US-09-422-978-3280	Sequence 3280, Ap	C 791	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
719	11	39.3	47	4	US-10-170-097-895	Sequence 895, App	C 792	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
720	11	39.3	49	4	US-09-710-000-7	Sequence 7, Appli	C 793	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
721	11	39.3	50	4	US-08-956-171B-2364	Sequence 2364, Ap	C 794	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
722	11	39.3	50	4	US-08-781-986A-2364	Sequence 2364, Ap	C 795	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
723	11	39.3	50	4	US-08-810-502-28	Sequence 28, Appl	C 796	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
724	11	39.3	50	4	US-08-485-629-18	Sequence 18, Appl	C 797	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
725	10.8	38.6	15	2	US-08-476-021A-18	Sequence 18, Appl	C 798	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
726	10.8	38.6	15	2	US-08-476-021A-18	Sequence 18, Appl	C 799	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
727	10.8	38.6	15	2	US-08-476-021A-18	Sequence 18, Appl	C 800	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
728	10.8	38.6	15	2	US-08-476-021A-18	Sequence 18, Appl	C 801	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
729	10.8	38.6	15	2	US-08-476-021A-18	Sequence 18, Appl	C 802	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
730	10.8	38.6	15	2	US-08-476-021A-18	Sequence 18, Appl	C 803	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
731	10.8	38.6	15	2	US-08-476-021A-18	Sequence 18, Appl	C 804	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
732	10.8	38.6	15	2	US-08-476-021A-18	Sequence 18, Appl	C 805	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
733	10.8	38.6	15	2	US-08-476-021A-18	Sequence 18, Appl	C 806	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
734	10.8	38.6	15	2	US-08-476-021A-18	Sequence 18, Appl	C 807	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
735	10.8	38.6	15	2	US-08-476-021A-18	Sequence 18, Appl	C 808	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
736	10.8	38.6	15	2	US-08-476-021A-18	Sequence 18, Appl	C 809	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
737	10.8	38.6	15	2	US-08-476-021A-18	Sequence 18, Appl	C 810	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
738	10.8	38.6	15	2	US-08-476-021A-18	Sequence 18, Appl	C 811	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
739	10.8	38.6	15	2	US-08-476-021A-18	Sequence 18, Appl	C 812	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
740	10.8	38.6	15	2	US-08-476-021A-18	Sequence 18, Appl	C 813	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
741	10.8	38.6	15	2	US-08-476-021A-18	Sequence 18, Appl	C 814	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
742	10.8	38.6	15	2	US-08-476-021A-18	Sequence 18, Appl	C 815	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
743	10.8	38.6	15	2	US-08-476-021A-18	Sequence 18, Appl	C 816	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
744	10.8	38.6	15	2	US-08-476-021A-18	Sequence 18, Appl	C 817	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
745	10.8	38.6	15	2	US-08-476-021A-18	Sequence 18, Appl	C 818	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
746	10.8	38.6	15	2	US-08-476-021A-18	Sequence 18, Appl	C 819	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
747	10.8	38.6	15	2	US-08-476-021A-18	Sequence 18, Appl	C 820	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
748	10.8	38.6	15	2	US-08-476-021A-18	Sequence 18, Appl	C 821	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
749	10.8	38.6	15	2	US-08-476-021A-18	Sequence 18, Appl	C 822	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
750	10.8	38.6	15	2	US-08-476-021A-18	Sequence 18, Appl	C 823	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
751	10.8	38.6	15	2	US-08-476-021A-18	Sequence 18, Appl	C 824	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
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753	10.8	38.6	15	2	US-08-476-021A-18	Sequence 18, Appl	C 826	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
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755	10.8	38.6	15	2	US-08-476-021A-18	Sequence 18, Appl	C 828	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
756	10.8	38.6	15	2	US-08-476-021A-18	Sequence 18, Appl	C 829	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl
757	10.8	38.6	15	2	US-08-476-021A-18	Sequence 18, Appl	C 830	10.8	38.6	24	4	US-09-723-909-53	Sequence 53, Appl

C 831	10.8	38.6	30	4	US-09-954-594A-18	Sequence 18, Appl	C 904	10.8	38.6	45	2	US-08-975-902-33	Sequence 33, Appl
C 832	10.8	38.6	30	4	US-09-574-779B-114	Sequence 114, App	C 905	10.8	38.6	45	3	US-09-251-565-33	Sequence 33, Appl
C 833	10.8	38.6	30	4	US-09-599-002-1	Sequence 1, Appli	906	10.8	38.6	45	3	US-09-224-426-7	Sequence 7, Appli
C 834	10.8	38.6	30	4	US-09-599-002-2	Sequence 2, Appli	907	10.8	38.6	45	3	US-09-478-601-7	Sequence 7, Appli
C 835	10.8	38.6	30	5	PCT-US92-02050-31	Sequence 31, Appl	908	10.8	38.6	45	3	US-03-478-602-7	Sequence 7, Appli
C 836	10.8	38.6	31	2	US-08-718-658-5	Sequence 5, Appli	909	10.8	38.6	45	4	US-03-885-478-7	Sequence 7, Appli
C 837	10.8	38.6	31	3	US-09-195-666A-39	Sequence 39, Appl	910	10.8	38.6	46	2	US-08-882-704A-8	Sequence 8, Appli
C 838	10.8	38.6	31	3	US-09-195-666A-42	Sequence 42, Appl	911	10.8	38.6	46	4	US-09-151-957-8	Sequence 8, Appli
C 839	10.8	38.6	31	3	US-08-840-456A-13	Sequence 13, Appl	912	10.8	38.6	46	4	US-10-195-158-8	Sequence 8, Appli
C 840	10.8	38.6	31	3	US-09-227-684-5	Sequence 5, Appli	913	10.8	38.6	47	1	US-07-933-469A-9	Sequence 9, Appli
C 841	10.8	38.6	31	3	US-09-635-705-39	Sequence 39, Appl	914	10.8	38.6	47	4	US-09-641-638-903	Sequence 903, App
C 842	10.8	38.6	31	3	US-09-635-705-42	Sequence 42, Appl	915	10.8	38.6	47	4	US-09-641-638-1110	Sequence 1110, Ap
C 843	10.8	38.6	31	4	US-09-696-188B-13	Sequence 13, Appl	C 916	10.8	38.6	47	4	US-09-422-978-1903	Sequence 1903, Ap
C 844	10.8	38.6	31	4	US-09-634-858A-39	Sequence 39, Appl	917	10.8	38.6	47	4	US-09-422-978-2425	Sequence 2425, Ap
C 845	10.8	38.6	31	4	US-09-634-858A-42	Sequence 42, Appl	C 918	10.8	38.6	47	4	US-09-422-978-3534	Sequence 3534, Ap
C 846	10.8	38.6	31	4	US-08-869-927C-39	Sequence 39, Appl	C 919	10.8	38.6	47	4	US-09-422-978-3816	Sequence 3816, Ap
C 847	10.8	38.6	31	4	US-08-869-927C-42	Sequence 42, Appl	920	10.8	38.6	47	4	US-10-170-097-903	Sequence 903, App
C 848	10.8	38.6	31	4	US-08-693-234-24	Sequence 24, Appl	921	10.8	38.6	47	4	US-10-170-097-1110	Sequence 1110, Ap
C 849	10.8	38.6	31	4	US-09-877-476-54	Sequence 54, Appl	922	10.8	38.6	48	1	US-08-285-936-36	Sequence 36, Appl
C 850	10.8	38.6	31	4	US-09-785-881-3	Sequence 3, Appli	923	10.8	38.6	48	1	US-08-487-860-36	Sequence 36, Appl
C 851	10.8	38.6	31	4	US-09-785-881-4	Sequence 4, Appli	C 924	10.8	38.6	48	4	US-09-500-123-3	Sequence 3, Appli
C 852	10.8	38.6	32	1	US-08-644-664B-39	Sequence 39, Appl	C 925	10.8	38.6	50	1	US-08-171-389-343	Sequence 343, App
C 853	10.8	38.6	32	2	US-08-761-277A-39	Sequence 39, Appl	C 926	10.8	38.6	50	1	US-08-123-936-343	Sequence 343, App
C 854	10.8	38.6	32	3	US-09-191-608-25	Sequence 25, Appl	C 927	10.8	38.6	50	2	US-08-475-228A-343	Sequence 343, App
C 855	10.8	38.6	33	1	US-08-218-933-4	Sequence 4, Appli	C 928	10.8	38.6	50	3	US-08-482-080A-343	Sequence 343, App
C 856	10.8	38.6	33	3	US-08-722-719-43	Sequence 43, Appl	929	10.8	38.6	50	3	US-09-298-886-13	Sequence 13, Appl
C 857	10.8	38.6	33	4	US-09-334-951-43	Sequence 43, Appl	C 930	10.8	38.6	50	3	US-09-354-947-343	Sequence 343, App
C 858	10.8	38.6	33	4	US-09-334-923A-43	Sequence 43, Appl	931	10.8	38.6	50	4	US-09-999-672-13	Sequence 13, Appl
C 859	10.8	38.6	33	4	US-09-689-693-34	Sequence 34, Appl	C 932	10.8	38.6	50	5	PCT-US93-12388-343	Sequence 343, App
C 860	10.8	38.6	33	4	US-09-334-954A-43	Sequence 43, Appl	C 933	10.6	37.9	17	4	US-09-866-108A-1625	Sequence 1625, Ap
C 861	10.8	38.6	33	5	PCT-US95-03918-4	Sequence 4, Appli	C 934	10.6	37.9	17	4	US-09-866-108A-1626	Sequence 1626, Ap
C 862	10.8	38.6	35	4	US-09-709-103-14	Sequence 14, Appl	C 935	10.6	37.9	18	4	US-09-375-248-23	Sequence 23, Appl
C 863	10.8	38.6	35	4	US-09-709-103-15	Sequence 15, Appl	936	10.6	37.9	19	1	US-08-582-539-31	Sequence 31, Appl
C 864	10.8	38.6	35	4	US-09-439-410A-14	Sequence 14, Appl	937	10.6	37.9	19	1	US-08-621-502A-10	Sequence 10, Appl
C 865	10.8	38.6	35	4	US-09-439-410A-15	Sequence 15, Appl	938	10.6	37.9	19	3	US-08-797-722-4	Sequence 4, Appli
C 866	10.8	38.6	36	3	US-09-455-960-25	Sequence 25, Appl	939	10.6	37.9	19	3	US-09-641-599-5	Sequence 5, Appli
C 867	10.8	38.6	36	4	US-10-051-325-25	Sequence 25, Appl	940	10.6	37.9	19	4	US-09-584-216-11	Sequence 11, Appl
C 868	10.8	38.6	36	6	5258287-12	Patent No. 5258287	941	10.6	37.9	20	1	US-08-208-795-3	Sequence 3, Appli
C 869	10.8	38.6	37	1	US-08-653-740-30	Sequence 30, Appl	C 942	10.6	37.9	20	2	US-08-463-418-9	Sequence 9, Appli
C 870	10.8	38.6	37	2	US-09-073-594-30	Sequence 30, Appl	C 943	10.6	37.9	20	2	US-08-368-704C-94	Sequence 94, Appl
C 871	10.8	38.6	37	2	US-09-019-201A-10	Sequence 10, Appl	C 944	10.6	37.9	20	3	US-09-596-938-8	Sequence 8, Appli
C 872	10.8	38.6	37	3	US-09-275-925-30	Sequence 30, Appl	C 945	10.6	37.9	20	4	US-09-657-452A-58	Sequence 58, Appl
C 873	10.8	38.6	37	4	US-09-842-164A-19	Sequence 19, Appl	C 946	10.6	37.9	20	4	US-09-360-416-121	Sequence 121, App
C 874	10.8	38.6	37	4	US-09-455-950-10	Sequence 10, Appl	947	10.6	37.9	20	4	US-08-887-497A-5	Sequence 5, Appli
C 875	10.8	38.6	38	4	US-09-877-476-56	Sequence 56, Appl	948	10.6	37.9	20	4	US-08-887-497A-74	Sequence 74, Appl
C 876	10.8	38.6	39	2	US-08-190-199A-27	Sequence 27, Appl	949	10.6	37.9	20	4	US-09-471-913-15	Sequence 15, Appl
C 877	10.8	38.6	40	1	US-07-959-941-6	Sequence 6, Appli	950	10.6	37.9	20	4	US-08-471-974-5	Sequence 5, Appli
C 878	10.8	38.6	40	1	US-08-259-924-6	Sequence 6, Appli	C 951	10.6	37.9	20	4	US-09-198-452A-2463	Sequence 2463, Ap
C 879	10.8	38.6	40	1	US-08-276-852-36	Sequence 36, Appl	952	10.6	37.9	20	4	US-09-198-452A-2733	Sequence 2733, Ap
C 880	10.8	38.6	40	1	US-08-133-011-108	Sequence 108, App	953	10.6	37.9	20	4	US-09-269-939A-28	Sequence 28, Appl
C 881	10.8	38.6	40	1	US-08-301-722A-6	Sequence 6, Appli	954	10.6	37.9	20	4	US-09-758-881-131	Sequence 131, App
C 882	10.8	38.6	40	1	US-08-322-730A-108	Sequence 108, App	C 955	10.6	37.9	21	3	US-08-835-728D-73	Sequence 73, Appl
C 883	10.8	38.6	40	1	US-08-387-874-80	Sequence 80, Appl	956	10.6	37.9	21	3	US-08-835-728D-177	Sequence 177, App
C 884	10.8	38.6	40	1	US-08-899-575-36	Sequence 36, Appl	C 957	10.6	37.9	21	3	US-09-490-558-177	Sequence 73, Appl
C 885	10.8	38.6	40	2	US-08-899-575-36	Sequence 36, Appl	958	10.6	37.9	21	3	US-09-490-558-177	Sequence 177, App
C 886	10.8	38.6	40	2	US-08-888-366-37	Sequence 108, App	959	10.6	37.9	21	3	US-08-887-497A-76	Sequence 76, Appl
C 887	10.8	38.6	40	2	US-08-888-366-37	Sequence 37, Appl	C 960	10.6	37.9	21	4	US-09-422-978-6753	Sequence 6753, Ap
C 888	10.8	38.6	40	3	US-08-820-970-5	Sequence 5, Appli	961	10.6	37.9	21	4	US-09-657-472-239	Sequence 239, App
C 889	10.8	38.6	40	3	US-08-646-538-20	Sequence 20, Appl	962	10.6	37.9	21	4	US-09-657-472-1555	Sequence 1555, Ap
C 890	10.8	38.6	40	3	US-08-646-538-23	Sequence 23, Appl	963	10.6	37.9	21	4	US-08-487-727A-11	Sequence 11, Appl
C 891	10.8	38.6	40	3	US-08-767-128-44	Sequence 44, Appl	C 964	10.6	37.9	24	2	US-08-487-727A-12	Sequence 12, Appl
C 892	10.8	38.6	40	3	US-09-075-272-10	Sequence 10, Appl	C 965	10.6	37.9	24	3	US-08-772-440-37	Sequence 37, Appl
C 893	10.8	38.6	40	3	US-08-907-739-108	Sequence 108, App	C 966	10.6	37.9	25	4	US-09-388-743-23	Sequence 23, Appl
C 894	10.8	38.6	40	3	US-09-503-222-20	Sequence 20, Appl	967	10.6	37.9	25	4	US-08-887-497A-8	Sequence 8, Appli
C 895	10.8	38.6	40	3	US-09-503-222-23	Sequence 23, Appl	968	10.6	37.9	25	4	US-08-887-497A-77	Sequence 77, Appl
C 896	10.8	38.6	40	3	US-08-972-564-20	Sequence 20, Appl	969	10.6	37.9	25	4	US-08-471-974-8	Sequence 8, Appli
C 897	10.8	38.6	40	4	US-09-729-597-108	Sequence 108, App	C 970	10.6	37.9	25	4	US-09-866-108A-4554	Sequence 4554, Ap
C 898	10.8	38.6	40	4	US-09-812-042A-1	Sequence 1, Appli	C 971	10.6	37.9	25	4	US-09-866-108A-4563	Sequence 4563, Ap
C 899	10.8	38.6	40	5	PCT-US93-08364-80	Sequence 80, Appl	C 972	10.6	37.9	25	4	US-10-044-543-23	Sequence 23, Appl
C 900	10.8	38.6	40	5	PCT-US95-00067-22	Sequence 22, Appl	C 973	10.6	37.9	26	1	US-08-531-556-91	Sequence 91, Appl
C 901	10.8	38.6	40	5	PCT-US95-08743-36	Sequence 36, Appl	C 974	10.6	37.9	26	1	US-08-472-416-91	Sequence 91, Appl
C 902	10.8	38.6	41	2	PCT-US95-08743-36	Sequence 36, Appl	975	10.6	37.9	26	2	US-08-859-998-1106	Sequence 1106, Ap
C 903	10.8	38.6	44	3	US-08-761-277A-69	Sequence 69, Appl	976	10.6	37.9	26	3	US-08-891-789B-12	Sequence 12, Appl

Sequence 1106, Ap  
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Sequence 78, Appl  
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Sequence 6, Appl  
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Sequence 79, Appl  
Sequence 10, Appl  
Sequence 6, Appl  
Sequence 756, Appl  
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Sequence 73, Appl  
Sequence 165, Appl  
Sequence 12, Appl  
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Sequence 85, Appl

ALIGNMENTS

RESULT 1  
US-09-422-978-1680  
; Sequence 1680, Application US/09422978  
; Patent No. 6537751  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Chumakov, Ilva  
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...  
; FILE REFERENCE: GENSET.020CF1  
; CURRENT APPLICATION NUMBER: US/09/422,978  
; CURRENT FILING DATE: 1999-10-20  
; EARLIER APPLICATION NUMBER: US 09/298,850  
; EARLIER FILING DATE: 1999-04-21  
; EARLIER APPLICATION NUMBER: US 60/109,732  
; EARLIER FILING DATE: 1998-11-23  
; EARLIER APPLICATION NUMBER: US 60/082,614  
; EARLIER FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 11796  
; SEQ ID NO 1680  
; LENGTH: 47  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 24  
; OTHER INFORMATION: 99-5604-376 : polymorphic base A or G  
US-09-422-978-1680  
Query Match 60.7%; Score 17; DB 4; Length 47;  
Best Local Similarity 74.1%; Pred. No. 43;  
Matches 20; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
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DB 8 GTATGCTATAGTACATGCTGT 34  
RESULT 2  
US-09-153-242-37/c  
; Sequence 37, Application US/09153242  
; Patent No. 6482592  
; GENERAL INFORMATION:  
; APPLICANT: Lundberg, Joakim

APPLICANT: Uhlen, Mathias  
; TITLE OF INVENTION: MODULAR PROBES II  
; FILE REFERENCE: 1181-242  
; CURRENT APPLICATION NUMBER: US/09/153,242  
; CURRENT FILING DATE: 1998-09-15  
; PRIOR APPLICATION NUMBER: PCT/GB97/02629  
; PRIOR FILING DATE: 1997-09-26  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 37  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: oligonucleotide H7  
US-09-153-242-37  
Query Match 53.6%; Score 15; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 TCGTGGGATAGTCG 18  
DB 15 TCGTGGGATAGTCG 1  
RESULT 3  
US-09-657-472-2496/c  
; Sequence 2496, Application US/09657472  
; Patent No. 6727063  
; GENERAL INFORMATION:  
; APPLICANT: Lander, Eric S.  
; APPLICANT: Cargill, Michele  
; APPLICANT: Ireland, James S.  
; APPLICANT: Bolk, Stacey  
; APPLICANT: Dailey, George Q.  
; APPLICANT: McCarthy, Jeanette J.  
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES  
; FILE REFERENCE: 2825.1027-001  
; CURRENT APPLICATION NUMBER: US/09/657,472  
; CURRENT FILING DATE: 2000-09-07  
; PRIOR APPLICATION NUMBER: US 60/153,357  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: US 60/220,947  
; PRIOR FILING DATE: 2000-07-26  
; PRIOR APPLICATION NUMBER: US 60/225,724  
; PRIOR FILING DATE: 2000-08-16  
; NUMBER OF SEQ ID NOS: 2551  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2496  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
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Best Local Similarity 81.0%; Pred. No. 5.2e+02;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2 GTTCGTGGGATAGTCGTCAT 22  
DB 21 GTTCGTGGAAATGTCGTCAT 1  
RESULT 4  
US-08-821-827c-25/c  
; Sequence 25, Application US/08821827C  
; Patent No. 6297425  
; GENERAL INFORMATION:  
; APPLICANT: Seelange, Christopher J.  
; APPLICANT: Bidney, Dennis L.  
; TITLE OF INVENTION: GENE ENCODING OXALATE DECARBOXYLASE FROM

; TITLE OF INVENTION: ASPERGILLUS PHOENICES  
; FILE REFERENCE: 0561A  
; CURRENT APPLICATION NUMBER: US/08/821.827C  
; CURRENT FILING DATE: 1997-03-21  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 25  
; LENGTH: 38  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: primer  
US-08-821-827C-25

Query Match 52.1%; Score 14.6; DB 3; Length 38;  
Best Local Similarity 81.0%; Pred. No. 5.7e+02;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GTTCGTGGGATAGTCCGTCAT 22  
Db 22 GATAGTGGGATGTGCGTCAT 2

## RESULT 5

US-09-290-202B-25/c  
; Sequence 25, Application US/09290202B  
; Patent No. 6303846  
; GENERAL INFORMATION:

; APPLICANT: Scelonge, Christopher J.

; APPLICANT: Bidney, Dennis L.

; TITLE OF INVENTION: GENE ENCODING OXALATE DECARBOXYLASE FROM

; FILE REFERENCE: 0561D

; CURRENT APPLICATION NUMBER: US/09/290.202B

; CURRENT FILING DATE: 1999-04-12

; PRIOR APPLICATION NUMBER: 08/821,827

; PRIOR FILING DATE: 1997-03-21

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 25

; LENGTH: 38

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: primer

US-09-290-202B-25

Query Match 52.1%; Score 14.6; DB 3; Length 38;  
Best Local Similarity 81.0%; Pred. No. 5.7e+02;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GTTCGTGGGATAGTCCGTCAT 22  
Db 22 GATAGTGGGATGTGCGTCAT 2

## RESULT 6

US-09-469-211A-14/c  
; Sequence 14, Application US/09469211A  
; Patent No. 6660524  
; GENERAL INFORMATION:

; APPLICANT: J. Turck

; APPLICANT: J. Archer

; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN EUKARYOTES

; FILE REFERENCE: 9341-021

; CURRENT APPLICATION NUMBER: US/09/469.211A

; CURRENT FILING DATE: 1999-12-22

; PRIOR APPLICATION NUMBER: UK 9828660.2

; PRIOR FILING DATE: 1998-12-24

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 14

; LENGTH: 50

; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial  
; OTHER INFORMATION: Sequence: CamVop2  
US-09-469-211A-14

Query Match 52.1%; Score 14.6; DB 4; Length 50;  
Best Local Similarity 81.0%; Pred. No. 6e+02;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GTTCGTGGGATAGTCCGTCAT 22  
Db 37 GATAGTGGGATGTGCGTCAT 17

## RESULT 7

US-08-833-167-78/c

; Sequence 78, Application US/08833167

; Patent No. 6100070

; GENERAL INFORMATION:

; APPLICANT: ZURELUH, LINDA L

; APPLICANT: MCWHERTER, CHARLES A

; APPLICANT: MCKEARN, JOHN P

; APPLICANT: KLEIN, BARBARA K

; APPLICANT: FENG, YIQING

; APPLICANT: BRAFORD-GOLDBERG, SARAH R

; APPLICANT: LEE, STEPHEN C

; TITLE OF INVENTION: G-CSF RECEPTOR AGONISTS

; NUMBER OF SEQUENCES: 129

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DENNIS A BENNETT, G.D. SEARLE & CO.,

; ADDRESSEE: CORPORATE PATENT DEPT.

; STREET: P.O. BOX 5110

; CITY: CHICAGO

; STATE: ILLINOIS

; COUNTRY: USA

; ZIP: 60680

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/833.167

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US 96/15935

; FILING DATE: 04-OCT-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/004,382

; FILING DATE: 05-OCT-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: BENNETT, DENNIS A

; REFERENCE/DOCKET NUMBER: 2907/1

; TELEPHONE: 314-694-5402

; TELEFAX: 314-694-9095

; INFORMATION FOR SEQ ID NO: 78:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 32 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: other nucleic acid

; DESCRIPTION: /desc = "DNA (synthetic)"

US-08-833-167-78

Query Match 51.4%; Score 14.4; DB 3; Length 32;  
Best Local Similarity 75.0%; Pred. No. 6.9e+02;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Wed Nov 24 08:46:11 2004

QY 2 GTTCGTGGATAGTCGTCATGGT 25  
Db 29 GGTGGTGGCAAGTCAGCCATGGT 6

RESULT 8  
US-09-344-837A-78/c  
; Sequence 78, Application US/09344837A  
; Patent No. 6358505  
; GENERAL INFORMATION:  
; APPLICANT: ZURFLOH, LINDA L  
; APPLICANT: MCWHERTER, CHARLES A  
; APPLICANT: MCKEARN, JOHN P  
; APPLICANT: KLEIN, BARBARA K  
; APPLICANT: FENG, YIONG  
; APPLICANT: BRAFORD-GOLDBERG, SARAH R  
; APPLICANT: LEE, STEPHEN C  
; TITLE OF INVENTION: G-CSF RECEPTOR AGONISTS  
; NUMBER OF SEQUENCES: 129  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: S. CHRISTOPHER BAUER  
; ADDRESSEE: MONSANTO/G. D. SEARLE & CO.,  
; ADDRESSEE: PATENT DEPARTMENT CENTRAL  
; STREET: P.O. BOX 5110  
; CITY: CHICAGO  
; STATE: ILLINOIS  
; COUNTRY: USA  
; ZIP: 60680  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/344,837A  
; FILING DATE: 25-JUN-1999  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US 96/15935  
; FILING DATE: 04-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/004,382  
; FILING DATE: 05-OCT-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: S. CHRISTOPHER BAUER  
; REFERENCE/DOCKET NUMBER: 2907/2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 636-737-6257  
; TELEFAX: 636-737-5452  
; INFORMATION FOR SEQ ID NO: 78:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 32 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA (synthetic)"  
US-09-344-837A-78

Query Match 51.4%; Score 14.4; DB 3; Length 32;  
Best Local Similarity 75.0%; Pred. No. 6.9e+02;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 GTTCGTGGATAGTCGTCATGGT 25  
Db 29 GGTGGTGGCAAGTCAGCCATGGT 6

RESULT 9  
US-08-985-337A-6/c  
; Sequence 6, Application US/08985337A  
; Patent No. 5932590  
; GENERAL INFORMATION:

; APPLICANT: Ciccarone, Terrence M.  
; APPLICANT: deSolms, S. Jane  
; TITLE OF INVENTION: INHIBITORS OF FARNESYL-PROTEIN  
; TITLE OF INVENTION: TRANSFERASE  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
; CITY: Rahway  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07065-0900  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/985,337A  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/032,578  
; FILING DATE: 05-DEC-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Muthard, David A  
; REGISTRATION NUMBER: 35,297  
; REFERENCE/DOCKET NUMBER: 19834Y  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 908-594-3903  
; TELEFAX: 908-594-4720  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 38 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Genomic DNA  
US-08-985-337A-6

Query Match 51.4%; Score 14.4; DB 2; Length 38;  
Best Local Similarity 93.8%; Pred. No. 7.1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 ATAGTCCGTCATGGTG 26  
||| ||||| ||||| |||||  
Db 28 ATATTCGTCATGGTG 13

RESULT 10  
US-08-985-124A-6/c  
; Sequence 6, Application US/08985124A  
; Patent No. 5972966  
; GENERAL INFORMATION:  
; APPLICANT: deSolms, S. Jane  
; TITLE OF INVENTION: INHIBITORS OF FARNESYL-PROTEIN  
; TITLE OF INVENTION: TRANSFERASE  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
; CITY: Rahway  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07065-0900  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/985,124A

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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/032,428
; FILING DATE: 05-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Muthard, David A
; REGISTRATION NUMBER: 35,297
; REFERENCE/DOCKET NUMBER: 19833Y
; TELEPHONE: 908-594-3903
; TELEFAX: 908-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; US-08-985-124A-6
;
; Query Match
; Best Local Similarity 51.4%; Score 14.4; DB 2; Length 38;
; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 11 ATAGTCCGTCATGGTG 26
; DB 28 ATATTCGTCATGGTG 13
;
; RESULT 11
; US-08-985-320A-6/c
; Sequence 6, Application US/08985320A
; Patent No. 5977134
; GENERAL INFORMATION:
; APPLICANT: Ciccarone, Terrence M.
; APPLICANT: Halczenko, Wasyli
; APPLICANT: Hutchinson, John H.
; APPLICANT: Lumma, Jr., William C.
; APPLICANT: Stokker, Gerald E.
; APPLICANT: Stump, Craig A.
; APPLICANT: Williams, Theresa M.
; TITLE OF INVENTION: INHIBITORS OF FARNESYL-PROTEIN
; TITLE OF INVENTION: TRANSFERASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,320A
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/032,579
; FILING DATE: 05-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Muthard, David A
; REGISTRATION NUMBER: 35,297
; REFERENCE/DOCKET NUMBER: 19850Y
; TELEPHONE: 908-594-3903
; TELEFAX: 908-594-4720
; TELEX:
;
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; US-08-985-124A-6
;
; Query Match
; Best Local Similarity 51.4%; Score 14.4; DB 3; Length 38;
; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 11 ATAGTCCGTCATGGTG 26
; DB 28 ATATTCGTCATGGTG 13
;
; RESULT 12
; US-08-984-732A-6/c
; Sequence 6, Application US/08984732A
; Patent No. 6015817
; GENERAL INFORMATION:
; APPLICANT: Halczenko, Wasyli
; APPLICANT: Stump, Craig A.
; TITLE OF INVENTION: INHIBITORS OF FARNESYL-PROTEIN
; TITLE OF INVENTION: TRANSFERASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/984,732A
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/032,126
; FILING DATE: 05-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Muthard, David A
; REGISTRATION NUMBER: 35,297
; REFERENCE/DOCKET NUMBER: 19849Y
; TELEPHONE: 908-594-3903
; TELEFAX: 908-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; US-08-984-732A-6
;
; Query Match
; Best Local Similarity 51.4%; Score 14.4; DB 3; Length 38;
; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 11 ATAGTCCGTCATGGTG 26
; DB 28 ATATTCGTCATGGTG 13
;
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; US-08-985-320A-6
;
; Query Match
; Best Local Similarity 51.4%; Score 14.4; DB 2; Length 38;
; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 11 ATAGTCCGTCATGGTG 26
; DB 28 ATATTCGTCATGGTG 13
```





; APPLICANT: Graham, Samuel L.  
; APPLICANT: Shaw, Anthony W.  
; APPLICANT: Ciccarone, Terrence M.  
; APPLICANT: Stokker, Gerald E.  
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN  
; TITLE OF INVENTION: TRANSFERASE  
; FILE REFERENCE: 20312Y  
; CURRENT APPLICATION NUMBER: US/09/456,153  
; CURRENT FILING DATE: 1999-12-07  
; EARLIER APPLICATION NUMBER: US 60/111,416  
; EARLIER FILING DATE: 1998-12-08  
; EARLIER APPLICATION NUMBER: US 60/129,282  
; EARLIER FILING DATE: 1999-04-14  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 13  
; LENGTH: 38  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: completely synthesized  
US-09-456-153-13

Query Match 51.4%; Score 14.4; DB 3; Length 38;  
Best Local Similarity 93.8%; Pred. No. 7.1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATAGTCCGTCATGGTG 26  
||| ||||| |||||  
Db 28 ATATTCGTCATGGTG 13

RESULT 18  
US-09-167-180-18/c  
; Sequence 18, Application US/09167180  
; Patent No. 6297239  
; GENERAL INFORMATION:  
; APPLICANT: deSolms, S. Jane  
; APPLICANT: Hutchinson, John H.  
; APPLICANT: Shaw, Anthony W.  
; APPLICANT: Graham, Samuel L.  
; APPLICANT: Ciccarone, Terrence M.  
; APPLICANT: Merck & Co., Inc.  
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE  
; FILE REFERENCE: 19928Y  
; CURRENT APPLICATION NUMBER: US/09/167,180  
; CURRENT FILING DATE: 1998-10-06  
; EARLIER APPLICATION NUMBER: 60/062,660  
; EARLIER FILING DATE: 1997-10-08  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 18  
; LENGTH: 38  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: completely synthesized  
US-09-167-180-18

Query Match 51.4%; Score 14.4; DB 3; Length 38;  
Best Local Similarity 93.8%; Pred. No. 7.1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATAGTCCGTCATGGTG 26  
||| ||||| |||||  
Db 28 ATATTCGTCATGGTG 13

RESULT 19  
US-09-455-627-13/c  
; Sequence 13, Application US/09455627  
; Patent No. 6316436  
; GENERAL INFORMATION:

; APPLICANT: deSolms, S. Jane  
; APPLICANT: Shaw, Anthony W.  
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN  
; TITLE OF INVENTION: TRANSFERASE  
; FILE REFERENCE: 20325  
; CURRENT APPLICATION NUMBER: US/09/455,627  
; CURRENT FILING DATE: 1999-12-07  
; EARLIER APPLICATION NUMBER: US 60/111,621  
; EARLIER FILING DATE: 1998-12-08  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 13  
; LENGTH: 38  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: completely synthesized  
US-09-455-627-13

Query Match 51.4%; Score 14.4; DB 3; Length 38;  
Best Local Similarity 93.8%; Pred. No. 7.1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATATCCGTCATGGTG 26  
||| ||||| |||||  
Db 28 ATATCCGTCATGGTG 13

RESULT 20  
US-09-426-533-13/c  
; Sequence 13, Application US/09426533  
; Patent No. 6329376  
; GENERAL INFORMATION:  
; APPLICANT: Bergman, Jeffrey M.  
; TITLE OF INVENTION: Inhibitors Of Prenyl-Protein Transferase  
; FILE REFERENCE: 20289  
; CURRENT APPLICATION NUMBER: US/09/426,533  
; CURRENT FILING DATE: 1999-10-26  
; EARLIER APPLICATION NUMBER: 60/101,177  
; EARLIER FILING DATE: 1998-10-29  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 13  
; LENGTH: 38  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: completely synthesized  
US-09-426-533-13

Query Match 51.4%; Score 14.4; DB 3; Length 38;  
Best Local Similarity 93.8%; Pred. No. 7.1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATAGTCCGTCATGGTG 26  
||| ||||| |||||  
Db 28 ATATTCGTCATGGTG 13

RESULT 21  
US-09-609-205-14/c  
; Sequence 14, Application US/09609205  
; Patent No. 6333335  
; GENERAL INFORMATION:  
; APPLICANT: Merck & Co., Inc.  
; APPLICANT: Dinmore, Christopher J.  
; APPLICANT: Graham, Samuel L.  
; APPLICANT: Williams, Theresa M.  
; TITLE OF INVENTION: PRENYL-PROTEIN TRANSFERASE INHIBITORS  
; FILE REFERENCE: 20488  
; CURRENT APPLICATION NUMBER: US/09/609,205  
; CURRENT FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 60/145,331

Wed Nov 24 08:46:11 2004

us-10-087-631b-9.max.rni

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; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Nucleotide Sequence
US-09-757-218-14

Query Match      51.4%; Score 14.4; DB 3; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      11 ATAGTCCGTCATGGTG 26
      ||| ||||| ||||| |||||
Db      28 ATATTCGGTCATGGTG 13

RESULT 24
US-09-516-757-13/c
; Sequence 13, Application US/09516757
; Patent No. 6355643
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Lumma, William C. Jr.
; APPLICANT: Sisko, John T.
; APPLICANT: Smith, Anthony M.
; APPLICANT: Tucker, Thomas J.
; APPLICANT: Bergman, Jeffrey M.
; APPLICANT: Dinsmore, Christopher J.
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 20399Y
; CURRENT APPLICATION NUMBER: US/09/516,757
; CURRENT FILING DATE: 2000-03-01
; EARLIER APPLICATION NUMBER: 60/122,771
; EARLIER FILING DATE: 1998-03-03
; EARLIER APPLICATION NUMBER: 60/127,257
; EARLIER FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthetic sequence
US-09-516-757-13

Query Match      51.4%; Score 14.4; DB 3; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      11 ATAGTCCGTCATGGTG 26
      ||| ||||| ||||| |||||
Db      28 ATATTCGGTCATGGTG 13

RESULT 25
US-09-516-750-13/c
; Sequence 13, Application US/09516750
; Patent No. 6358956
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Hartman, George D.
; APPLICANT: Lumma, William C. Jr.
; APPLICANT: Sisko, John T.
; APPLICANT: Smith, Anthony M.
; APPLICANT: Stocker, Gerald E.
; APPLICANT: Tucker, Thomas J.
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 20393Y
; CURRENT APPLICATION NUMBER: US/09/516,750
; CURRENT FILING DATE: 2000-03-01
; EARLIER APPLICATION NUMBER: 60/122,768
; EARLIER FILING DATE: 1998-03-03
; SEQ ID NO 14

; PRIOR FILING DATE: 1999-07-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthetic sequence
US-09-609-205-14

Query Match      51.4%; Score 14.4; DB 3; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      11 ATAGTCCGTCATGGTG 26
      ||| ||||| ||||| |||||
Db      28 ATATTCGGTCATGGTG 13

RESULT 22
US-09-516-945-13/c
; Sequence 13, Application US/09516945
; Patent No. 6335343
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Lumma, William C. Jr.
; APPLICANT: Smith, Anthony M.
; APPLICANT: Sisko, John T.
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 20335Y
; CURRENT APPLICATION NUMBER: US/09/516,945
; CURRENT FILING DATE: 2000-03-01
; EARLIER APPLICATION NUMBER: 60/122,970
; EARLIER FILING DATE: 1998-03-03
; EARLIER APPLICATION NUMBER: 60/127,259
; EARLIER FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthetic sequence
US-09-516-945-13

Query Match      51.4%; Score 14.4; DB 3; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      11 ATAGTCCGTCATGGTG 26
      ||| ||||| ||||| |||||
Db      28 ATATTCGGTCATGGTG 13

RESULT 23
US-09-757-218-14/c
; Sequence 14, Application US/09757218
; Patent No. 6350755
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: S. Jane desolms
; APPLICANT: Anthony W. Shaw
; APPLICANT: Anthony W. Shaw
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 20613
; CURRENT APPLICATION NUMBER: US/09/757,218
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/175,703
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
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; EARLIER APPLICATION NUMBER: 60/127,253  
; EARLIER FILING DATE: 1999-03-31  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 38  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: completely synthetic sequence  
US-09-516-750-13

Query Match 51.4%; Score 14.4; DB 3; Length 38;  
Best Local Similarity 93.8%; Pred. No. 7.1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATAGTCGTCATGGTG 26  
Db 28 ATATTCGTCATGGTG 13

RESULT 26  
US-09-342-577-14/c  
; Sequence 14, Application US/09342577  
; Patent No. 6358985  
; GENERAL INFORMATION:  
; APPLICANT: Merck & Co., Inc.  
; APPLICANT: Anthony, Neville J.  
; APPLICANT: Bell, Ian M.  
; APPLICANT: Beshore, Douglas C.  
; APPLICANT: Ciccarone, Terrence M.  
; APPLICANT: desolms, S. Jane  
; APPLICANT: Dinsmore, Christopher J.  
; APPLICANT: Stokker, Gerald E.  
; TITLE OF INVENTION: INHIBITORS OF FARNESYL-PROTEIN  
; TITLE OF INVENTION: TRANSFERASE  
; FILE REFERENCE: 20275Y  
; CURRENT APPLICATION NUMBER: US/09/342,577  
; CURRENT FILING DATE: 1999-06-29  
; EARLIER APPLICATION NUMBER: 60/091,513  
; EARLIER FILING DATE: 1998-07-02  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 14  
; LENGTH: 38  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: completely synthetic sequence  
US-09-342-577-14

Query Match 51.4%; Score 14.4; DB 3; Length 38;  
Best Local Similarity 93.8%; Pred. No. 7.1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATAGTCGTCATGGTG 26  
Db 28 ATATTCGTCATGGTG 13

RESULT 27  
US-09-516-756-13/c  
; Sequence 13, Application US/09516756  
; Patent No. 6376496  
; GENERAL INFORMATION:  
; APPLICANT: Merck & Co., Inc.  
; APPLICANT: Hartman, George D.  
; APPLICANT: Lumma, William C. Jr.  
; APPLICANT: Sisko, John T.  
; APPLICANT: Smith, Anthony M.  
; APPLICANT: Tucker, Thomas J.  
; APPLICANT: Bergman, Jeffrey M.  
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE

; FILE REFERENCE: 20288Y  
; CURRENT APPLICATION NUMBER: US/09/516,756  
; CURRENT FILING DATE: 2000-03-01  
; EARLIER APPLICATION NUMBER: 60/122,968  
; EARLIER FILING DATE: 1998-03-03  
; EARLIER APPLICATION NUMBER: 60/127,132  
; EARLIER FILING DATE: 1999-03-31  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 38  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: completely synthetic sequence  
US-09-516-756-13

Query Match 51.4%; Score 14.4; DB 3; Length 38;  
Best Local Similarity 93.8%; Pred. No. 7.1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATAGTCGTCATGGTG 26  
Db 28 ATATTCGTCATGGTG 13

RESULT 28  
US-09-828-061A-14/c  
; Sequence 14, Application US/09828061A  
; Patent No. 6380228  
; GENERAL INFORMATION:  
; APPLICANT: Merck & Co., Inc.  
; APPLICANT: Craig A. Stump  
; APPLICANT: Theresa M. Williams  
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE  
; FILE REFERENCE: 20635Y  
; CURRENT APPLICATION NUMBER: US/09/828,061A  
; CURRENT FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/196,231  
; PRIOR FILING DATE: 2000-04-10  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 38  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sense Nucleotide Sequence  
US-09-828-061A-14

Query Match 51.4%; Score 14.4; DB 3; Length 38;  
Best Local Similarity 93.8%; Pred. No. 7.1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATAGTCGTCATGGTG 26  
Db 28 ATATTCGTCATGGTG 13

RESULT 29  
US-09-463-917-13/c  
; Sequence 13, Application US/09463917  
; Patent No. 6387903  
; GENERAL INFORMATION:  
; APPLICANT: Merck & Co., Inc.  
; APPLICANT: Dinsmore, Christopher J.  
; APPLICANT: Hutchinson, John H.  
; APPLICANT: Williams, Theresa M.  
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE  
; FILE REFERENCE: 20040Y  
; CURRENT APPLICATION NUMBER: US/09/463,917  
; CURRENT FILING DATE: 2000-02-01  
; PRIOR APPLICATION NUMBER: 60/057,080

us-10-087-631b-9.max.rni

Wed Nov 24 08:46:11 2004

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;
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Nucleotide Sequence
US-09-757-213-14
Query Match 51.4%; Score 14.4; DB 4; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 ATAGTCGTCATGGTG 26
   ||| ||||| ||||| |||||
Db 28 ATATCCGTCATGGTG 13

RESULT 32
US-09-656-653-13/c
; Sequence 13, Application US/09656653
; Patent No. 6441017
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Bell, Ian M.
; APPLICANT: Beshore, Douglas C.
; APPLICANT: Gallicchio, Steven N.
; APPLICANT: Zartman, C. Blair
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 20292Y
; CURRENT APPLICATION NUMBER: US/09/656,653
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/153,017
; PRIOR FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthesized
US-09-656-653-13
Query Match 51.4%; Score 14.4; DB 4; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 ATAGTCGTCATGGTG 26
   ||| ||||| ||||| |||||
Db 28 ATATCCGTCATGGTG 13

RESULT 33
US-09-757-251-14/c
; Sequence 14, Application US/09757251
; Patent No. 6525074
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: S. Jane deSolms
; APPLICANT: Suzanne C. MacTough
; APPLICANT: Anthony W. Shaw
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 20604Y
; CURRENT APPLICATION NUMBER: US/09/757,251
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/175,784
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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;
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthesized nucleotide sequence
US-09-463-917-13
Query Match 51.4%; Score 14.4; DB 3; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 ATAGTCGTCATGGTG 26
   ||| ||||| ||||| |||||
Db 28 ATATCCGTCATGGTG 13

RESULT 30
US-09-347-673-14/c
; Sequence 14, Application US/09347673
; Patent No. 6410534
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Dinmore, Christopher J.
; APPLICANT: Bell, Ian M.
; APPLICANT: Beshore, Douglas C.
; APPLICANT: Williams, Theresa M.
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 20236Y
; CURRENT APPLICATION NUMBER: US/09/347,673
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: 60/091,596
; EARLIER FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthetic sequence
US-09-347-673-14
Query Match 51.4%; Score 14.4; DB 4; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 ATAGTCGTCATGGTG 26
   ||| ||||| ||||| |||||
Db 28 ATATCCGTCATGGTG 13

RESULT 31
US-09-757-213-14/c
; Sequence 14, Application US/09757213
; Patent No. 6413964
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: S. Jane deSolms
; APPLICANT: Suzanne C. MacTough
; APPLICANT: Anthony W. Shaw
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 20605Y
; CURRENT APPLICATION NUMBER: US/09/757,213
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/175,708
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
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; OTHER INFORMATION: Artificial Nucleotide Sequence  
US-09-757-251-14

Query Match 51.4%; Score 14.4; DB 4; Length 38;  
Best Local Similarity 93.8%; Pred. No. 7.1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATAGTCGTCATGGTG 26  
||| |||||  
Db 28 ATATTCGTCATGGTG 13

## RESULT 34

US-09-828-259A-14/c  
; Sequence 14, Application US/09828259A

; Patent No. 6534506

; GENERAL INFORMATION:

; APPLICANT: Merck & Co., Inc.

; APPLICANT: Diem N. Nguyen

; APPLICANT: Theresa M. Williams

; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE

; FILE REFERENCE: 20637Y

; CURRENT APPLICATION NUMBER: US/09/828,259A

; CURRENT FILING DATE: 2001-04-09

; PRIOR APPLICATION NUMBER: 60/195,951

; PRIOR FILING DATE: 2000-04-10

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 14

; LENGTH: 38

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Artificial Nucleotide Sequence

US-09-828-259A-14

Query Match 51.4%; Score 14.4; DB 4; Length 38;  
Best Local Similarity 93.8%; Pred. No. 7.1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATAGTCGTCATGGTG 26  
||| |||||  
Db 28 ATATTCGTCATGGTG 13

## RESULT 35

US-09-719-878-14/c

; Sequence 14, Application US/09719878

; Patent No. 6562823

; GENERAL INFORMATION:

; APPLICANT: Merck & Co., Inc.

; APPLICANT: Dinsmore, Christopher J.

; APPLICANT: Bergman, Jeffrey M.

; APPLICANT: Graham, Samuel L.

; APPLICANT: Nguyen, Diem N.

; APPLICANT: Stokker, Gerald E.

; APPLICANT: Williams, Theresa M.

; APPLICANT: Zartman, C. Blair

; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE

; FILE REFERENCE: 20205Y

; CURRENT APPLICATION NUMBER: US/09/719,878

; CURRENT FILING DATE: 1999-06-29

; PRIOR APPLICATION NUMBER: 60/091,629

; PRIOR FILING DATE: 1998-07-02

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 14

; LENGTH: 38

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: completely synthetic sequence

US-09-719-878-14

Query Match 51.4%; Score 14.4; DB 4; Length 38;  
Best Local Similarity 93.8%; Pred. No. 7.1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATAGTCGTCATGGTG 26  
||| |||||  
Db 28 ATATTCGTCATGGTG 13

## RESULT 36

US-09-757-217A-14/c

; Sequence 14, Application US/09757217A

; Patent No. 6566385

; GENERAL INFORMATION:

; APPLICANT: Merck & Co., Inc.

; APPLICANT: S. Jane deSolms

; APPLICANT: Gerald E. Stokker

; APPLICANT: Anthony W. Shaw

; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE

; FILE REFERENCE: 20603Y

; CURRENT APPLICATION NUMBER: US/09/757,217A

; CURRENT FILING DATE: 2001-06-25

; PRIOR APPLICATION NUMBER: 60/175,801

; PRIOR FILING DATE: 2000-01-12

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 14

; LENGTH: 38

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Artificial Nucleotide Sequence

US-09-757-217A-14

Query Match 51.4%; Score 14.4; DB 4; Length 38;  
Best Local Similarity 93.8%; Pred. No. 7.1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 ATAGTCGTCATGGTG 26  
||| |||||  
Db 28 ATATTCGTCATGGTG 13

## RESULT 37

US-09-828-325A-14/c

; Sequence 14, Application US/09828325A

; Patent No. 6610722

; GENERAL INFORMATION:

; APPLICANT: Merck & Co., Inc.

; APPLICANT: Craig A. Stump

; APPLICANT: Theresa M. Williams

; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE

; FILE REFERENCE: 20636Y

; CURRENT APPLICATION NUMBER: US/09/828,325A

; CURRENT FILING DATE: 2001-08-17

; PRIOR APPLICATION NUMBER: 60/196,244

; PRIOR FILING DATE: 2000-04-10

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 14

; LENGTH: 38

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic Sense Nucleotide Sequence

US-09-828-325A-14

Query Match 51.4%; Score 14.4; DB 4; Length 38;  
Best Local Similarity 93.8%; Pred. No. 7.1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

us-10-087-631b-9.max.rni

Wed Nov 24 08:46:11 2004

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;
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligo)
US-08-333-565-58

Query Match      50.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      7 TGGGATAGTCCGTCATGGT 25
      ||| ||||| ||||| |||||
Db      2 TGAGGTAGTCTGTCATGGT 20

RESULT 40
US-08-661-479-58
; Sequence 58, Application US/08661479
; Patent No. 5834209
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
; TITLE OF INVENTION: REGULATOR
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/661,479
; FILING DATE: 11-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 08/333,565
; FILING DATE: 31-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000700
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligo)
US-08-661-479-58

Query Match      50.7%; Score 14.2; DB 2; Length 20;
Best Local Similarity 84.2%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      7 TGGGATAGTCCGTCATGGT 25
      ||| ||||| ||||| |||||
Db      2 TGAGGTAGTCTGTCATGGT 20

Search completed: November 23, 2004, 22:26:55
Job time : 37.4045 secs
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;
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligo)
US-08-333-565-58

Query Match      51.4%; Score 14.4; DB 4; Length 38;
Best Local Similarity 93.8%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      11 ATAGTCCGTCATGGT 26
      ||| ||||| ||||| |||||
Db      28 ATATCCGTCATGGT 13

RESULT 39
US-08-333-565-58
; Sequence 58, Application US/08333565
; Patent No. 5622852
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
; TITLE OF INVENTION: REGULATOR
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/333,565
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000700
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
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;
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligo)
US-08-333-565-58

Query Match      50.7%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      7 TGGGATAGTCCGTCATGGT 25
      ||| ||||| ||||| |||||
Db      2 TGAGGTAGTCTGTCATGGT 20

RESULT 40
US-08-661-479-58
; Sequence 58, Application US/08661479
; Patent No. 5834209
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
; TITLE OF INVENTION: REGULATOR
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/661,479
; FILING DATE: 11-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 08/333,565
; FILING DATE: 31-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000700
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligo)
US-08-661-479-58

Query Match      50.7%; Score 14.2; DB 2; Length 20;
Best Local Similarity 84.2%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      7 TGGGATAGTCCGTCATGGT 25
      ||| ||||| ||||| |||||
Db      2 TGAGGTAGTCTGTCATGGT 20

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Job time : 37.4045 secs
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 18:47:33 ; Search time 131.296 Seconds  
(without alignments)  
1152.370 Million cell updates/sec

Title: US-10-087-631B-9

Perfect score: 28

Sequence: 1 cgttcgtgggtagtcgtagtggtt 28

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3627888 seqs, 2701811610 residues

Total number of hits satisfying chosen parameters: 1987578

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications NA:\*

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2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*  
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6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*  
14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*  
17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*  
18: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
19: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*  
20: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
21: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	28	14	US-10-087-631B-9
2	28	100.0	28	15	US-10-419-022-9
3	21	75.0	21	18	US-10-444-853A-208
4	21	75.0	21	18	US-10-444-853A-209
5	21	75.0	21	18	US-10-444-853A-210
c 6	21	75.0	21	18	US-10-444-853A-217
7	21	75.0	21	18	US-10-667-271-1465
8	21	75.0	21	18	US-10-667-271-1466
9	21	75.0	21	18	US-10-667-271-1467
c 10	21	75.0	21	18	US-10-667-271-1474
c 11	20	71.4	21	18	US-10-444-853A-216
c 12	20	71.4	21	18	US-10-667-271-1473

Sequence 161, App	13	19	67.9	21	18	US-10-444-853A-161	Sequence 161, App
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Sequence 1648, App	c 60	18	64.3	21	18	US-10-667-271-1648	Sequence 1648, App
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Sequence 1546, App	c 64	17	60.7	21	18	US-10-667-271-1546	Sequence 1546, App
Sequence 1592, App	c 65	17	60.7	21	18	US-10-667-271-1592	Sequence 1592, App
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Sequence 14, Appl	c 73	14.4	51.4	38	9	US-09-828-061A-14	Sequence 14, Appl
Sequence 14, Appl	c 74	14.4	51.4	38	9	US-09-757-251-14	Sequence 14, Appl
Sequence 13, Appl	c 75	14.4	51.4	38	9	US-09-784-897A-13	Sequence 13, Appl
Sequence 13, Appl	c 76	14.4	51.4	38	9	US-09-770-983-13	Sequence 13, Appl
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Sequence 14, Appl	c 78	14.4	51.4	38	9	US-09-757-217A-14	Sequence 14, Appl
Sequence 14, Appl	c 79	14.4	51.4	38	9	US-09-828-259A-14	Sequence 14, Appl
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C 86	14	50.0	21	18	US-10-667-271-1547	Sequence 1547, Ap	159	13	46.4	25	15	US-10-098-263B-122919	Sequence 122919,
C 87	14	50.0	21	18	US-10-667-271-1584	Sequence 1584, Ap	160	13	46.4	25	15	US-10-098-263B-122920	Sequence 122920,
C 88	14	50.0	21	18	US-10-667-271-1593	Sequence 1593, Ap	161	13	46.4	26	15	US-10-010-476-91	Sequence 91, Appl
C 89	14	50.0	21	18	US-10-667-271-1596	Sequence 1596, Ap	162	13	46.4	36	9	US-09-084-491A-13	Sequence 13, Appl
C 90	14	50.0	21	18	US-10-667-271-1605	Sequence 1605, Ap	163	13	46.4	36	9	US-09-084-491A-15	Sequence 15, Appl
C 91	14	50.0	21	18	US-10-667-271-1605	Sequence 1605, Ap	164	13	46.4	36	9	US-10-102-704-13	Sequence 13, Appl
C 92	13.8	49.3	25	15	US-10-215-112-721	Sequence 721, Appl	165	13	46.4	36	13	US-10-102-704-15	Sequence 15, Appl
C 93	13.8	49.3	25	15	US-10-098-263B-95814	Sequence 95814, A	166	13	46.4	36	13	US-10-057-951-13	Sequence 13, Appl
C 94	13.8	49.3	26	10	US-09-754-853A-640	Sequence 640, Appl	167	13	46.4	36	13	US-10-057-951-15	Sequence 15, Appl
C 95	13.6	48.6	20	9	US-10-436-782-30	Sequence 30, Appl	168	13	46.4	47	15	US-10-128-590-8	Sequence 8, Appl
C 96	13.6	48.6	20	9	US-09-790-417-182	Sequence 417, Appl	169	13	46.4	47	15	US-10-128-590-8	Sequence 8, Appl
C 97	13.6	48.6	20	10	US-09-780-863-44	Sequence 863, Ap	170	13	46.4	47	15	US-10-128-590-8	Sequence 8, Appl
C 98	13.6	48.6	21	18	US-10-786-720-2932	Sequence 2932, Ap	171	12.8	45.7	24	9	US-09-733-692A-44	Sequence 44, Appl
C 99	13.6	48.6	21	18	US-10-786-720-2934	Sequence 2934, Ap	172	12.8	45.7	25	15	US-10-098-263B-22676	Sequence 22676, A
C 100	13.6	48.6	21	18	US-10-786-720-2977	Sequence 2977, Ap	173	12.8	45.7	25	15	US-10-098-263B-29099	Sequence 29099, A
C 101	13.6	48.6	21	18	US-10-786-720-2979	Sequence 2979, Ap	174	12.8	45.7	25	15	US-10-098-263B-30292	Sequence 30292, A
C 102	13.6	48.6	21	18	US-10-786-720-3181	Sequence 3181, Ap	175	12.8	45.7	25	15	US-10-098-263B-31664	Sequence 31664, A
C 103	13.6	48.6	21	18	US-10-786-720-3183	Sequence 3183, Ap	176	12.8	45.7	25	15	US-10-098-263B-66649	Sequence 66649, A
C 104	13.6	48.6	21	18	US-10-786-720-3286	Sequence 3286, Ap	177	12.8	45.7	25	15	US-10-098-263B-66650	Sequence 66650, A
C 105	13.6	48.6	21	18	US-10-786-720-3286	Sequence 3286, Ap	178	12.8	45.7	25	15	US-10-098-263B-78471	Sequence 78471, A
C 106	13.6	48.6	25	15	US-10-098-263B-7349	Sequence 7349, Ap	179	12.8	45.7	25	15	US-10-098-263B-113338	Sequence 113338,
C 107	13.6	48.6	25	15	US-10-098-263B-32620	Sequence 32620, A	180	12.8	45.7	25	15	US-10-098-263B-116616	Sequence 116616,
C 108	13.6	48.6	25	15	US-10-098-263B-61422	Sequence 61422, A	181	12.8	45.7	25	15	US-10-098-263B-116616	Sequence 116616,
C 109	13.6	48.6	25	15	US-10-098-263B-127891	Sequence 127891, A	182	12.8	45.7	25	15	US-10-098-263B-116616	Sequence 116616,
C 110	13.6	48.6	25	16	US-10-204-889-1	Sequence 1, Appl	183	12.8	45.7	25	15	US-10-098-263B-116616	Sequence 116616,
C 111	13.6	48.6	25	17	US-10-829-430-1	Sequence 1, Appl	184	12.8	45.7	25	15	US-10-098-263B-116616	Sequence 116616,
C 112	13.6	48.6	27	9	US-09-789-054A-51	Sequence 51, Appl	185	12.8	45.7	25	15	US-10-098-263B-116616	Sequence 116616,
C 113	13.6	48.6	27	10	US-09-911-904-195	Sequence 195, Appl	186	12.8	45.7	25	15	US-10-098-263B-116616	Sequence 116616,
C 114	13.6	48.6	39	10	US-10-628-969-51	Sequence 51, Appl	187	12.8	45.7	25	15	US-10-098-263B-116616	Sequence 116616,
C 115	13.6	48.6	39	17	US-09-966-459A-30	Sequence 30, Appl	188	12.8	45.7	25	15	US-10-098-263B-116616	Sequence 116616,
C 116	13.6	48.6	42	14	US-10-323-413-30	Sequence 30, Appl	189	12.8	45.7	25	15	US-10-098-263B-116616	Sequence 116616,
C 117	13.6	48.6	42	15	US-10-044-692-272	Sequence 272, Appl	190	12.8	45.7	25	15	US-10-098-263B-116616	Sequence 116616,
C 118	13.6	48.6	42	15	US-10-044-692-272	Sequence 272, Appl	191	12.8	45.7	25	15	US-10-098-263B-116616	Sequence 116616,
C 119	13.6	48.6	42	15	US-10-325-810-505	Sequence 505, Appl	192	12.8	45.7	25	15	US-10-098-263B-116616	Sequence 116616,
C 120	13.6	48.6	50	15	US-10-322-360-184	Sequence 184, Appl	193	12.8	45.7	25	15	US-10-098-263B-116616	Sequence 116616,
C 121	13.4	47.9	25	15	US-10-098-263B-15203	Sequence 15203, A	194	12.8	45.7	25	15	US-10-098-263B-116616	Sequence 116616,
C 122	13.4	47.9	25	15	US-10-098-263B-15204	Sequence 15204, A	195	12.8	45.7	25	15	US-10-098-263B-116616	Sequence 116616,
C 123	13.4	47.9	25	15	US-10-098-263B-17049	Sequence 17049, A	196	12.8	45.7	25	15	US-10-098-263B-116616	Sequence 116616,
C 124	13.4	47.9	25	15	US-10-098-263B-42006	Sequence 42006, A	197	12.8	45.7	25	15	US-10-098-263B-116616	Sequence 116616,
C 125	13.4	47.9	31	9	US-10-098-263B-123733	Sequence 123733, A	198	12.8	45.7	25	15	US-10-098-263B-116616	Sequence 116616,
C 126	13.4	47.9	31	9	US-09-801-274-358	Sequence 358, Appl	199	12.8	45.7	25	15	US-10-098-263B-116616	Sequence 116616,
C 127	13.4	47.9	39	15	US-10-005-956-1495	Sequence 1495, Ap	200	12.8	45.7	25	15	US-10-098-263B-116616	Sequence 116616,
C 128	13.4	47.9	39	15	US-10-005-956-1505	Sequence 1505, Ap	201	12.8	45.7	25	15	US-10-098-263B-116616	Sequence 116616,
C 129	13.4	47.9	48	10	US-09-766-167-20	Sequence 20, Appl	202	12.8	45.7	25	15	US-10-098-263B-116616	Sequence 116616,
C 130	13.4	47.9	48	15	US-10-208-557-20	Sequence 20, Appl	203	12.8	45.7	25	15	US-10-098-263B-116616	Sequence 116616,
C 131	13.4	47.9	48	17	US-10-774-938-20	Sequence 20, Appl	204	12.8	45.7	25	15	US-10-098-263B-116616	Sequence 116616,
C 132	13.2	47.1	20	15	US-10-062-188-78	Sequence 40, Appl	205	12.8	45.7	25	15	US-10-098-263B-116616	Sequence 116616,
C 133	13.2	47.1	24	15	US-10-126-355-4	Sequence 4, Appl	206	12.8	45.7	25	15	US-10-098-263B-116616	Sequence 116616,
C 134	13.2	47.1	24	15	US-10-126-355-4	Sequence 4, Appl	207	12.8	45.7	25	15	US-10-098-263B-116616	Sequence 116616,
C 135	13.2	47.1	25	14	US-10-215-112-5488	Sequence 5488, Ap	208	12.6	45.0	21	18	US-10-786-720-2978	Sequence 2978, Ap
C 136	13.2	47.1	25	15	US-10-098-263B-52644	Sequence 52644, A	209	12.6	45.0	21	18	US-10-786-720-3182	Sequence 3182, Ap
C 137	13.2	47.1	25	15	US-10-098-263B-79603	Sequence 79603, A	210	12.6	45.0	21	18	US-10-786-720-3287	Sequence 3287, Ap
C 138	13.2	47.1	25	15	US-10-098-263B-116085	Sequence 116085, A	211	12.6	45.0	25	15	US-10-098-263B-6804	Sequence 6804, Ap
C 139	13.2	47.1	25	15	US-10-098-263B-116086	Sequence 116086, A	212	12.6	45.0	25	15	US-10-098-263B-6804	Sequence 6804, Ap
C 140	13.2	47.1	25	15	US-10-336-638-11	Sequence 11, Appl	213	12.6	45.0	25	15	US-10-098-263B-42667	Sequence 42667, A
C 141	13.2	47.1	39	17	US-10-018-245A-16	Sequence 16, Appl	214	12.6	45.0	25	15	US-10-098-263B-42668	Sequence 42668, A
C 142	13.2	47.1	45	14	US-10-111-069-37	Sequence 37, Appl	215	12.6	45.0	25	15	US-10-098-263B-113159	Sequence 113159,
C 143	13.2	47.1	50	16	US-10-220-373-27	Sequence 27, Appl	216	12.6	45.0	25	15	US-10-098-263B-126105	Sequence 126105,
C 144	13	46.4	23	17	US-10-168-533C-27	Sequence 27, Appl	217	12.6	45.0	25	16	US-10-098-263B-126106	Sequence 126106,
C 145	13	46.4	23	16	US-10-429-555-12	Sequence 12, Appl	218	12.6	45.0	25	16	US-10-250-823-20	Sequence 20, Appl
C 146	13	46.4	24	16	US-10-429-555-12	Sequence 12, Appl	219	12.6	45.0	25	17	US-10-775-169-708	Sequence 708, Appl
C 147	13	46.4	25	14	US-10-060-756A-2155	Sequence 2155, Ap	220	12.6	45.0	25	17	US-10-775-169-708	Sequence 708, Appl
C 148	13	46.4	25	14	US-10-060-756A-2156	Sequence 2156, Ap	221	12.6	45.0	30	14	US-10-133-934-11	Sequence 11, Appl
C 149	13	46.4	25	14	US-10-060-756A-2157	Sequence 2157, Ap	222	12.6	45.0	30	14	US-10-072-438-33	Sequence 33, Appl
C 150	13	46.4	25	14	US-10-060-756A-2158	Sequence 2158, Ap	223	12.6	45.0	30	14	US-10-105-697-11	Sequence 11, Appl
C 151	13	46.4	25	14	US-10-060-756A-2159	Sequence 2159, Ap	224	12.6	45.0	30	14	US-10-120-630-11	Sequence 11, Appl
C 152	13	46.4	25	14	US-10-060-756A-2160	Sequence 2160, Ap	225	12.6	45.0	30	14	US-10-137-765-25	Sequence 25, Appl
C 153	13	46.4	25	14	US-10-215-112-1607	Sequence 1607, Ap	226	12.6	45.0	30	14	US-10-146-337-45	Sequence 45, Appl
C 154	13	46.4	25	14	US-10-215-112-1607	Sequence 1607, Ap	227	12.6	45.0	30	14	US-10-154-671-11	Sequence 11, Appl
C 155	13	46.4	25	15	US-10-098-263B-22004	Sequence 22004, A	228	12.6	45.0	30	14	US-10-142-077-11	Sequence 11, Appl
C 156	13	46.4	25	15	US-10-098-263B-41172	Sequence 41172, A	229	12.6	45.0	30	14	US-10-236-508-19	Sequence 19, Appl
C 157	13	46.4	25	15	US-10-098-263B-102984	Sequence 102984, A	230	12.6	45.0	31	15	US-10-304-059-44	Sequence 44, Appl
C 158	13	46.4	25	15	US-10-098-263B-122283	Sequence 122283, A	231	12.6	45.0	39	9	US-10-797-941A-29	Sequence 29, Appl

C 232	12.6	45.0	41	9	US-09-811-094-34	Sequence 34, Appl	C 305	12.2	43.6	22	10	US-09-532-708-8	Sequence 8, Appl
C 233	12.6	45.0	41	9	US-09-810-644-34	Sequence 34, Appl	C 306	12.2	43.6	23	9	US-09-305-856B-110	Sequence 110, App
C 234	12.6	45.0	42	9	US-09-811-094-28	Sequence 28, Appl	C 307	12.2	43.6	23	15	US-10-247-159-110	Sequence 110, App
C 235	12.6	45.0	42	9	US-09-810-644-28	Sequence 28, Appl	308	12.2	43.6	24	15	US-10-052-578-74	Sequence 74, Appl
C 236	12.6	45.0	42	9	US-09-185-904A-28	Sequence 28, Appl	309	12.2	43.6	24	15	US-10-053-520-74	Sequence 74, Appl
C 237	12.6	45.0	42	16	US-10-437-708-63	Sequence 63, Appl	310	12.2	43.6	24	15	US-10-053-498B-74	Sequence 74, Appl
C 238	12.6	45.0	42	16	US-10-395-402-63	Sequence 63, Appl	C 311	12.2	43.6	24	16	US-10-269-021B-19	Sequence 19, Appl
C 239	12.6	45.0	45	10	US-09-824-438-4	Sequence 4, Appl	312	12.2	43.6	25	8	US-08-887-497A-52	Sequence 52, Appl
C 240	12.6	45.0	46	15	US-10-374-600-92	Sequence 92, Appl	C 313	12.2	43.6	25	14	US-10-136-427-52	Sequence 52, Appl
C 241	12.6	45.0	46	16	US-10-374-601-92	Sequence 92, Appl	C 314	12.2	43.6	25	15	US-10-098-263B-6990	Sequence 6990, App
C 242	12.6	45.0	47	16	US-10-349-143-1173	Sequence 1173, Ap	315	12.2	43.6	25	15	US-10-098-263B-26757	Sequence 26757, A
C 243	12.6	45.0	50	16	US-10-131-827-4735	Sequence 4735, Ap	316	12.2	43.6	25	15	US-10-098-263B-26758	Sequence 26758, A
C 244	12.4	44.3	25	14	US-10-215-112-847	Sequence 847, App	317	12.2	43.6	25	15	US-10-098-263B-43709	Sequence 43709, A
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C 271	12.4	44.3	40	16	US-10-411-066-59	Sequence 59, Appl	C 344	12.2	43.6	43	10	US-09-924-981-37	Sequence 37, Appl
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c 382	12	42.9	25	15	US-10-098-263B-108432	Sequence 108432, A	c 455	12	42.9	49	10	US-09-902-903-380	Sequence 380, App
c 383	12	42.9	25	15	US-10-098-263B-127892	Sequence 127892, A	c 456	12	42.9	49	10	US-09-903-749A-238	Sequence 238, App
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c 449	12	42.9	49	10	US-09-906-646-238	Sequence 238, App	c 522	12	42.9	49	10	US-09-903-806-238	Sequence 238, App
c 450	12	42.9	49	10	US-09-906-646-380	Sequence 380, App	c 523	12	42.9	49	10	US-09-903-806-380	Sequence 380, App

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C 526	12	42.9	49	10	US-09-904-838-238	Sequence 238, App	C 599	11.8	42.1	25	14	US-10-215-112-13215	Sequence 13215, A
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C 528	12	42.9	49	10	US-09-906-777-238	Sequence 238, App	601	11.8	42.1	25	15	US-10-098-263B-9557	Sequence 9557, Ap
C 529	12	42.9	49	10	US-09-906-777-380	Sequence 238, App	602	11.8	42.1	25	15	US-10-098-263B-9833	Sequence 9833, Ap
C 530	12	42.9	49	10	US-09-903-603A-238	Sequence 238, App	603	11.8	42.1	25	15	US-10-098-263B-12032	Sequence 12032, A
C 531	12	42.9	49	10	US-09-903-603A-380	Sequence 238, App	C 604	11.8	42.1	25	15	US-10-098-263B-17050	Sequence 17050, A
C 532	12	42.9	49	10	US-09-904-532-238	Sequence 238, App	C 605	11.8	42.1	25	15	US-10-098-263B-22305	Sequence 22305, A
C 533	12	42.9	49	10	US-09-904-532-380	Sequence 238, App	C 606	11.8	42.1	25	15	US-10-098-263B-32110	Sequence 32110, A
C 534	12	42.9	49	10	US-09-904-766-238	Sequence 238, App	C 607	11.8	42.1	25	15	US-10-098-263B-37829	Sequence 37829, A
C 535	12	42.9	49	10	US-09-904-766-380	Sequence 238, App	C 608	11.8	42.1	25	15	US-10-098-263B-38417	Sequence 38417, A
C 536	12	42.9	49	10	US-09-904-920A-238	Sequence 238, App	C 609	11.8	42.1	25	15	US-10-098-263B-39045	Sequence 39045, A
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C 554	12	42.9	49	15	US-10-299-976-238	Sequence 238, App	627	11.8	42.1	25	15	US-10-098-263B-105117	Sequence 105117, A
C 555	12	42.9	49	15	US-10-299-976-380	Sequence 238, App	628	11.8	42.1	25	15	US-10-098-263B-105743	Sequence 105743, A
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C 561	12	42.9	49	15	US-10-448-923-380	Sequence 238, App	634	11.8	42.1	25	17	US-10-723-361-13626	Sequence 13626, A
C 562	12	42.9	49	16	US-10-449-656-238	Sequence 238, App	635	11.8	42.1	25	17	US-10-723-361-13627	Sequence 13627, A
C 563	12	42.9	49	16	US-10-449-656-380	Sequence 238, App	636	11.8	42.1	25	17	US-10-723-361-13628	Sequence 13628, A
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C 565	12	42.9	49	16	US-10-448-713-380	Sequence 238, App	638	11.8	42.1	26	16	US-10-072-012-943	Sequence 943, App
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C 567	12	42.9	49	16	US-10-425-447-380	Sequence 238, App	640	11.8	42.1	28	15	US-10-157-899A-23	Sequence 23, Appli
C 568	12	42.9	49	17	US-10-215-371-238	Sequence 238, App	641	11.8	42.1	28	15	US-10-157-899A-24	Sequence 24, Appli
C 569	12	42.9	49	17	US-10-215-371-380	Sequence 238, App	642	11.8	42.1	28	15	US-10-157-305A-200	Sequence 200, App
C 570	12	42.9	49	17	US-10-771-187-238	Sequence 238, App	643	11.8	42.1	28	15	US-10-157-391-200	Sequence 200, App
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C 572	12	42.9	50	16	US-10-131-827-250	Sequence 238, App	645	11.8	42.1	28	15	US-10-157-302-200	Sequence 200, App
C 573	12	42.9	50	16	US-10-131-827-1030	Sequence 1030, Ap	646	11.8	42.1	28	15	US-10-157-215A-200	Sequence 200, App
C 574	12	42.9	50	16	US-10-131-827-2977	Sequence 2977, Ap	647	11.8	42.1	28	15	US-10-157-299-200	Sequence 200, App
C 575	12	42.9	50	16	US-10-131-827-3057	Sequence 3057, Ap	648	11.8	42.1	28	15	US-10-154-951B-200	Sequence 200, App
C 576	12	42.9	50	16	US-10-131-827-4763	Sequence 4763, Ap	649	11.8	42.1	28	15	US-10-156-831-200	Sequence 200, App
C 577	12	42.9	50	16	US-10-131-827-6474	Sequence 6474, Ap	650	11.8	42.1	28	15	US-10-157-147-200	Sequence 200, App
C 578	12	42.9	50	16	US-10-062-188-30	Sequence 6864, Ap	651	11.8	42.1	28	15	US-10-157-166-200	Sequence 200, App
C 579	12	42.9	50	16	US-10-062-188-30	Sequence 30, Appli	652	11.8	42.1	28	15	US-10-156-902-200	Sequence 200, App
C 580	11.8	42.1	17	10	US-09-740-332-1153	Sequence 1153, Ap	653	11.8	42.1	28	15	US-10-157-318-200	Sequence 200, App
C 581	11.8	42.1	17	10	US-09-740-332-3402	Sequence 3402, Ap	654	11.8	42.1	28	15	US-10-157-318-200	Sequence 200, App
C 582	11.8	42.1	17	10	US-09-817-879-1153	Sequence 1153, Ap	655	11.8	42.1	28	15	US-10-156-792A-200	Sequence 200, App
C 583	11.8	42.1	17	10	US-09-817-879-3402	Sequence 3402, Ap	656	11.8	42.1	28	15	US-10-157-811-200	Sequence 200, App
C 584	11.8	42.1	17	17	US-10-669-841-3746	Sequence 3746, Ap	657	11.8	42.1	28	15	US-10-157-073-200	Sequence 200, App
C 585	11.8	42.1	17	17	US-10-669-841-5995	Sequence 5995, Ap	658	11.8	42.1	28	15	US-10-157-073-200	Sequence 200, App
C 586	11.8	42.1	18	15	US-10-388-263-251	Sequence 251, App	659	11.8	42.1	28	15	US-10-157-106A-200	Sequence 200, App
C 587	11.8	42.1	20	9	US-09-735-368-6	Sequence 6, Appli	660	11.8	42.1	28	15	US-10-157-320A-200	Sequence 200, App
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C 589	11.8	42.1	21	10	US-09-374-046A-199	Sequence 199, App	662	11.8	42.1	28	15	US-10-157-171-200	Sequence 200, App
C 590	11.8	42.1	21	15	US-10-229-346-22	Sequence 22, Appli	663	11.8	42.1	28	15	US-10-157-317-200	Sequence 200, App
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C 594	11.8	42.1	25	8	US-08-647-444-7	Sequence 7, Appli	667	11.8	42.1	30	15	US-10-157-305A-202	Sequence 202, App
C 595	11.8	42.1	25	9	US-09-866-108-13626	Sequence 13626, A	668	11.8	42.1	30	15	US-10-157-391-202	Sequence 202, App
C 596	11.8	42.1	25	9	US-09-866-108-13627	Sequence 13627, A	669	11.8	42.1	30	15	US-10-272-865-26	Sequence 26, Appli

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670	11.8	42.1	30	15	US-10-157-096-202	Sequence 202, App	c 743	11.8	42.1	45	17	US-10-776-311-88	Sequence 88, Appl
671	11.8	42.1	30	15	US-10-157-302-202	Sequence 202, App	c 744	11.8	42.1	47	16	US-10-349-143-786	Sequence 786, App
672	11.8	42.1	30	15	US-10-157-202-202	Sequence 202, App	c 745	11.8	42.1	47	16	US-10-294-934-804	Sequence 804, App
673	11.8	42.1	30	15	US-10-157-215A-202	Sequence 202, App	c 746	11.8	42.1	50	9	US-09-909-496-6	Sequence 6, Appl
674	11.8	42.1	30	15	US-10-157-399-202	Sequence 202, App	c 747	11.8	42.1	50	9	US-09-909-496-6	Sequence 8, Appl
675	11.8	42.1	30	15	US-10-154-951B-202	Sequence 202, App	c 748	11.8	42.1	50	9	US-09-909-496-6	Sequence 10, Appl
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681	11.8	42.1	30	15	US-10-156-178-202	Sequence 202, App	c 754	11.8	42.1	50	13	US-10-103-002-11	Sequence 11, Appl
682	11.8	42.1	30	15	US-10-156-792A-202	Sequence 202, App	c 755	11.8	42.1	50	14	US-10-269-229-6	Sequence 6, Appl
683	11.8	42.1	30	15	US-10-157-213-202	Sequence 202, App	c 756	11.8	42.1	50	14	US-10-269-229-10	Sequence 10, Appl
684	11.8	42.1	30	15	US-10-156-811-202	Sequence 202, App	c 757	11.8	42.1	50	15	US-10-189-211-6	Sequence 6, Appl
685	11.8	42.1	30	15	US-10-157-073-202	Sequence 202, App	c 758	11.8	42.1	50	15	US-10-189-211-6	Sequence 8, Appl
686	11.8	42.1	30	15	US-10-157-106A-202	Sequence 202, App	c 759	11.8	42.1	50	15	US-10-438-151-6	Sequence 8, Appl
687	11.8	42.1	30	15	US-10-157-320A-202	Sequence 202, App	c 760	11.8	42.1	50	15	US-10-438-151-8	Sequence 10, Appl
688	11.8	42.1	30	15	US-10-157-418A-202	Sequence 202, App	c 761	11.8	42.1	50	15	US-10-438-151-10	Sequence 24, Appl
689	11.8	42.1	30	15	US-10-422-671-26	Sequence 26, Appl	c 762	11.8	42.1	50	16	US-10-177-029-24	Sequence 26, Appl
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691	11.8	42.1	30	15	US-10-157-491-202	Sequence 202, App	c 764	11.6	41.4	19	9	US-09-725-752A-11	Sequence 1394, Ap
692	11.8	42.1	30	16	US-10-157-317-202	Sequence 202, App	c 765	11.6	41.4	20	16	US-10-289-762-1394	Sequence 151, App
693	11.8	42.1	31	9	US-09-801-274-1702	Sequence 1702, Ap	c 766	11.6	41.4	20	16	US-10-037-417-151	Sequence 14, Appl
694	11.8	42.1	34	16	US-10-433-238-47	Sequence 47, Appl	c 767	11.6	41.4	21	15	US-10-380-931-14	Sequence 2803, Ap
695	11.8	42.1	36	15	US-10-267-074-6	Sequence 6, Appl	c 768	11.6	41.4	21	18	US-10-786-720-2803	Sequence 2804, Ap
696	11.8	42.1	36	15	US-10-274-638-12	Sequence 12, Appl	c 769	11.6	41.4	21	18	US-10-786-720-2804	Sequence 2805, Ap
697	11.8	42.1	36	15	US-10-418-183-70	Sequence 70, Appl	c 770	11.6	41.4	21	18	US-10-786-720-2805	Sequence 2935, Ap
698	11.8	42.1	36	15	US-10-418-183-346	Sequence 346, App	c 771	11.6	41.4	21	18	US-10-786-720-2935	Sequence 2965, Ap
699	11.8	42.1	37	9	US-09-939-581A-16	Sequence 16, Appl	c 772	11.6	41.4	21	18	US-10-786-720-2965	Sequence 2966, Ap
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701	11.8	42.1	37	17	US-10-287-913-108	Sequence 108, App	c 774	11.6	41.4	21	18	US-10-786-720-3013	Sequence 3013, Ap
702	11.8	42.1	37	17	US-10-628-969-61	Sequence 61, Appl	c 775	11.6	41.4	21	18	US-10-786-720-3014	Sequence 3014, Ap
703	11.8	42.1	38	9	US-09-770-967-16	Sequence 16, Appl	c 776	11.6	41.4	21	18	US-10-786-720-3015	Sequence 3015, Ap
704	11.8	42.1	38	9	US-09-858-369-16	Sequence 16, Appl	c 777	11.6	41.4	21	18	US-10-786-720-3015	Sequence 3184, Ap
705	11.8	42.1	38	9	US-09-819-522-16	Sequence 16, Appl	c 778	11.6	41.4	21	18	US-10-786-720-3184	Sequence 3256, Ap
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707	11.8	42.1	38	9	US-09-757-251-17	Sequence 17, Appl	c 780	11.6	41.4	21	18	US-10-786-720-3257	Sequence 3258, Ap
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709	11.8	42.1	38	9	US-09-770-983-16	Sequence 16, Appl	c 782	11.6	41.4	22	15	US-10-325-403-27	Sequence 196, App
710	11.8	42.1	38	9	US-09-828-325A-17	Sequence 17, Appl	c 783	11.6	41.4	22	15	US-10-025-806-196	Sequence 27, Appl
711	11.8	42.1	38	9	US-09-757-217A-17	Sequence 17, Appl	c 784	11.6	41.4	22	16	US-10-325-403-27	Sequence 10, Appl
712	11.8	42.1	38	9	US-09-838-359A-17	Sequence 17, Appl	c 785	11.6	41.4	23	9	US-09-725-897-10	Sequence 48, Appl
713	11.8	42.1	38	9	US-09-784-818-16	Sequence 16, Appl	c 786	11.6	41.4	23	10	US-09-291-417-48	Sequence 10, Appl
714	11.8	42.1	38	10	US-09-756-248-16	Sequence 16, Appl	c 787	11.6	41.4	23	15	US-10-244-367-10	Sequence 18, Appl
715	11.8	42.1	38	11	US-09-828-317A-17	Sequence 17, Appl	c 788	11.6	41.4	23	15	US-10-143-897-18	Sequence 13, Appl
716	11.8	42.1	39	16	US-10-244-215-82	Sequence 82, Appl	c 789	11.6	41.4	23	16	US-10-311-129-13	Sequence 48, Appl
717	11.8	42.1	39	16	US-10-435-935-9	Sequence 9, Appl	c 790	11.6	41.4	23	18	US-10-725-329-48	Sequence 4555, Ap
718	11.8	42.1	40	16	US-10-411-066-76	Sequence 76, Appl	c 791	11.6	41.4	25	9	US-09-866-108-4555	Sequence 4556, Ap
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720	11.8	42.1	40	18	US-10-748-055-4	Sequence 4, Appl	c 793	11.6	41.4	25	9	US-09-866-108-4558	Sequence 4559, Ap
721	11.8	42.1	41	9	US-09-770-967-11	Sequence 11, Appl	c 794	11.6	41.4	25	9	US-09-866-108-4559	Sequence 4561, Ap
722	11.8	42.1	41	9	US-09-858-369-11	Sequence 11, Appl	c 795	11.6	41.4	25	9	US-09-866-108-4560	Sequence 4562, Ap
723	11.8	42.1	41	9	US-09-819-522-11	Sequence 11, Appl	c 796	11.6	41.4	25	9	US-09-866-108-4561	Sequence 4562, Ap
724	11.8	42.1	41	9	US-09-828-061A-12	Sequence 12, Appl	c 797	11.6	41.4	25	9	US-09-866-108-4562	Sequence 4562, Ap
725	11.8	42.1	41	9	US-09-757-251-12	Sequence 12, Appl	c 798	11.6	41.4	25	9	US-09-866-108-4562	Sequence 4562, Ap
726	11.8	42.1	41	9	US-09-784-897A-11	Sequence 11, Appl	c 799	11.6	41.4	25	14	US-10-215-112-1310	Sequence 4562, Ap
727	11.8	42.1	41	9	US-09-770-983-11	Sequence 11, Appl	c 800	11.6	41.4	25	14	US-10-215-112-1310	Sequence 4562, Ap
728	11.8	42.1	41	9	US-09-828-325A-12	Sequence 12, Appl	c 801	11.6	41.4	25	14	US-10-215-112-1310	Sequence 4562, Ap
729	11.8	42.1	41	9	US-09-757-217A-12	Sequence 12, Appl	c 802	11.6	41.4	25	14	US-10-215-112-1310	Sequence 4562, Ap
730	11.8	42.1	41	9	US-09-828-259A-12	Sequence 12, Appl	c 803	11.6	41.4	25	14	US-10-215-112-1310	Sequence 4562, Ap
731	11.8	42.1	41	9	US-09-925-664-66	Sequence 66, Appl	c 804	11.6	41.4	25	14	US-10-215-112-1310	Sequence 4562, Ap
732	11.8	42.1	41	9	US-09-784-818-11	Sequence 11, Appl	c 805	11.6	41.4	25	14	US-10-215-112-1310	Sequence 4562, Ap
733	11.8	42.1	41	10	US-09-756-248-11	Sequence 11, Appl	c 806	11.6	41.4	25	14	US-10-215-112-1310	Sequence 4562, Ap
734	11.8	42.1	41	11	US-09-925-192-66	Sequence 66, Appl	c 807	11.6	41.4	25	14	US-10-215-112-1310	Sequence 4562, Ap
735	11.8	42.1	41	11	US-09-828-317A-12	Sequence 12, Appl	c 808	11.6	41.4	25	14	US-10-215-112-1310	Sequence 4562, Ap
736	11.8	42.1	41	15	US-10-244-215-77	Sequence 77, Appl	c 809	11.6	41.4	25	14	US-10-215-112-1310	Sequence 4562, Ap
737	11.8	42.1	41	16	US-10-035-833A-1445	Sequence 1446, Ap	c 810	11.6	41.4	25	15	US-10-098-263B-1232	Sequence 1232, Ap
738	11.8	42.1	41	16	US-10-035-833A-3943	Sequence 3943, Ap	c 811	11.6	41.4	25	15	US-10-098-263B-1232	Sequence 1232, Ap
739	11.8	42.1	41	16	US-10-381-779-155	Sequence 155, App	c 812	11.6	41.4	25	15	US-10-098-263B-1232	Sequence 1232, Ap
740	11.8	42.1	42	13	US-10-001-051B-8	Sequence 8, Appl	c 813	11.6	41.4	25	15	US-10-098-263B-1232	Sequence 1232, Ap
741	11.8	42.1	45	15	US-10-060-793-21	Sequence 21, Appl	c 814	11.6	41.4	25	15	US-10-098-263B-1232	Sequence 1232, Ap
742	11.8	42.1	45	17	US-10-606-133-21	Sequence 21, Appl	c 815	11.6	41.4	25	15	US-10-098-263B-1232	Sequence 1232, Ap





## ALIGNMENTS

Qy 1 CGTTCGTGGATAGTCCGTCATGGTGT 28  
db 1 CGTTCGTGGATAGTCCGTCATGGTGT 28

RESULT 3  
US-10-444-853A-208  
; Sequence 208, Application US/10444853A  
; Publication No. US20040192626A1  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: Haerberli, Peter  
; APPLICANT: McSwiggen, James  
; APPLICANT: Beigelman, Leonid  
; APPLICANT: Macejak, Dennis  
; APPLICANT: Zinnen, Shawn  
; APPLICANT: Pavco, Pamela  
; APPLICANT: Morrissey, David  
; APPLICANT: Fosnaugh, Kathy  
; APPLICANT: Mokler, Victor  
; APPLICANT: Jamison, Sharon  
; APPLICANT: Vaish, Narendra  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using  
; TITLE OF INVENTION: Chemically Modified Short Interfering Nucleic Acid (siNA)  
; FILE REFERENCE: 400/114 (MBHB03-465)  
; CURRENT APPLICATION NUMBER: US/10/444,853A  
; CURRENT FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: US 10/417,012  
; PRIOR FILING DATE: 2003-04-16  
; PRIOR APPLICATION NUMBER: PCT/US03/05346  
; PRIOR FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: PCT/US03/05028  
; PRIOR FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: US 60/358,580  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: US 60/363,124  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: US 60/386,782  
; PRIOR FILING DATE: 2002-06-06  
; PRIOR APPLICATION NUMBER: US 60/406,784  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: US 60/408,378  
; PRIOR FILING DATE: 2002-09-05



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; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 208
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
US-10-444-853A-208

Query Match          75.0%; Score 21; DB 18; Length 21;
Best Local Similarity 66.7%; Pred. No. 8.5;
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GGGATAGTCGTCATGCGTGT 28
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Db 1 GGGGAUAGUCCGCAUGGUGU 21

RESULT 4
US-10-444-853A-209
; Sequence 209, Application US/10444853A
; Publication No. US20040192626A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Haerberli, Peter
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Macejak, Dennis
; APPLICANT: Zinnen, Shawn
; APPLICANT: Pavco, Pamela
; APPLICANT: Morrissey, David
; APPLICANT: Fossnaugh, Kathy
; APPLICANT: Mokler, Victor
; APPLICANT: Jamison, Sharon
; APPLICANT: Vaish, Narendra
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using
; FILE REFERENCE: 400/114 (MBHB03-465)
; CURRENT APPLICATION NUMBER: US/10/444,853A
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 209
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
US-10-444-853A-209

Query Match          75.0%; Score 21; DB 18; Length 21;
Best Local Similarity 66.7%; Pred. No. 8.5;
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GGGATAGTCGTCATGCGTGT 28
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Db 1 GGGGAUAGUCCGCAUGGUGU 21

RESULT 5
US-10-444-853A-210
; Sequence 210, Application US/10444853A
; Publication No. US20040192626A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Haerberli, Peter
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Macejak, Dennis
; APPLICANT: Zinnen, Shawn
; APPLICANT: Pavco, Pamela
; APPLICANT: Morrissey, David
; APPLICANT: Fossnaugh, Kathy
; APPLICANT: Mokler, Victor
; APPLICANT: Jamison, Sharon
; APPLICANT: Vaish, Narendra
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using
; FILE REFERENCE: 400/114 (MBHB03-465)
; CURRENT APPLICATION NUMBER: US/10/444,853A
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 210
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
US-10-444-853A-210

Query Match          75.0%; Score 21; DB 18; Length 21;
Best Local Similarity 71.4%; Pred. No. 8.5;
Matches 15; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GTGGGATAGTCGTCATGCGT 26
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Db 1 GUGGAUAGUCCGCAUGGUG 21
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
US-10-444-853A-209

Query Match          75.0%; Score 21; DB 18; Length 21;
Best Local Similarity 66.7%; Pred. No. 8.5;
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TGGGATAGTCGTCATGCGT 27
    |||||:||||:||||:|:|:|
Db 1 UGGGAUAGUCCGCAUGGUGU 21

RESULT 5
US-10-444-853A-210
; Sequence 210, Application US/10444853A
; Publication No. US20040192626A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Haerberli, Peter
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Macejak, Dennis
; APPLICANT: Zinnen, Shawn
; APPLICANT: Pavco, Pamela
; APPLICANT: Morrissey, David
; APPLICANT: Fossnaugh, Kathy
; APPLICANT: Mokler, Victor
; APPLICANT: Jamison, Sharon
; APPLICANT: Vaish, Narendra
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using
; FILE REFERENCE: 400/114 (MBHB03-465)
; CURRENT APPLICATION NUMBER: US/10/444,853A
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 210
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
US-10-444-853A-210

Query Match          75.0%; Score 21; DB 18; Length 21;
Best Local Similarity 71.4%; Pred. No. 8.5;
Matches 15; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GTGGGATAGTCGTCATGCGT 26
    |||||:||||:||||:|:|:|
Db 1 GUGGAUAGUCCGCAUGGUG 21
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us-10-087-631b-9.max.rnpb

Wed Nov 24 08:46:11 2004

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; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MEHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1465
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
; US-10-667-271-1465

Query Match 75.0%; Score 21; DB 18; Length 21;
Best Local Similarity 66.7%; Pred. No. 8.5;
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 8 GGGATAGTCGTCATGCTGTT 28
DB 1 GGGATAGTCGTCATGCTGTT 21

RESULT 8
US-10-667-271-1466
; Sequence 1466, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MEHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 217
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
; US-10-444-853A-217

Query Match 75.0%; Score 21; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GGGATAGTCGTCATGCTGTT 28
DB 21 GGGATAGTCGTCATGCTGTT 1

RESULT 7
US-10-667-271-1465
; Sequence 1465, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/114 (MEHB03-465)
; CURRENT APPLICATION NUMBER: US/10/444,853A
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/440,129
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 217
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
; US-10-444-853A-217

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;; PRIOR APPLICATION NUMBER: USSN 60/386,782  
;; PRIOR FILING DATE: 2002-06-06  
;; PRIOR APPLICATION NUMBER: USSN 60/406,784  
;; PRIOR FILING DATE: 2002-08-29  
;; PRIOR APPLICATION NUMBER: USSN 60/408,378  
;; PRIOR FILING DATE: 2002-09-05  
;; PRIOR APPLICATION NUMBER: USSN 60/409,293  
;; PRIOR FILING DATE: 2002-09-09  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 1705  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO 1466  
;; LENGTH: 21  
;; TYPE: RNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region  
US-10-667-271-1466

Query Match 75.0%; Score 21; DB 18; Length 21;  
Best Local Similarity 66.7%; Pred. No. 8.5;  
Matches 14; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TGGGATAGTCGTCATGCTGT 27  
:||||:||||:||||:||||:|  
Db 1 UGGGAUAGUCCGCAUGGUGU 21

RESULT 9  
US-10-667-271-1467  
; Sequence 1467, Application US/10667271  
; Publication No. US20040209831A1  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics  
; APPLICANT: McSwiggen, James  
; APPLICANT: Macejak, Dennis  
; APPLICANT: Beigelman, Leonid  
; APPLICANT: Morrissey, David  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)  
; FILE REFERENCE: 400/129 (WBH02-763B)  
; CURRENT APPLICATION NUMBER: US/10/667,271  
; CURRENT FILING DATE: 2003-09-16  
; PRIOR APPLICATION NUMBER: US 10/444,853  
; PRIOR FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: PCT / US03/05043  
; PRIOR FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: PCT / US02/09187  
; PRIOR FILING DATE: 2002-03-26  
; PRIOR APPLICATION NUMBER: USSN 60/401,104  
; PRIOR FILING DATE: 2002-08-05  
; PRIOR APPLICATION NUMBER: USSN 60/358,580  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: USSN 60/363,124  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: USSN 60/386,782  
; PRIOR FILING DATE: 2002-06-06  
; PRIOR APPLICATION NUMBER: USSN 60/406,784  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: USSN 60/408,378  
; PRIOR FILING DATE: 2002-09-05  
; PRIOR APPLICATION NUMBER: USSN 60/409,293  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1705  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1467  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region  
US-10-667-271-1467

Query Match 75.0%; Score 21; DB 18; Length 21;  
Best Local Similarity 71.4%; Pred. No. 8.5;  
Matches 15; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GTGGATAGTCGTCATGCTGTG 26  
:||||:||||:||||:||||:|  
Db 1 GUGGAUAGUCCGCAUGGUG 21

RESULT 10  
US-10-667-271-1474/c  
; Sequence 1474, Application US/10667271  
; Publication No. US20040209831A1  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics  
; APPLICANT: McSwiggen, James  
; APPLICANT: Macejak, Dennis  
; APPLICANT: Beigelman, Leonid  
; APPLICANT: Morrissey, David  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)  
; FILE REFERENCE: 400/129 (WBH02-763B)  
; CURRENT APPLICATION NUMBER: US/10/667,271  
; CURRENT FILING DATE: 2003-09-16  
; PRIOR APPLICATION NUMBER: US 10/444,853  
; PRIOR FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: PCT / US03/05043  
; PRIOR FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: PCT / US02/09187  
; PRIOR FILING DATE: 2002-03-26  
; PRIOR APPLICATION NUMBER: USSN 60/401,104  
; PRIOR FILING DATE: 2002-08-05  
; PRIOR APPLICATION NUMBER: USSN 60/358,580  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: USSN 60/363,124  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: USSN 60/386,782  
; PRIOR FILING DATE: 2002-06-06  
; PRIOR APPLICATION NUMBER: USSN 60/406,784  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: USSN 60/408,378  
; PRIOR FILING DATE: 2002-09-05  
; PRIOR APPLICATION NUMBER: USSN 60/409,293  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1705  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1474  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region  
US-10-667-271-1474

Query Match 75.0%; Score 21; DB 18; Length 21;  
Best Local Similarity 100.0%; Pred. No. 8.5;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GGGATAGTCGTCATGCTGTT 28  
:||||:||||:||||:||||:|  
Db 21 GGGATAGTCGTCATGCTGTT 1

RESULT 11  
US-10-444-853A-216/c  
; Sequence 216, Application US/10444853A  
; Publication No. US20040192626A1  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics, Inc.  
; APPLICANT: Haeblerli, Peter  
; APPLICANT: McSwiggen, James

```

; APPLICANT: Beigelman, Leonid
; APPLICANT: Macejak, Dennis
; APPLICANT: Zinnen, Shawn
; APPLICANT: Pavco, Pamela
; APPLICANT: Morrissey, David
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: Mokler, Victor
; APPLICANT: Jamison, Sharon
; APPLICANT: Vaish, Narendra
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using
; FILE REFERENCE: 400/114 (MEHB03-465)
; CURRENT APPLICATION NUMBER: US/10/444,853A
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 216
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-444-853A-216

Query Match 71.4%; Score 20; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGATAGTCGTCATGCTGTT 28
Db 21 GGATAGTCGTCATGCTGTT 2

RESULT 12
US-10-667-271-1473/c
; Sequence 1473, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Macejak, Dennis
; APPLICANT: Zinnen, Shawn
; APPLICANT: Pavco, Pamela
; APPLICANT: Morrissey, David
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: Mokler, Victor
; APPLICANT: Jamison, Sharon
; APPLICANT: Vaish, Narendra
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using
; FILE REFERENCE: 400/129 (MEHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
;
; APPLICANT: Beigelman, Leonid
; APPLICANT: Macejak, Dennis
; APPLICANT: Zinnen, Shawn
; APPLICANT: Pavco, Pamela
; APPLICANT: Morrissey, David
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: Mokler, Victor
; APPLICANT: Jamison, Sharon
; APPLICANT: Vaish, Narendra
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/114 (MEHB03-465)
; CURRENT APPLICATION NUMBER: US/10/444,853A
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 216
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-444-853A-216

Query Match 71.4%; Score 20; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGATAGTCGTCATGCTGTT 28
Db 21 GGATAGTCGTCATGCTGTT 2

RESULT 13
US-10-444-853A-161
; Sequence 161, Application US/10444853A
; Publication No. US20040192628A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Haeblerli, Peter
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Macejak, Dennis
; APPLICANT: Zinnen, Shawn
; APPLICANT: Pavco, Pamela
; APPLICANT: Morrissey, David
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: Mokler, Victor
; APPLICANT: Jamison, Sharon
; APPLICANT: Vaish, Narendra
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using
; FILE REFERENCE: 400/114 (MEHB03-465)
; CURRENT APPLICATION NUMBER: US/10/444,853A
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 216
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-444-853A-216
```

```
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 161
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: inverted control/siNA sense
; NAME/KEY: misc feature
; LOCATION: (1)-(2)
; OTHER INFORMATION: n stands for thymidine
US-10-444-853A-161

Query Match      67.9%; Score 19; DB 18; Length 21;
Best Local Similarity 73.7%; Pred. NO. 69;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GCGATAGTCGTCATGGTG 26
Db 3 GCGAUGUCCGUCGUAUGGUG 21
||||:||||:||||:||||:|

RESULT 14
US-10-444-853A-162
; Sequence 162, Application US/10444853A
; Publication No. US20040192626A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Haerberli, Peter
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Macejak, Dennis
; APPLICANT: Zinnen, Shawn
; APPLICANT: Pavco, Pamela
; APPLICANT: Morrissey, David
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: Mokler, Victor
; APPLICANT: Jamison, Sharon
; APPLICANT: Vaish, Nerendra
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using
; FILE REFERENCE: 400/114 (MEH803-465)
; CURRENT APPLICATION NUMBER: US/10/444,853A
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 161
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: inverted control/siNA sense
```

```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 162
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: inverted control/siNA sense
; NAME/KEY: misc feature
; LOCATION: (1)-(2)
; OTHER INFORMATION: n stands for thymidine
US-10-444-853A-162

Query Match      67.9%; Score 19; DB 18; Length 21;
Best Local Similarity 68.4%; Pred. NO. 69;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GCGATAGTCGTCATGGTGT 27
Db 3 GGAUAGUCCGUCGUAUGGUGU 21
||||:||||:||||:||||:|

RESULT 15
US-10-444-853A-163
; Sequence 163, Application US/10444853A
; Publication No. US20040192626A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Haerberli, Peter
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Macejak, Dennis
; APPLICANT: Zinnen, Shawn
; APPLICANT: Pavco, Pamela
; APPLICANT: Morrissey, David
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: Mokler, Victor
; APPLICANT: Jamison, Sharon
; APPLICANT: Vaish, Nerendra
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using
; FILE REFERENCE: 400/114 (MEH803-465)
; CURRENT APPLICATION NUMBER: US/10/444,853A
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 163
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: inverted control/siNA sense
```

Wed Nov 24 08:46:11 2004

us-10-087-631b-9.max.rnpb

Best Local Similarity 67.9%; Score 19; DB 18; Length 21;  
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;  
Query Match

FEATURE: NAME/KEY: misc\_feature  
LOCATION: (1)..(2)  
OTHER INFORMATION: n stands for thymidine  
US-10-444-853A-163

QY 10 GATAGTCGTCATGGTGT 28  
DB 3 GAUAGUCGUGGUGUU 21

RESULT 16  
US-10-444-853A-168/c  
Sequence 168, Application US/10444853A  
Publication No. US20040192626A1

GENERAL INFORMATION:

APPLICANT: Sirna Therapeutics, Inc.

APPLICANT: Haerberli, Peter

APPLICANT: McSwiggen, James

APPLICANT: Beigelman, Leonid

APPLICANT: Macejak, Dennis

APPLICANT: Zinnen, Shawn

APPLICANT: Pavco, Pamela

APPLICANT: Morrissey, David

APPLICANT: Fossnaugh, Kathy

APPLICANT: Mokier, Victor

APPLICANT: Jamison, Sharon

APPLICANT: Valsh, Nereandra

TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using

TITLE OF INVENTION: Chemically Modified Short Interfering Nucleic Acid (siNA)

FILE REFERENCE: 400/114 (MBHB03-465)

CURRENT APPLICATION NUMBER: US/10/444,853A

CURRENT FILING DATE: 2003-05-23

PRIOR APPLICATION NUMBER: US 10/417,012

PRIOR FILING DATE: 2003-04-16

PRIOR APPLICATION NUMBER: PCT/US03/05346

PRIOR FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: PCT/US03/05028

PRIOR FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: US 60/358,580

PRIOR FILING DATE: 2002-02-20

PRIOR APPLICATION NUMBER: US 60/363,124

PRIOR FILING DATE: 2002-03-11

PRIOR APPLICATION NUMBER: US 60/386,782

PRIOR FILING DATE: 2002-06-06

PRIOR APPLICATION NUMBER: US 60/406,784

PRIOR FILING DATE: 2002-08-29

PRIOR APPLICATION NUMBER: US 60/408,378

PRIOR FILING DATE: 2002-09-05

PRIOR APPLICATION NUMBER: US 60/409,293

PRIOR FILING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: US 60/440,129

PRIOR FILING DATE: 2003-01-15

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 626

SOFTWARE: Patentin version 3.2

SEQ ID NO 168

LENGTH: 21

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: inverted control/siNA antise

FEATURE:

NAME/KEY: misc feature

LOCATION: (1)..(2)

OTHER INFORMATION: n stands for thymidine

US-10-444-853A-168

Query Match

67.9%; Score 19; DB 18; Length 21;

Best Local Similarity 100.0%; Pred. No. 69;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 GGGATAGTCGTCATGGTG 26  
DB 21 GGGATAGTCGTCATGGTG 3

RESULT 17  
US-10-444-853A-169/c  
Sequence 169, Application US/10444853A  
Publication No. US20040192626A1

GENERAL INFORMATION:

APPLICANT: Sirna Therapeutics, Inc.

APPLICANT: Haerberli, Peter

APPLICANT: McSwiggen, James

APPLICANT: Beigelman, Leonid

APPLICANT: Macejak, Dennis

APPLICANT: Zinnen, Shawn

APPLICANT: Pavco, Pamela

APPLICANT: Morrissey, David

APPLICANT: Fossnaugh, Kathy

APPLICANT: Mokier, Victor

APPLICANT: Jamison, Sharon

APPLICANT: Valsh, Nereandra

TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using

TITLE OF INVENTION: Chemically Modified Short Interfering Nucleic Acid (siNA)

FILE REFERENCE: 400/114 (MBHB03-465)

CURRENT APPLICATION NUMBER: US/10/444,853A

CURRENT FILING DATE: 2003-05-23

PRIOR APPLICATION NUMBER: US 10/417,012

PRIOR FILING DATE: 2003-04-16

PRIOR APPLICATION NUMBER: PCT/US03/05346

PRIOR FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: PCT/US03/05028

PRIOR FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: US 60/358,580

PRIOR FILING DATE: 2002-02-20

PRIOR APPLICATION NUMBER: US 60/363,124

PRIOR FILING DATE: 2002-03-11

PRIOR APPLICATION NUMBER: US 60/386,782

PRIOR FILING DATE: 2002-06-06

PRIOR APPLICATION NUMBER: US 60/406,784

PRIOR FILING DATE: 2002-08-29

PRIOR APPLICATION NUMBER: US 60/408,378

PRIOR FILING DATE: 2002-09-05

PRIOR APPLICATION NUMBER: US 60/409,293

PRIOR FILING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: US 60/440,129

PRIOR FILING DATE: 2003-01-15

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 626

SOFTWARE: Patentin version 3.2

SEQ ID NO 169

LENGTH: 21

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: inverted control/siNA antise

FEATURE:

NAME/KEY: misc feature

LOCATION: (1)..(2)

OTHER INFORMATION: n stands for thymidine

US-10-444-853A-169

Query Match

67.9%; Score 19; DB 18; Length 21;

Best Local Similarity 100.0%; Pred. No. 69;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGGATAGTCGTCATGGTG 27

DB 21 GGGATAGTCGTCATGGTG 3

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RESULT 19
US-10-444-853A-170/c
; Sequence 170, Application US/10444853A
; Publication No. US20040192626A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Haerberli, Peter
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Macejak, Dennis
; APPLICANT: Zinnen, Shawn
; APPLICANT: Pavco, Pamela
; APPLICANT: Morrissey, David
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: Mokler, Victor
; APPLICANT: Jamison, Sharon
; APPLICANT: Vaish, Nerendra
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using
; FILE REFERENCE: 400/114 (MBHB03-465)
; CURRENT APPLICATION NUMBER: US/10/444,853A
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 170
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: n stands for thymidine
US-10-444-853A-170

Query Match 67.9%; Score 19; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 10 GATAGTCGTCATGGTGT 28
Db 21 GATAGTCGTCATGGTGT 3

RESULT 19
US-10-444-853A-215/c
; Sequence 215, Application US/10444853A
; Publication No. US20040192626A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Haerberli, Peter
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Macejak, Dennis
; APPLICANT: Zinnen, Shawn
; APPLICANT: Pavco, Pamela
; APPLICANT: Morrissey, David
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: Mokler, Victor
; APPLICANT: Jamison, Sharon
; APPLICANT: Vaish, Nerendra
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using
; FILE REFERENCE: 400/114 (MBHB03-465)
; CURRENT APPLICATION NUMBER: US/10/444,853A
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 170
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: n stands for thymidine
US-10-444-853A-170

Query Match 67.9%; Score 19; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 10 GATAGTCGTCATGGTGT 28
Db 21 GATAGTCGTCATGGTGT 3

RESULT 20
US-10-444-853A-477
; Sequence 477, Application US/10444853A
; Publication No. US20040192626A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Haerberli, Peter
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Macejak, Dennis
; APPLICANT: Zinnen, Shawn
; APPLICANT: Pavco, Pamela
; APPLICANT: Morrissey, David
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: Mokler, Victor
; APPLICANT: Jamison, Sharon
; APPLICANT: Vaish, Nerendra
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using
; FILE REFERENCE: 400/114 (MBHB03-465)
; CURRENT APPLICATION NUMBER: US/10/444,853A
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 215
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-444-853A-215

Query Match 67.9%; Score 19; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 10 GATAGTCGTCATGGTGT 28
Db 21 GATAGTCGTCATGGTGT 3

RESULT 20
US-10-444-853A-477
; Sequence 477, Application US/10444853A
; Publication No. US20040192626A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Haerberli, Peter
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Macejak, Dennis
; APPLICANT: Zinnen, Shawn
; APPLICANT: Pavco, Pamela
; APPLICANT: Morrissey, David
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: Mokler, Victor
; APPLICANT: Jamison, Sharon
; APPLICANT: Vaish, Nerendra
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1  
Db  
US-10-444-853A-478/c  
Sequence 478, Application US/10444853A  
Publication No. US20040192626A1  
GENERAL INFORMATION:  
APPLICANT: Sirna Therapeutics, Inc.  
APPLICANT: Haeblerli, Peter  
APPLICANT: McSwiggen, James  
APPLICANT: Beigelman, Leonid  
APPLICANT: Macejak, Dennis  
APPLICANT: Zinnen, Shawn  
APPLICANT: Pavco, Pamela  
APPLICANT: Morrissey, David  
APPLICANT: Fosnaugh, Kathy  
APPLICANT: Mokler, Victor  
APPLICANT: Jamison, Sharon  
APPLICANT: Vaish, Narendra  
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using  
FILE REFERENCE: 400/114 (MBHB03-465)  
CURRENT APPLICATION NUMBER: US/10/444,853A  
CURRENT FILING DATE: 2003-05-23  
PRIOR APPLICATION NUMBER: US 10/417,012  
PRIOR FILING DATE: 2003-04-16  
PRIOR APPLICATION NUMBER: PCT/US03/05346  
PRIOR FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: PCT/US03/05028  
PRIOR FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: US 60/358,580  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: US 60/363,124  
PRIOR FILING DATE: 2002-03-11  
PRIOR APPLICATION NUMBER: US 60/386,782  
PRIOR FILING DATE: 2002-06-06  
PRIOR APPLICATION NUMBER: US 60/406,784  
PRIOR FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: US 60/408,378  
PRIOR FILING DATE: 2002-09-05  
PRIOR APPLICATION NUMBER: US 60/409,293  
PRIOR FILING DATE: 2002-09-09  
PRIOR APPLICATION NUMBER: US 60/440,129  
PRIOR FILING DATE: 2003-01-15  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 626  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 477  
LENGTH: 21  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: siNA inverted control/siNA  
NAME/KEY: misc\_feature  
LOCATION: (1)..(1)  
OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (2)..(4)  
OTHER INFORMATION: 2'-O-methyl  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (6)..(6)  
OTHER INFORMATION: 2'-O-methyl  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (11)..(11)  
OTHER INFORMATION: 2'-O-methyl  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (14)..(16)  
OTHER INFORMATION: 2'-O-methyl  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (18)..(19)  
OTHER INFORMATION: 2'-O-methyl  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (20)..(21)  
OTHER INFORMATION: n stands for thymidine  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (21)..(21)  
OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety  
US-10-444-853A-477  
Query Match 67.9%; Score 19; DB 18; Length 21;  
Best Local Similarity 68.4%; Pred. No. 69;  
Matches 13; Conservative 0; Mismatches 0; Gaps 0;  
2 GTTCGTGGGATAGTCGTC 20

1  
Db  
US-10-444-853A-478/c  
Sequence 478, Application US/10444853A  
Publication No. US20040192626A1  
GENERAL INFORMATION:  
APPLICANT: Sirna Therapeutics, Inc.  
APPLICANT: Haeblerli, Peter  
APPLICANT: McSwiggen, James  
APPLICANT: Beigelman, Leonid  
APPLICANT: Macejak, Dennis  
APPLICANT: Zinnen, Shawn  
APPLICANT: Pavco, Pamela  
APPLICANT: Morrissey, David  
APPLICANT: Fosnaugh, Kathy  
APPLICANT: Mokler, Victor  
APPLICANT: Jamison, Sharon  
APPLICANT: Vaish, Narendra  
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using  
FILE REFERENCE: 400/114 (MBHB03-465)  
CURRENT APPLICATION NUMBER: US/10/444,853A  
CURRENT FILING DATE: 2003-05-23  
PRIOR APPLICATION NUMBER: US 10/417,012  
PRIOR FILING DATE: 2003-04-16  
PRIOR APPLICATION NUMBER: PCT/US03/05346  
PRIOR FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: PCT/US03/05028  
PRIOR FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: US 60/358,580  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: US 60/363,124  
PRIOR FILING DATE: 2002-03-11  
PRIOR APPLICATION NUMBER: US 60/386,782  
PRIOR FILING DATE: 2002-06-06  
PRIOR APPLICATION NUMBER: US 60/406,784  
PRIOR FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: US 60/408,378  
PRIOR FILING DATE: 2002-09-05  
PRIOR APPLICATION NUMBER: US 60/409,293  
PRIOR FILING DATE: 2002-09-09  
PRIOR APPLICATION NUMBER: US 60/440,129  
PRIOR FILING DATE: 2003-01-15  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 626  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 478  
LENGTH: 21  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: siNA inverted control/siNA  
NAME/KEY: misc\_feature  
LOCATION: (3)..(3)  
OTHER INFORMATION: 2'-O-methyl  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (7)..(8)  
OTHER INFORMATION: 2'-O-methyl  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (10)..(13)  
OTHER INFORMATION: 2'-O-methyl  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (15)..(15)  
OTHER INFORMATION: 2'-O-methyl  
FEATURE:  
NAME/KEY: misc\_feature

LOCATION: (19)..(19)  
OTHER INFORMATION: 2'-O-methyl  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (20)..(21)  
OTHER INFORMATION: n stands for thymidine  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (20)..(20)  
OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage  
US-10-444-853A-478

Query Match 67.9%; Score 19; DB 18; Length 21;  
Best Local Similarity 100.0%; Pred. No. 69;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTCGTGGGATAGTCGTC 20  
|||||  
Db 19 GTTCGTGGGATAGTCGTC 1

## RESULT 22

US-10-667-271-1439  
Sequence 1439, Application US/10667271  
Publication No. US20040209831A1  
GENERAL INFORMATION:  
APPLICANT: Sirna Therapeutics  
APPLICANT: McSwiggen, James  
APPLICANT: Macejak, Dennis  
APPLICANT: Beigelman, Leonid  
APPLICANT: Morrissey, David  
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)  
TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)  
FILE REFERENCE: 400/129 (MBHB02-763B)  
CURRENT APPLICATION NUMBER: US/10/667,271  
CURRENT FILING DATE: 2003-09-16  
PRIOR APPLICATION NUMBER: US 10/444,853  
PRIOR FILING DATE: 2003-05-23  
PRIOR APPLICATION NUMBER: PCT / US03/05043  
PRIOR FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: PCT / US02/09187  
PRIOR FILING DATE: 2002-03-26  
PRIOR APPLICATION NUMBER: USN 60/401,104  
PRIOR FILING DATE: 2002-08-05  
PRIOR APPLICATION NUMBER: USN 60/358,580  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: USN 60/363,124  
PRIOR FILING DATE: 2002-03-11  
PRIOR APPLICATION NUMBER: USN 60/386,782  
PRIOR FILING DATE: 2002-06-06  
PRIOR APPLICATION NUMBER: USN 60/406,784  
PRIOR FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: USN 60/408,378  
PRIOR FILING DATE: 2002-09-05  
PRIOR APPLICATION NUMBER: USN 60/409,293  
PRIOR FILING DATE: 2002-09-09  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 1705  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1439  
LENGTH: 21  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: siNA sense region  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(2)  
OTHER INFORMATION: n stands for thymidine  
US-10-667-271-1439

Query Match 67.9%; Score 19; DB 18; Length 21;  
Best Local Similarity 73.7%; Pred. No. 69;

Qy 2 GTTCGTGGGATAGTCGTC 20  
|||||  
Db 19 GTTCGTGGGATAGTCGTC 1

Query Match 67.9%; Score 19; DB 18; Length 21;  
Best Local Similarity 73.7%; Pred. No. 69;

Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
Qy 8 GGGATAGTCGTCATGGTG 26  
|||||  
Db 3 GGAUAGUCCGUAUGGUG 21

## RESULT 23

US-10-667-271-1440  
Sequence 1440, Application US/10667271  
Publication No. US20040209831A1  
GENERAL INFORMATION:  
APPLICANT: Sirna Therapeutics  
APPLICANT: McSwiggen, James  
APPLICANT: Macejak, Dennis  
APPLICANT: Beigelman, Leonid  
APPLICANT: Morrissey, David  
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)  
TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)  
FILE REFERENCE: 400/129 (MBHB02-763B)  
CURRENT APPLICATION NUMBER: US/10/667,271  
CURRENT FILING DATE: 2003-09-16  
PRIOR APPLICATION NUMBER: US 10/444,853  
PRIOR FILING DATE: 2003-05-23  
PRIOR APPLICATION NUMBER: PCT / US03/05043  
PRIOR FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: PCT / US02/09187  
PRIOR FILING DATE: 2002-03-26  
PRIOR APPLICATION NUMBER: USN 60/401,104  
PRIOR FILING DATE: 2002-08-05  
PRIOR APPLICATION NUMBER: USN 60/358,580  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: USN 60/363,124  
PRIOR FILING DATE: 2002-03-11  
PRIOR APPLICATION NUMBER: USN 60/386,782  
PRIOR FILING DATE: 2002-06-06  
PRIOR APPLICATION NUMBER: USN 60/406,784  
PRIOR FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: USN 60/408,378  
PRIOR FILING DATE: 2002-09-05  
PRIOR APPLICATION NUMBER: USN 60/409,293  
PRIOR FILING DATE: 2002-09-09  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 1705  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1440  
LENGTH: 21  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: siNA sense region  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(2)  
OTHER INFORMATION: n stands for thymidine  
US-10-667-271-1440

Query Match 67.9%; Score 19; DB 18; Length 21;  
Best Local Similarity 68.4%; Pred. No. 69;  
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GGATAGTCGTCATGGTGT 27  
|||||  
Db 3 GGAUAGUCCGUAUGGUG 21

## RESULT 24

US-10-667-271-1441  
Sequence 1441, Application US/10667271  
Publication No. US20040209831A1  
GENERAL INFORMATION:  
APPLICANT: Sirna Therapeutics  
APPLICANT: McSwiggen, James  
APPLICANT: Macejak, Dennis  
APPLICANT: Beigelman, Leonid  
APPLICANT: Morrissey, David  
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)  
TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)  
FILE REFERENCE: 400/129 (MBHB02-763B)  
CURRENT APPLICATION NUMBER: US/10/667,271  
CURRENT FILING DATE: 2003-09-16  
PRIOR APPLICATION NUMBER: US 10/444,853  
PRIOR FILING DATE: 2003-05-23  
PRIOR APPLICATION NUMBER: PCT / US03/05043  
PRIOR FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: PCT / US02/09187  
PRIOR FILING DATE: 2002-03-26  
PRIOR APPLICATION NUMBER: USN 60/401,104  
PRIOR FILING DATE: 2002-08-05  
PRIOR APPLICATION NUMBER: USN 60/358,580  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: USN 60/363,124  
PRIOR FILING DATE: 2002-03-11  
PRIOR APPLICATION NUMBER: USN 60/386,782  
PRIOR FILING DATE: 2002-06-06  
PRIOR APPLICATION NUMBER: USN 60/406,784  
PRIOR FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: USN 60/408,378  
PRIOR FILING DATE: 2002-09-05  
PRIOR APPLICATION NUMBER: USN 60/409,293  
PRIOR FILING DATE: 2002-09-09  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 1705  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1440  
LENGTH: 21  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: siNA sense region  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(2)  
OTHER INFORMATION: n stands for thymidine  
US-10-667-271-1440

Query Match 67.9%; Score 19; DB 18; Length 21;  
Best Local Similarity 68.4%; Pred. No. 69;  
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GGATAGTCGTCATGGTGT 27  
|||||  
Db 3 GGAUAGUCCGUAUGGUG 21

## RESULT 25

US-10-667-271-1441  
Sequence 1441, Application US/10667271  
Publication No. US20040209831A1  
GENERAL INFORMATION:  
APPLICANT: Sirna Therapeutics  
APPLICANT: McSwiggen, James  
APPLICANT: Macejak, Dennis  
APPLICANT: Beigelman, Leonid  
APPLICANT: Morrissey, David  
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)  
TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)  
FILE REFERENCE: 400/129 (MBHB02-763B)  
CURRENT APPLICATION NUMBER: US/10/667,271  
CURRENT FILING DATE: 2003-09-16  
PRIOR APPLICATION NUMBER: US 10/444,853  
PRIOR FILING DATE: 2003-05-23  
PRIOR APPLICATION NUMBER: PCT / US03/05043  
PRIOR FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: PCT / US02/09187  
PRIOR FILING DATE: 2002-03-26  
PRIOR APPLICATION NUMBER: USN 60/401,104  
PRIOR FILING DATE: 2002-08-05  
PRIOR APPLICATION NUMBER: USN 60/358,580  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: USN 60/363,124  
PRIOR FILING DATE: 2002-03-11  
PRIOR APPLICATION NUMBER: USN 60/386,782  
PRIOR FILING DATE: 2002-06-06  
PRIOR APPLICATION NUMBER: USN 60/406,784  
PRIOR FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: USN 60/408,378  
PRIOR FILING DATE: 2002-09-05  
PRIOR APPLICATION NUMBER: USN 60/409,293  
PRIOR FILING DATE: 2002-09-09  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 1705  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1441  
LENGTH: 21  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: siNA sense region  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(2)  
OTHER INFORMATION: n stands for thymidine  
US-10-667-271-1441

Query Match 67.9%; Score 19; DB 18; Length 21;  
Best Local Similarity 68.4%; Pred. No. 69;  
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GGATAGTCGTCATGGTGT 27  
|||||  
Db 3 GGAUAGUCCGUAUGGUG 21

## RESULT 26

US-10-667-271-1441  
Sequence 1441, Application US/10667271  
Publication No. US20040209831A1  
GENERAL INFORMATION:  
APPLICANT: Sirna Therapeutics  
APPLICANT: McSwiggen, James  
APPLICANT: Macejak, Dennis  
APPLICANT: Beigelman, Leonid  
APPLICANT: Morrissey, David  
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)  
TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)  
FILE REFERENCE: 400/129 (MBHB02-763B)  
CURRENT APPLICATION NUMBER: US/10/667,271  
CURRENT FILING DATE: 2003-09-16  
PRIOR APPLICATION NUMBER: US 10/444,853  
PRIOR FILING DATE: 2003-05-23  
PRIOR APPLICATION NUMBER: PCT / US03/05043  
PRIOR FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: PCT / US02/09187  
PRIOR FILING DATE: 2002-03-26  
PRIOR APPLICATION NUMBER: USN 60/401,104  
PRIOR FILING DATE: 2002-08-05  
PRIOR APPLICATION NUMBER: USN 60/358,580  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: USN 60/363,124  
PRIOR FILING DATE: 2002-03-11  
PRIOR APPLICATION NUMBER: USN 60/386,782  
PRIOR FILING DATE: 2002-06-06  
PRIOR APPLICATION NUMBER: USN 60/406,784  
PRIOR FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: USN 60/408,378  
PRIOR FILING DATE: 2002-09-05  
PRIOR APPLICATION NUMBER: USN 60/409,293  
PRIOR FILING DATE: 2002-09-09  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 1705  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1441  
LENGTH: 21  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: siNA sense region  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(2)  
OTHER INFORMATION: n stands for thymidine  
US-10-667-271-1441

Query Match 67.9%; Score 19; DB 18; Length 21;  
Best Local Similarity 73.7%; Pred. No. 69;

Wed Nov 24 08:46:11 2004

us-10-087-631b-9.max.rnpb

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; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/129 (MEHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1441
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: n stands for thymidine
US-10-667-271-1441

Query Match 67.9%; Score 19; DB 18; Length 21;
Best Local Similarity 63.2%; Pred. No. 69;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 10 GATAGTCGCGTCATGTTT 28
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3 GAUAGUCCGCAUGGUGUU 21

Db 3 GAUAGUCCGCAUGGUGUU 21

RESULT 25
US-10-667-271-1446/c
; Sequence 1446, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/129 (MEHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1441
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: n stands for thymidine
US-10-667-271-1441

Query Match 67.9%; Score 19; DB 18; Length 21;
Best Local Similarity 63.2%; Pred. No. 69;
Matches 12; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 10 GATAGTCGCGTCATGTTT 28
|||:||||:||||:||||:
3 GAUAGUCCGCAUGGUGUU 21

Db 3 GAUAGUCCGCAUGGUGUU 21

RESULT 26
US-10-667-271-1447/c
; Sequence 1447, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/129 (MEHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1446
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: n stands for thymidine
US-10-667-271-1446

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; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 1705  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1447

; LENGTH: 21

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: sRNA antisense region

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)..(2)

; OTHER INFORMATION: n stands for thymidine

US-10-667-271-1447

Query Match 67.9%; Score 19; DB 18; Length 21;

Best Local Similarity 100.0%; Pred. No. 69;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GGATAGTCCGTCATGGTGT 27

Db 21 GGATAGTCCGTCATGGTGT 3  
|||||

#### RESULT 27

US-10-667-271-1448/c

; Sequence 1448, Application US/10667271

; Publication No. US20040209831A1

; GENERAL INFORMATION:

; APPLICANT: Sirna Therapeutics

; APPLICANT: McSwiggen, James

; APPLICANT: Macejak, Dennis

; APPLICANT: Beigelman, Leonid

; APPLICANT: Morrissey, David

; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)

; FILE REFERENCE: 400/129 (MBHB02-763B)

; CURRENT FILING DATE: 2003-09-16

; PRIOR APPLICATION NUMBER: US/10/667,271

; PRIOR FILING DATE: 2003-09-16

; PRIOR APPLICATION NUMBER: US 10/444,853

; PRIOR FILING DATE: 2003-05-23

; PRIOR APPLICATION NUMBER: PCT / US03/05043

; PRIOR FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: PCT / US02/09187

; PRIOR FILING DATE: 2002-03-26

; PRIOR APPLICATION NUMBER: USSN 60/401,104

; PRIOR FILING DATE: 2002-08-05

; PRIOR APPLICATION NUMBER: USSN 60/358,580

; PRIOR FILING DATE: 2002-02-20

; PRIOR APPLICATION NUMBER: USSN 60/363,124

; PRIOR FILING DATE: 2002-03-11

; PRIOR APPLICATION NUMBER: USSN 60/386,782

; PRIOR FILING DATE: 2002-06-06

; PRIOR APPLICATION NUMBER: USSN 60/406,784

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: USSN 60/408,378

; PRIOR FILING DATE: 2002-09-05

; PRIOR APPLICATION NUMBER: USSN 60/409,293

; PRIOR FILING DATE: 2002-09-09

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 1705

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1448

; LENGTH: 21

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: sRNA antisense region

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)..(2)

; OTHER INFORMATION: n stands for thymidine

US-10-667-271-1448

Query Match

Best Local Similarity 67.9%; Score 19; DB 18; Length 21;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GATAGTCCGTCATGGTGT 28

Db 21 GATAGTCCGTCATGGTGT 3  
|||||

#### RESULT 28

US-10-667-271-1472/c

; Sequence 1472, Application US/10667271

; Publication No. US20040209831A1

; GENERAL INFORMATION:

; APPLICANT: Sirna Therapeutics

; APPLICANT: McSwiggen, James

; APPLICANT: Macejak, Dennis

; APPLICANT: Beigelman, Leonid

; APPLICANT: Morrissey, David

; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)

; FILE REFERENCE: 400/129 (MBHB02-763B)

; CURRENT APPLICATION NUMBER: US/10/667,271

; CURRENT FILING DATE: 2003-09-16

; PRIOR APPLICATION NUMBER: US 10/444,853

; PRIOR FILING DATE: 2003-05-23

; PRIOR APPLICATION NUMBER: PCT / US03/05043

; PRIOR FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: PCT / US02/09187

; PRIOR FILING DATE: 2002-03-26

; PRIOR APPLICATION NUMBER: USSN 60/401,104

; PRIOR FILING DATE: 2002-08-05

; PRIOR APPLICATION NUMBER: USSN 60/358,580

; PRIOR FILING DATE: 2002-02-20

; PRIOR APPLICATION NUMBER: USSN 60/363,124

; PRIOR FILING DATE: 2002-03-11

; PRIOR APPLICATION NUMBER: USSN 60/386,782

; PRIOR FILING DATE: 2002-06-06

; PRIOR APPLICATION NUMBER: USSN 60/406,784

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: USSN 60/408,378

; PRIOR FILING DATE: 2002-09-05

; PRIOR APPLICATION NUMBER: USSN 60/409,293

; PRIOR FILING DATE: 2002-09-09

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 1705

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1472

; LENGTH: 21

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: sRNA antisense region

US-10-667-271-1472

Query Match

Best Local Similarity 67.9%; Score 19; DB 18; Length 21;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GATAGTCCGTCATGGTGT 28

Db 21 GATAGTCCGTCATGGTGT 3  
|||||

#### RESULT 29

US-10-667-271-1528

; Sequence 1528, Application US/10667271

; Publication No. US20040209831A1

; GENERAL INFORMATION:

; APPLICANT: Sirna Therapeutics

; APPLICANT: McSwiggen, James

; APPLICANT: Macejak, Dennis

```

; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1528
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)..(5)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6)..(6)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)..(8)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)..(11)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12)..(12)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15)..(15)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1528
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)..(5)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6)..(6)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)..(8)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)..(11)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12)..(12)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15)..(15)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:

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; NAME/KEY: misc_feature
; LOCATION: (16)..(16)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (17)..(18)
; OTHER INFORMATION: 2'-deoxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety
; US-10-667-271-1528
Query Match 67.9%; Score 19; DB 18; Length 21;
Best Local Similarity 68.4%; Pred. No. 69;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
Qy 7 TGGGATAGTCCGTCATGGT 25
Db 1 UGGGAUAGUCCGUAUGGU 19
:||||:||||:||||:
:||||:||||:||||:
RESULT 30
US-10-667-271-1529
; Sequence 1529, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1529
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:

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OTHER INFORMATION: Description of Artificial Sequence: sRNA sense region

FEATURE: NAME/KEY: misc feature  
LOCATION: (1)..(1)  
OTHER INFORMATION: 2'-deoxy  
FEATURE: NAME/KEY: misc feature  
LOCATION: (1)..(1)  
OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety  
FEATURE: NAME/KEY: misc feature  
LOCATION: (2)..(2)  
OTHER INFORMATION: 2'-deoxy-2'-fluoro  
FEATURE: NAME/KEY: misc feature  
LOCATION: (3)..(6)  
OTHER INFORMATION: 2'-deoxy  
FEATURE: NAME/KEY: misc feature  
LOCATION: (7)..(7)  
OTHER INFORMATION: 2'-deoxy-2'-fluoro  
FEATURE: NAME/KEY: misc feature  
LOCATION: (8)..(9)  
OTHER INFORMATION: 2'-deoxy  
FEATURE: NAME/KEY: misc feature  
LOCATION: (10)..(12)  
OTHER INFORMATION: 2'-deoxy-2'-fluoro  
FEATURE: NAME/KEY: misc feature  
LOCATION: (13)..(13)  
OTHER INFORMATION: 2'-deoxy  
FEATURE: NAME/KEY: misc feature  
LOCATION: (14)..(15)  
OTHER INFORMATION: 2'-deoxy-2'-fluoro  
FEATURE: NAME/KEY: misc feature  
LOCATION: (16)..(16)  
OTHER INFORMATION: 2'-deoxy  
FEATURE: NAME/KEY: misc feature  
LOCATION: (17)..(17)  
OTHER INFORMATION: 2'-deoxy-2'-fluoro  
FEATURE: NAME/KEY: misc feature  
LOCATION: (17)..(17)  
OTHER INFORMATION: 2'-deoxy  
FEATURE: NAME/KEY: misc feature  
LOCATION: (18)..(19)  
OTHER INFORMATION: 2'-deoxy  
FEATURE: NAME/KEY: misc feature  
LOCATION: (20)..(21)  
OTHER INFORMATION: n stands for thymidine  
FEATURE: NAME/KEY: misc feature  
LOCATION: (21)..(21)  
OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety  
US-10-667-271-1529

Query Match 67.9%; Score 19; DB 18; Length 21;  
Best Local Similarity 73.7%; Pred No. 69;  
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GTGGGATAGTCGTCATCG 24  
|:||||:|:|:|:|:|:|:|:|:|  
Db 1 GUGGGAUAGUCGCAUGG 19

RESULT 31

US-10-667-271-1530  
; Sequence 1530, Application US/10667271  
; Publication No. US20040209831A1  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics  
; APPLICANT: McSwiggen, James  
; APPLICANT: Macejak, Dennis  
; APPLICANT: Beigelman, Leonid  
; APPLICANT: Morrissey, David  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)  
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)  
; FILE REFERENCE: 400/129 (MEH02-763B)  
; CURRENT APPLICATION NUMBER: US/10/667,271  
; CURRENT FILING DATE: 2003-09-16  
; PRIOR APPLICATION NUMBER: US 10/444,853  
; PRIOR FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: PCT / US03/05043  
; PRIOR FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: PCT / US02/09187  
; PRIOR FILING DATE: 2002-03-26  
; PRIOR APPLICATION NUMBER: USSN 60/401,104  
; PRIOR FILING DATE: 2002-08-05  
; PRIOR APPLICATION NUMBER: USSN 60/358,580  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: USSN 60/363,124  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: USSN 60/386,782  
; PRIOR FILING DATE: 2002-06-06  
; PRIOR APPLICATION NUMBER: USSN 60/406,784  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: USSN 60/408,378  
; PRIOR FILING DATE: 2002-09-05  
; PRIOR APPLICATION NUMBER: USSN 60/409,293  
; PRIOR FILING DATE: 2002-09-09  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1705  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1530  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: sRNA sense region  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: 2'-deoxy-2'-fluoro  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (2)..(2)  
; OTHER INFORMATION: 2'-deoxy  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (3)..(3)  
; OTHER INFORMATION: 2'-deoxy-2'-fluoro  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (4)..(7)  
; OTHER INFORMATION: 2'-deoxy  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (8)..(8)  
; OTHER INFORMATION: 2'-deoxy-2'-fluoro  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (9)..(10)  
; OTHER INFORMATION: 2'-deoxy  
; FEATURE:  
; NAME/KEY: misc feature

Wed Nov 24 08:46:11 2004

LOCATION: (11)..(13)  
OTHER INFORMATION: 2'-deoxy-2'-fluoro  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (14)..(14)  
OTHER INFORMATION: 2'-deoxy  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (15)..(16)  
OTHER INFORMATION: 2'-deoxy-2'-fluoro  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (17)..(17)  
OTHER INFORMATION: 2'-deoxy  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (18)..(18)  
OTHER INFORMATION: 2'-deoxy-2'-fluoro  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (19)..(19)  
OTHER INFORMATION: 2'-deoxy  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (20)..(21)  
OTHER INFORMATION: n stands for thymidine  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (21)..(21)  
OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety  
US-10-667-271-1530

Query Match 67.9%; Score 19; DB 18; Length 21;  
Best Local Similarity 73.7%; Pred. No. 69;  
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CGTGGGATAGTCCTCATG 23  
Db 1 CGUGGGAUAGUCCGUCAUG 19

RESULT 32  
US-10-667-271-1531  
Sequence 1531, Application US/10667271  
Publication No. US2004020983A1  
GENERAL INFORMATION:  
APPLICANT: Sirna Therapeutics  
APPLICANT: McSwiggen, James  
APPLICANT: Macejak, Dennis  
APPLICANT: Beigelman, Leonid  
APPLICANT: Morrissey, David  
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)  
FILE REFERENCE: 400/129 (MBH02-763B)  
CURRENT APPLICATION NUMBER: US/10/667.271  
CURRENT FILING DATE: 2003-09-16  
PRIOR APPLICATION NUMBER: US 10/444,853  
PRIOR FILING DATE: 2003-05-23  
PRIOR APPLICATION NUMBER: PCT / US03/05043  
PRIOR FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: PCT / US02/09187  
PRIOR FILING DATE: 2002-03-26  
PRIOR APPLICATION NUMBER: USSN 60/401,104  
PRIOR FILING DATE: 2002-08-05  
PRIOR APPLICATION NUMBER: USSN 60/358,580  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: USSN 60/363,124  
PRIOR FILING DATE: 2002-03-11  
PRIOR APPLICATION NUMBER: USSN 60/386,782  
PRIOR FILING DATE: 2002-06-06  
PRIOR APPLICATION NUMBER: USSN 60/406,784  
PRIOR FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: USSN 60/408,378

PRIOR FILING DATE: 2002-09-05  
PRIOR APPLICATION NUMBER: USSN 60/409,293  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 1705  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1531  
LENGTH: 21  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: siNA sense region  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(2)  
OTHER INFORMATION: 2'-deoxy-2'-fluoro  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(1)  
OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (3)..(3)  
OTHER INFORMATION: 2'-deoxy  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (4)..(4)  
OTHER INFORMATION: 2'-deoxy-2'-fluoro  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (5)..(8)  
OTHER INFORMATION: 2'-deoxy  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (9)..(9)  
OTHER INFORMATION: 2'-deoxy-2'-fluoro  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (10)..(11)  
OTHER INFORMATION: 2'-deoxy  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (12)..(14)  
OTHER INFORMATION: 2'-deoxy-2'-fluoro  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (15)..(15)  
OTHER INFORMATION: 2'-deoxy  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (16)..(17)  
OTHER INFORMATION: 2'-deoxy-2'-fluoro  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (18)..(18)  
OTHER INFORMATION: 2'-deoxy  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (19)..(19)  
OTHER INFORMATION: 2'-deoxy-2'-fluoro  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (20)..(21)  
OTHER INFORMATION: n stands for thymidine  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (21)..(21)  
OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety  
US-10-667-271-1531

Query Match 67.9%; Score 19; DB 18; Length 21;  
Best Local Similarity 68.4%; Pred. No. 69;  
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;



Qy 4 TCGTGGGATAGTCGGTAT 22  
:||||:||||:  
Db 1 UCGUGGGAUAGUCCGUCAU 19

## RESULT 33

US-10-667-271-1532  
; Sequence 1532, Application US/10667271  
; Publication No. US20040209831A1

## GENERAL INFORMATION:

; APPLICANT: Sirna Therapeutics  
; APPLICANT: McSwiggen, James  
; APPLICANT: Macejak, Dennis  
; APPLICANT: Beigelman, Leonid  
; APPLICANT: Morrissey, David

; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)  
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)

; FILE REFERENCE: 400/129 (MHB02-763B)

; CURRENT APPLICATION NUMBER: US/10/667,271

; PRIOR FILING DATE: 2003-09-16

; PRIOR APPLICATION NUMBER: US 10/444,853

; PRIOR FILING DATE: 2003-05-23

; PRIOR APPLICATION NUMBER: PCT / US03/05043

; PRIOR FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: PCT / US02/09187

; PRIOR FILING DATE: 2002-03-26

; PRIOR APPLICATION NUMBER: USSN 60/401,104

; PRIOR FILING DATE: 2002-08-05

; PRIOR APPLICATION NUMBER: USSN 60/358,580

; PRIOR FILING DATE: 2002-02-20

; PRIOR APPLICATION NUMBER: USSN 60/363,124

; PRIOR FILING DATE: 2002-03-11

; PRIOR APPLICATION NUMBER: USSN 60/386,782

; PRIOR FILING DATE: 2002-06-06

; PRIOR APPLICATION NUMBER: USSN 60/406,784

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: USSN 60/408,378

; PRIOR FILING DATE: 2002-09-05

; PRIOR APPLICATION NUMBER: USSN 60/409,293

; PRIOR FILING DATE: 2002-09-09

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 1705

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1532

; LENGTH: 21

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region

; NAME/KEY: misc feature

; LOCATION: (1)..(1)

; OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)..(1)

; OTHER INFORMATION: 2'-deoxy

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (2)..(4)  
; OTHER INFORMATION: 2'-deoxy-2'-fluoro

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (5)..(5)

; OTHER INFORMATION: 2'-deoxy

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (6)..(6)

; OTHER INFORMATION: 2'-deoxy-2'-fluoro

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (7)..(10)

; OTHER INFORMATION: 2'-deoxy  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (11)..(11)  
; OTHER INFORMATION: 2'-deoxy-2'-fluoro  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (12)..(13)  
; OTHER INFORMATION: 2'-deoxy  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (14)..(16)  
; OTHER INFORMATION: 2'-deoxy-2'-fluoro  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (17)..(17)  
; OTHER INFORMATION: 2'-deoxy  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (18)..(19)  
; OTHER INFORMATION: 2'-deoxy-2'-fluoro  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (20)..(21)  
; OTHER INFORMATION: n stands for thymidine  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (21)..(21)  
; OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety  
US-10-667-271-1532

Query Match 67.9%; Score 19; DB 18; Length 21;  
Best Local Similarity 68.4%; Pred. No. 69;  
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTCGCGGATAGTCGGTC 20

:||||:||||:||||:

Db 1 GUUCGUGGGAUAGUCCGUC 19

## RESULT 34

US-10-667-271-1533

; Sequence 1533, Application US/10667271

; Publication No. US20040209831A1

; GENERAL INFORMATION:

; APPLICANT: Sirna Therapeutics

; APPLICANT: McSwiggen, James

; APPLICANT: Macejak, Dennis

; APPLICANT: Beigelman, Leonid

; APPLICANT: Morrissey, David

; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)

; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)

; FILE REFERENCE: 400/129 (MHB02-763B)

; CURRENT APPLICATION NUMBER: US/10/667,271

; CURRENT FILING DATE: 2003-09-16

; PRIOR APPLICATION NUMBER: US 10/444,853

; PRIOR FILING DATE: 2003-05-23

; PRIOR APPLICATION NUMBER: PCT / US03/05043

; PRIOR FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: PCT / US02/09187

; PRIOR FILING DATE: 2002-03-26

; PRIOR APPLICATION NUMBER: USSN 60/401,104

; PRIOR FILING DATE: 2002-08-05

; PRIOR APPLICATION NUMBER: USSN 60/358,580

; PRIOR FILING DATE: 2002-02-20

; PRIOR APPLICATION NUMBER: USSN 60/363,124

; PRIOR FILING DATE: 2002-03-11

; PRIOR APPLICATION NUMBER: USSN 60/386,782

; PRIOR FILING DATE: 2002-06-06

; PRIOR APPLICATION NUMBER: USSN 60/406,784

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: USSN 60/408,378

; PRIOR FILING DATE: 2002-09-05

PRIOR APPLICATION NUMBER: USSN 60/409,293	
PRIOR FILING DATE: 2002-09-09	
Remaining Prior Application data removed - See File Wrapper or PALM.	
NUMBER OF SEQ ID NOS: 1705	
SOFTWARE: PatentIn version 3.2	
SEQ ID NO 1533	
LENGTH: 21	
TYPE: RNA	
ORGANISM: Artificial Sequence	
FEATURE:	
OTHER INFORMATION: Description of Artificial Sequence: siNA sense region	
FEATURE:	
NAME/KEY: misc.feature	
LOCATION: (1)..(1)	
OTHER INFORMATION: 2'-deoxy-2'-fluoro	
FEATURE:	
NAME/KEY: misc.feature	
LOCATION: (1)..(1)	
OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety	
FEATURE:	
NAME/KEY: misc.feature	
LOCATION: (2)..(2)	
OTHER INFORMATION: 2'-deoxy	
FEATURE:	
NAME/KEY: misc.feature	
LOCATION: (3)..(5)	
OTHER INFORMATION: 2'-deoxy-2'-fluoro	
FEATURE:	
NAME/KEY: misc.feature	
LOCATION: (7)..(7)	
OTHER INFORMATION: 2'-deoxy-2'-fluoro	
FEATURE:	
NAME/KEY: misc.feature	
LOCATION: (6)..(6)	
OTHER INFORMATION: 2'-deoxy	
FEATURE:	
NAME/KEY: misc.feature	
LOCATION: (8)..(11)	
OTHER INFORMATION: 2'-deoxy	
FEATURE:	
NAME/KEY: misc.feature	
LOCATION: (12)..(12)	
OTHER INFORMATION: 2'-deoxy-2'-fluoro	
FEATURE:	
NAME/KEY: misc.feature	
LOCATION: (13)..(14)	
OTHER INFORMATION: 2'-deoxy	
FEATURE:	
NAME/KEY: misc.feature	
LOCATION: (15)..(17)	
OTHER INFORMATION: 2'-deoxy-2'-fluoro	
FEATURE:	
NAME/KEY: misc.feature	
LOCATION: (18)..(18)	
OTHER INFORMATION: 2'-deoxy	
FEATURE:	
NAME/KEY: misc.feature	
LOCATION: (19)..(19)	
OTHER INFORMATION: 2'-deoxy-2'-fluoro	
FEATURE:	
NAME/KEY: misc.feature	
LOCATION: (20)..(21)	
OTHER INFORMATION: n stands for thymidine	
FEATURE:	
NAME/KEY: misc.feature	
LOCATION: (21)..(21)	
OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety	
US-10-667-271-1533	
Query Match	67.9%; Score 19; DB 18; Length 21;
Best Local Similarity	68.4%; Pred. No. 69;
Matches 13; Conservative	6; Mismatches 0; Indels 0; Gaps 0;

FEATURE: ;  
NAME/KEY: misc\_feature ;  
LOCATION: (9)..(11) ;  
OTHER INFORMATION: 2'-O-methyl ;  
FEATURE: ;  
NAME/KEY: misc\_feature ;  
LOCATION: (12)..(13) ;  
OTHER INFORMATION: 2'-deoxy-2'-fluoro ;  
FEATURE: ;  
NAME/KEY: misc\_feature ;  
LOCATION: (14)..(14) ;  
OTHER INFORMATION: 2'-O-methyl ;  
FEATURE: ;  
NAME/KEY: misc\_feature ;  
LOCATION: (15)..(18) ;  
OTHER INFORMATION: 2'-deoxy-2'-fluoro ;  
FEATURE: ;  
NAME/KEY: misc\_feature ;  
LOCATION: (19)..(19) ;  
OTHER INFORMATION: 2'-O-methyl ;  
FEATURE: ;  
NAME/KEY: misc\_feature ;  
LOCATION: (20)..(20) ;  
OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage ;  
FEATURE: ;  
NAME/KEY: misc\_feature ;  
LOCATION: (20)..(21) ;  
OTHER INFORMATION: n stands for thymidine ;  
US-10-667-271-1540

Query Match 67.9%; Score 19; DB 18; Length 21;  
Best Local Similarity 100.0%; Pred. No. 69;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TGGGATAGTCCTCATGGT 25  
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DB 19 TGGGATAGTCCTCATGGT 1

RESULT 36  
US-10-667-271-1541/c  
Sequence 1541, Application US/10667271  
Publication No. US20040209831A1  
GENERAL INFORMATION:  
APPLICANT: McSwiggen, James  
APPLICANT: Macejak, Dennis  
APPLICANT: Beigelman, Leonid  
APPLICANT: Morrissey, David  
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)  
FILE REFERENCE: 400/129 (MBH02-763B)  
CURRENT APPLICATION NUMBER: US/10/667,271  
CURRENT FILING DATE: 2003-09-16  
PRIOR APPLICATION NUMBER: US 10/444,853  
PRIOR FILING DATE: 2003-05-23  
PRIOR APPLICATION NUMBER: PCT / US03/05043  
PRIOR FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: PCT / US02/09187  
PRIOR FILING DATE: 2002-03-26  
PRIOR APPLICATION NUMBER: USSN 60/401,104  
PRIOR FILING DATE: 2002-08-05  
PRIOR APPLICATION NUMBER: USSN 60/358,580  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: USSN 60/363,124  
PRIOR FILING DATE: 2002-03-11  
PRIOR APPLICATION NUMBER: USSN 60/386,782  
PRIOR FILING DATE: 2002-06-06  
PRIOR APPLICATION NUMBER: USSN 60/406,784  
PRIOR FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: USSN 60/408,378  
PRIOR FILING DATE: 2002-09-05  
PRIOR APPLICATION NUMBER: USSN 60/409,293

PRIOR FILING DATE: 2002-09-09  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 1705  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1541  
LENGTH: 21  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE: ;  
OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region  
FEATURE: ;  
NAME/KEY: misc\_feature ;  
LOCATION: (1)..(2) ;  
OTHER INFORMATION: 2'-deoxy-2'-fluoro ;  
FEATURE: ;  
NAME/KEY: misc\_feature ;  
LOCATION: (3)..(3) ;  
OTHER INFORMATION: 2'-O-methyl ;  
FEATURE: ;  
NAME/KEY: misc\_feature ;  
LOCATION: (4)..(4) ;  
OTHER INFORMATION: 2'-deoxy-2'-fluoro ;  
FEATURE: ;  
NAME/KEY: misc\_feature ;  
LOCATION: (5)..(6) ;  
OTHER INFORMATION: 2'-O-methyl ;  
FEATURE: ;  
NAME/KEY: misc\_feature ;  
LOCATION: (7)..(7) ;  
OTHER INFORMATION: 2'-deoxy-2'-fluoro ;  
FEATURE: ;  
NAME/KEY: misc\_feature ;  
LOCATION: (8)..(10) ;  
OTHER INFORMATION: 2'-O-methyl ;  
FEATURE: ;  
NAME/KEY: misc\_feature ;  
LOCATION: (11)..(12) ;  
OTHER INFORMATION: 2'-deoxy-2'-fluoro ;  
FEATURE: ;  
NAME/KEY: misc\_feature ;  
LOCATION: (13)..(13) ;  
OTHER INFORMATION: 2'-O-methyl ;  
FEATURE: ;  
NAME/KEY: misc\_feature ;  
LOCATION: (14)..(17) ;  
OTHER INFORMATION: 2'-deoxy-2'-fluoro ;  
FEATURE: ;  
NAME/KEY: misc\_feature ;  
LOCATION: (18)..(18) ;  
OTHER INFORMATION: 2'-O-methyl ;  
FEATURE: ;  
NAME/KEY: misc\_feature ;  
LOCATION: (19)..(19) ;  
OTHER INFORMATION: 2'-deoxy-2'-fluoro ;  
FEATURE: ;  
NAME/KEY: misc\_feature ;  
LOCATION: (20)..(20) ;  
OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage  
FEATURE: ;  
NAME/KEY: misc\_feature ;  
LOCATION: (20)..(21) ;  
OTHER INFORMATION: n stands for thymidine ;  
US-10-667-271-1541

Query Match 67.9%; Score 19; DB 18; Length 21;  
Best Local Similarity 100.0%; Pred. No. 69;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 GTGGGATAGTCCTCATGG 24  
|||||  
DB 19 GTGGGATAGTCCTCATGG 1

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RESULT 37
US-10-667-271-1542/c
; Sequence 1542, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/129 (MEHB02-763B)
; CURRENT FILING DATE: 2003-09-16
; PRIOR FILING DATE: 2003-05-23
; PRIOR FILING DATE: 2003-02-20
; PRIOR FILING DATE: 2003-02-20
; PRIOR FILING DATE: 2002-03-26
; PRIOR FILING DATE: 2002-03-11
; PRIOR FILING DATE: 2002-08-05
; PRIOR FILING DATE: 2002-02-20
; PRIOR FILING DATE: 2002-06-06
; PRIOR FILING DATE: 2002-08-29
; PRIOR FILING DATE: 2002-09-05
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1542
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6)..(6)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)..(9)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(11)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12)..(12)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
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; NAME/KEY: misc_feature
; LOCATION: (13)..(16)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (17)..(17)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (18)..(18)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; US-10-667-271-1542
Query Match 67.9%; Score 19; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 COTGGGATAGTCCGTCATG 23
Db 19 COTGGGATAGTCCGTCATG 1
|||||||
RESULT 38
US-10-667-271-1543/c
; Sequence 1543, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/129 (MEHB02-763B)
; CURRENT FILING DATE: 2003-09-16
; PRIOR FILING DATE: 2003-09-16
; PRIOR FILING DATE: 2003-05-23
; PRIOR FILING DATE: 2003-05-23
; PRIOR FILING DATE: 2003-02-20
; PRIOR FILING DATE: 2003-02-20
; PRIOR FILING DATE: 2003-03-26
; PRIOR FILING DATE: 2002-03-26
; PRIOR FILING DATE: 2002-08-05
; PRIOR FILING DATE: 2002-08-05
; PRIOR FILING DATE: 2002-02-20
; PRIOR FILING DATE: 2002-03-11
; PRIOR FILING DATE: 2002-03-11
; PRIOR FILING DATE: 2002-06-06
; PRIOR FILING DATE: 2002-08-29
; PRIOR FILING DATE: 2002-09-05
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1543
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; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3)..(4)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6)..(8)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)..(10)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)..(11)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12)..(15)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16)..(16)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (17)..(17)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (18)..(19)
; OTHER INFORMATION: 2'-O-methyl
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
US-10-667-271-1543
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Query Match      67.9%; Score 19; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      4 TCGTGGGATAGTCCGTCAT 22
         |||||
Db      19 TCGTGGGATAGTCCGTCAT 1
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RESULT 39
US-10-667-271-1544/c
; Sequence 1544, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
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; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1544
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
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US-10-667-271-1544

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Best Local Similarity 100.0%; Pred.No. 69;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 19 GTTCGTGGGATAGTCGCTC 1

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; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
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; SOFTWARE: PatentIn version 3.2
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; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
US-10-667-271-1545

Query Match 67.9%; Score 19; DB 18; Length 21;
Best Local Similarity 100.0%; Pred.No. 69;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCGTGGGATAGTCGCT 19
Db 19 CGTTCGTGGGATAGTCGCT 1

Search completed: November 24, 2004, 03:43:09
Job time : 140.396 secs
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:59:28 ; Search time 1342.43 Seconds  
(without alignments)  
760.051 Million cell updates/sec

Title: US-10-087-631B-9

Perfect score: 28  
Sequence: 1 cgttcgtgggatagcgcgtcatgtgtt 28

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 158194

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : EST:\*

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gsl:\*  
9: gb\_gsl2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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us-10-087-631b-9-max.rst

Wed Nov 24 08:46:12 2004

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C 154	11.2	40.0	50	1	AU104318	1M0165E16	C 227	10.8	38.6	37	1	AI000163	os44d06.8
C 155	11.2	40.0	50	1	AU104318	1M0165E16	C 228	10.8	38.6	37	1	AI000163	os44d06.8
C 156	11.2	40.0	50	1	AU104318	1M0165E16	C 229	10.8	38.6	37	1	AI000163	os44d06.8
C 157	11.2	40.0	50	1	AU104318	1M0165E16	C 230	10.8	38.6	37	1	AI000163	os44d06.8
C 158	11.2	40.0	50	1	AU104318	1M0165E16	C 231	10.8	38.6	37	1	AI000163	os44d06.8
C 159	11.2	40.0	50	1	AU104318	1M0165E16	C 232	10.8	38.6	37	1	AI000163	os44d06.8
C 160	11.2	40.0	50	1	AU104318	1M0165E16	C 233	10.8	38.6	37	1	AI000163	os44d06.8
C 161	11.2	40.0	50	1	AU104318	1M0165E16	C 234	10.8	38.6	37	1	AI000163	os44d06.8
C 162	11.2	40.0	50	1	AU104318	1M0165E16	C 235	10.8	38.6	37	1	AI000163	os44d06.8
C 163	11.2	40.0	50	1	AU104318	1M0165E16	C 236	10.8	38.6	37	1	AI000163	os44d06.8
C 164	11.2	40.0	50	1	AU104318	1M0165E16	C 237	10.8	38.6	37	1	AI000163	os44d06.8
C 165	11.2	40.0	50	1	AU104318	1M0165E16	C 238	10.8	38.6	37	1	AI000163	os44d06.8
C 166	11.2	40.0	50	1	AU104318	1M0165E16	C 239	10.8	38.6	37	1	AI000163	os44d06.8
C 167	11.2	40.0	50	1	AU104318	1M0165E16	C 240	10.8	38.6	37	1	AI000163	os44d06.8
C 168	11.2	40.0	50	1	AU104318	1M0165E16	C 241	10.8	38.6	37	1	AI000163	os44d06.8
C 169	11.2	40.0	50	1	AU104318	1M0165E16	C 242	10.8	38.6	37	1	AI000163	os44d06.8
C 170	11.2	40.0	50	1	AU104318	1M0165E16	C 243	10.8	38.6	37	1	AI000163	os44d06.8

C 244	10.6	37.9	43	9	BX892893	BX892893 Arabidops	317	10.4	37.1	42	9	BX532481	BX532481 Arabidops
C 245	10.6	37.9	44	9	BX532319	BX532319 Arabidops	C 318	10.4	37.1	43	8	DNE545209	AJ545209 Drosophill
C 246	10.6	37.9	44	9	TA129804P	AL463981 T. brucei	C 319	10.4	37.1	43	8	AZ365276	1M011C24
C 247	10.6	37.9	45	1	AV961530	AV961530 Arabidops	C 320	10.4	37.1	43	9	BX661340	Arabidops
C 248	10.6	37.9	45	8	AZ385914	AZ385914 Arabidops	C 321	10.4	37.1	44	5	BX625656	BX625656
C 249	10.6	37.9	45	9	BX229715	BX229715 Arabidops	C 322	10.4	37.1	44	8	AZ340483	1M0072N19
C 250	10.6	37.9	45	9	AG202104	AG202104 Arabidops	C 323	10.4	37.1	44	8	AZ347569	1M00803P11
C 251	10.6	37.9	46	1	AI196568	AI196568 Arabidops	C 324	10.4	37.1	44	8	AZ628166	1M0480C12
C 252	10.6	37.9	46	1	AA389458	AA389458 Arabidops	C 325	10.4	37.1	44	8	CC199999	XH435 Bay
C 253	10.6	37.9	46	1	AZ429933	AZ429933 Arabidops	C 326	10.4	37.1	44	8	BX654077	Arabidops
C 254	10.6	37.9	46	9	AL760236	AL760236 Arabidops	C 327	10.4	37.1	45	1	AJ2339826	AJ2339826
C 255	10.6	37.9	46	9	CG805368	CG805368 Arabidops	C 328	10.4	37.1	45	8	AZ764357	1M0560G35
C 256	10.6	37.9	47	8	BH790193	BH790193 Arabidops	C 329	10.4	37.1	45	8	BH907586	SALK_0431
C 257	10.6	37.9	47	8	BZ663870	BZ663870 Arabidops	C 330	10.4	37.1	45	8	BZ596472	SALK_0431
C 258	10.6	37.9	47	9	AJ588138	AJ588138 Arabidops	C 331	10.4	37.1	45	9	CG728115	11190980
C 259	10.6	37.9	47	9	DR46K238	DR46K238 Arabidops	C 332	10.4	37.1	46	1	AA932841	oe57a07_s
C 260	10.6	37.9	47	9	CL302815	CL302815 Arabidops	C 333	10.4	37.1	46	1	AA991225	oe40e03_s
C 261	10.6	37.9	47	9	CL528024	CL528024 Arabidops	C 334	10.4	37.1	46	7	CO790652	NT010B_A0
C 262	10.6	37.9	48	1	AA501194	AA501194 Arabidops	C 335	10.4	37.1	46	9	BX003177	Arabidops
C 263	10.6	37.9	48	9	TA278009P	TA278009P Arabidops	C 336	10.4	37.1	46	9	CR397736	Arabidops
C 264	10.6	37.9	49	1	AI16542	AI16542 Arabidops	C 337	10.4	37.1	47	4	BG777442	602664745
C 265	10.6	37.9	49	1	AI883392	AI883392 Arabidops	C 338	10.4	37.1	47	6	CF293703	30DGS--02
C 266	10.6	37.9	49	2	BE914650	BE914650 Arabidops	C 339	10.4	37.1	47	8	BH903786	SALK_1033
C 267	10.6	37.9	49	8	AZ395400	AZ395400 Arabidops	C 340	10.4	37.1	47	9	BX130256	Danio rer
C 268	10.6	37.9	49	8	BH901678	BH901678 Arabidops	C 341	10.4	37.1	48	1	AV959231	AV959231
C 269	10.6	37.9	49	9	BX891921	BX891921 Arabidops	C 342	10.4	37.1	48	8	AZ412179	1M0185H06
C 270	10.6	37.9	50	1	AU102314	AU102314 Arabidops	C 343	10.4	37.1	48	8	AZ576812	01d05 Sho
C 271	10.6	37.9	50	1	AU102316	AU102316 Arabidops	C 344	10.4	37.1	48	8	BH792289	SALK_0633
C 272	10.6	37.9	50	1	AU102317	AU102317 Arabidops	C 345	10.4	37.1	48	8	CC459378	SALK_1279
C 273	10.6	37.9	50	1	AU102317	AU102317 Arabidops	C 346	10.4	37.1	48	9	AG197101	Pan trogl
C 274	10.6	37.9	50	1	AU102632	AU102632 Arabidops	C 347	10.4	37.1	49	1	AA934271	SWOVL3CAN
C 275	10.6	37.9	50	7	CN850182	CN850182 Arabidops	C 348	10.4	37.1	49	1	AL047237	DKFZP586N
C 276	10.6	37.9	50	8	AZ654289	AZ654289 Arabidops	C 349	10.4	37.1	49	5	BQ548140	rd20h05_Y
C 277	10.6	37.9	50	8	AZ931879	AZ931879 Arabidops	C 350	10.4	37.1	49	9	BX289417	Arabidops
C 278	10.6	37.9	50	8	CC456725	CC456725 Arabidops	C 351	10.4	37.1	49	9	BX531841	Arabidops
C 279	10.6	37.9	50	9	CL679776	CL679776 Arabidops	C 352	10.4	37.1	50	1	AU012341	AU012341
C 280	10.4	37.1	22	8	AZ854926	AZ854926 Arabidops	C 353	10.4	37.1	50	1	AU012398	AU012398
C 281	10.4	37.1	28	9	AZ450102	AZ450102 Arabidops	C 354	10.4	37.1	50	1	AU104771	AU104771
C 282	10.4	37.1	28	9	AG193662	AG193662 Arabidops	C 355	10.4	37.1	50	1	AU107570	AU107570
C 283	10.4	37.1	29	8	BH865195	BH865195 Arabidops	C 356	10.4	37.1	50	1	AU255974	AU255974
C 284	10.4	37.1	30	2	AW246919	AW246919 Arabidops	C 357	10.4	37.1	50	2	BF861971	963030H05
C 285	10.4	37.1	31	9	AL756692	AL756692 Arabidops	C 358	10.4	37.1	50	8	AZ592438	1M0403D22
C 286	10.4	37.1	32	8	AZ513719	AZ513719 Arabidops	C 359	10.4	37.1	50	9	AJ622111	Drosophill
C 287	10.4	37.1	33	8	AZ455934	AZ455934 Arabidops	C 360	10.4	37.1	50	9	AJ622124	Drosophill
C 288	10.4	37.1	33	8	AZ489295	AZ489295 Arabidops	C 361	10.4	37.1	50	9	AL947641	Arabidops
C 289	10.4	37.1	33	8	AZ662153	AZ662153 Arabidops	C 362	10.4	37.1	50	9	BX984033	Reverse s
C 290	10.4	37.1	33	8	BZ357116	BZ357116 Arabidops	C 363	10.4	37.1	50	9	CR404841	Arabidops
C 291	10.4	37.1	34	1	AI366127	AI366127 Arabidops	C 364	10.2	36.4	22	8	AZ647408	Arabidops
C 292	10.4	37.1	34	8	AZ624946	AZ624946 Arabidops	C 365	10.2	36.4	23	8	AZ780690	2M0018E06
C 293	10.4	37.1	35	8	BH902525	BH902525 Arabidops	C 366	10.2	36.4	23	9	TA372F07P	TA372F07P
C 294	10.4	37.1	35	9	AL768191	AL768191 Arabidops	C 367	10.2	36.4	24	8	AZ807089	2M0069003
C 295	10.4	37.1	35	9	AG193215	AG193215 Arabidops	C 368	10.2	36.4	24	8	AZ831914	2M0111L20
C 296	10.4	37.1	36	9	AG202742	AG202742 Arabidops	C 369	10.2	36.4	24	9	AG193817	Pan trogl
C 297	10.4	37.1	37	1	AA056316	AA056316 Arabidops	C 370	10.2	36.4	25	1	AI660931	wf2aall.x
C 298	10.4	37.1	37	7	T70764	T70764 Arabidops	C 371	10.2	36.4	25	8	AZ817189	2M0086E24
C 299	10.4	37.1	37	8	BH811969	BH811969 Arabidops	C 372	10.2	36.4	25	8	BH910108	SALK_0577
C 300	10.4	37.1	37	9	BX285355	BX285355 Arabidops	C 373	10.2	36.4	26	8	AZ387156	1M0146E19
C 301	10.4	37.1	37	9	DME546370	DME546370 Arabidops	C 374	10.2	36.4	26	8	AZ760876	1M0554J20
C 302	10.4	37.1	37	9	TA322H02Q	TA322H02Q Arabidops	C 375	10.2	36.4	26	8	BH910109	SALK_0577
C 303	10.4	37.1	37	9	TA58H04Q	TA58H04Q Arabidops	C 376	10.2	36.4	26	8	BH910398	SALK_0594
C 304	10.4	37.1	38	9	AG22374	AG22374 Arabidops	C 377	10.2	36.4	28	8	AZ628209	1M0480L12
C 305	10.4	37.1	39	1	AV851787	AV851787 Arabidops	C 378	10.2	36.4	29	8	AZ635260	1M0491E06
C 306	10.4	37.1	39	5	BX554651	BX554651 Arabidops	C 379	10.2	36.4	29	8	AZ831916	2M0135P09
C 307	10.4	37.1	39	8	AZ435630	AZ435630 Arabidops	C 380	10.2	36.4	30	9	CG717040	1119046G1
C 308	10.4	37.1	39	8	BH906658	BH906658 Arabidops	C 381	10.2	36.4	31	1	AI004493	ot57c08_s
C 309	10.4	37.1	39	9	TA65G07P	TA65G07P Arabidops	C 382	10.2	36.4	31	8	AQ254745	EP(3)3682
C 310	10.4	37.1	39	9	AG203895	AG203895 Arabidops	C 383	10.2	36.4	32	6	CF531013	09A03 Ara
C 311	10.4	37.1	40	1	AA911268	AA911268 Arabidops	C 384	10.2	36.4	32	6	CF329231	NACL--04
C 312	10.4	37.1	40	1	AZ226145	AZ226145 Arabidops	C 385	10.2	36.4	32	8	BH909978	SALK_0568
C 313	10.4	37.1	40	8	AZ784839	AZ784839 Arabidops	C 386	10.2	36.4	32	9	AL949878	Arabidops
C 314	10.4	37.1	41	8	CC182322	CC182322 Arabidops	C 387	10.2	36.4	33	1	AJ649239	AJ649239
C 315	10.4	37.1	42	8	CC050109	CC050109 Arabidops	C 388	10.2	36.4	33	5	BQ595597	E014690-0
C 316	10.4	37.1	42	9	AL947400	AL947400 Arabidops	C 389	10.2	36.4	34	1	AI798272	tr32e04.x

390	10.2	36.4	34	8	A2845465	A2845465	2M0145H18	463	10	35.7	19	8	AZ491592	AZ491592	IM0325F16
391	10.2	36.4	35	8	A2477231	A2477231	IM0296A11	464	10	35.7	21	6	AZ645644	AZ645644	IM0511N11
392	10.2	36.4	35	8	A2504484	A2504484	IM0344M18	C 465	10	35.7	19	6	CF281815	CF281815	14ETL--09
393	10.2	36.4	36	9	CT796901	CT796901	SALK 1442	C 466	10	35.7	22	8	AZ761328	AZ761328	IM0555A11
394	10.2	36.4	37	1	AA972483	AA972483	qp42d12.s	C 467	10	35.7	25	8	AZ345848	AZ345848	IM0080C16
395	10.2	36.4	37	1	AI185944	AI185944	qp29b02.s	C 468	10	35.7	25	8	AZ792292	AZ792292	IM0043H11
396	10.2	36.4	37	1	AV833316	AV833316	AV833316	C 469	10	35.7	26	8	BH610036	BH610036	KG00300.5
397	10.2	36.4	37	1	AV833316	AV833316	AV833316	C 470	10	35.7	26	8	TA95C11P	TA95C11P	T. brucei
398	10.2	36.4	38	8	AZ806056	AZ806056	IM0302F18	C 471	10	35.7	27	1	AZ603545	AZ603545	IM0422O19
399	10.2	36.4	38	8	AZ806456	AZ806456	IM0302F18	C 472	10	35.7	27	1	AI538375	AI538375	IM0422O19
400	10.2	36.4	40	1	AA133553	AA133553	zo14b11.r	C 473	10	35.7	28	8	AZ781477	AZ781477	IM0019H24
401	10.2	36.4	40	1	AA133553	AA133553	zo14b11.r	C 474	10	35.7	28	8	BH861588	BH861588	SALK 0875
402	10.2	36.4	40	7	R34628	R34628	YS7C12.r1	C 475	10	35.7	29	9	TA91B11P	TA91B11P	T. brucei
403	10.2	36.4	41	1	AG203784	AG203784	Pan trogl	C 476	10	35.7	31	1	AI793821	AI793821	IC54610.x
404	10.2	36.4	41	1	AG203784	AG203784	Pan trogl	C 477	10	35.7	31	1	AI793821	AI793821	IC54610.x
405	10.2	36.4	41	7	T98725	T98725	Y6G103.r1	C 478	10	35.7	32	6	CF291137	CF291137	14ROOT--0
406	10.2	36.4	41	8	CL639523	CL639523	Q009D01 G	C 479	10	35.7	32	6	CF291137	CF291137	14ROOT--0
407	10.2	36.4	42	9	CL639523	CL639523	Q009D01 G	C 480	10	35.7	32	8	AZ519233	AZ519233	IM0402F21
408	10.2	36.4	42	8	AZ427649	AZ427649	IM0209A15	C 481	10	35.7	32	8	AZ810628	AZ810628	IM0076H18
409	10.2	36.4	42	8	AZ993438	AZ993438	2M0278A04	C 482	10	35.7	33	8	AZ514079	AZ514079	IM0360P07
410	10.2	36.4	43	1	CG778648	CG778648	1123029F0	C 483	10	35.7	33	8	AZ841576	AZ841576	IM0360P07
411	10.2	36.4	43	1	AI663963	AI663963	u11507.r	C 484	10	35.7	34	1	AA929647	AA929647	VY81F07.r
412	10.2	36.4	43	8	AZ308202	AZ308202	IM0010R20	C 485	10	35.7	34	1	AI082825	AI082825	OX78B07.x
413	10.2	36.4	43	9	AG217315	AG217315	Drosophila	C 486	10	35.7	34	5	Q0586749	Q0586749	IM02389-0
414	10.2	36.4	43	9	AG217315	AG217315	Drosophila	C 487	10	35.7	34	7	CO784715	CO784715	BL281C.A0
415	10.2	36.4	44	1	AV952167	AV952167	AV952167	C 488	10	35.7	34	9	AJ598642	AJ598642	Arabidops
416	10.2	36.4	44	9	CL256331	CL256331	AB0029.Sa	C 489	10	35.7	34	9	AJ598642	AJ598642	Arabidops
417	10.2	36.4	44	9	CL256331	CL256331	AB0029.Sa	C 490	10	35.7	34	9	AJ598642	AJ598642	Arabidops
418	10.2	36.4	45	7	N48168	N48168	Yz02G09.s1	C 491	10	35.7	35	2	BE545364	BE545364	601078624
419	10.2	36.4	45	8	AZ371100	AZ371100	IM0122G06	C 492	10	35.7	35	8	AQ06431	AQ06431	ms(3) 0509
420	10.2	36.4	45	8	AZ513376	AZ513376	IM0359N23	C 493	10	35.7	35	8	AZ767704	AZ767704	IM0567B11
421	10.2	36.4	45	9	DM545559	DM545559	Arabidops	C 494	10	35.7	35	8	BZ661989	BZ661989	SALK 0254
422	10.2	36.4	45	9	TA372A04P	TA372A04P	Arabidops	C 495	10	35.7	35	8	BZ661989	BZ661989	SALK 0254
423	10.2	36.4	45	9	AA903958	AA903958	Arabidops	C 496	10	35.7	36	2	BE395465	BE395465	601309990
424	10.2	36.4	46	1	AA436017	AA436017	Arabidops	C 497	10	35.7	36	8	BZ287056	BZ287056	SALK 0204
425	10.2	36.4	46	8	AZ36017	AZ36017	Arabidops	C 498	10	35.7	36	8	CL528584	CL528584	ASV21E09.
426	10.2	36.4	46	8	AZ36017	AZ36017	Arabidops	C 499	10	35.7	36	8	CL528584	CL528584	ASV21E09.
427	10.2	36.4	46	8	AZ778033	AZ778033	2M0013D03	C 500	10	35.7	37	8	BH789296	BH789296	SALK 0016
428	10.2	36.4	46	9	AJ592635	AJ592635	Arabidops	C 501	10	35.7	37	8	BH789296	BH789296	SALK 0016
429	10.2	36.4	47	8	AZ624454	AZ624454	IM0463I10	C 502	10	35.7	38	2	BF663249	BF663249	602144367
430	10.2	36.4	47	8	AZ624454	AZ624454	IM0463I10	C 503	10	35.7	38	2	BF663249	BF663249	602144367
431	10.2	36.4	47	9	TA347C08Q	TA347C08Q	Arabidops	C 504	10	35.7	38	9	TA117B04P	TA117B04P	Arabidops
432	10.2	36.4	47	9	CL521062	CL521062	DAJ2H03.F	C 505	10	35.7	38	9	TA117B04P	TA117B04P	Arabidops
433	10.2	36.4	48	8	AZ818575	AZ818575	2M0088M10	C 506	10	35.7	39	8	AZ818545	AZ818545	2M0083B19
434	10.2	36.4	48	9	AJ587603	AJ587603	Arabidops	C 507	10	35.7	39	8	BZ665538	BZ665538	EY01063-3
435	10.2	36.4	48	9	AJ594944	AJ594944	Arabidops	C 508	10	35.7	39	8	CC060041	CC060041	EY00755-5
436	10.2	36.4	48	1	AA882475	AA882475	Arabidops	C 509	10	35.7	39	9	AJ943084	AJ943084	Arabidops
437	10.2	36.4	49	1	AA882475	AA882475	Arabidops	C 510	10	35.7	39	9	CG722883	CG722883	1119073H0
438	10.2	36.4	49	1	AI326039	AI326039	mr66C09.x	C 511	10	35.7	39	9	AG198386	AG198386	Pan trogl
439	10.2	36.4	49	1	AA140338	AA140338	Arabidops	C 512	10	35.7	40	1	AI538827	AI538827	tp61b08.x
440	10.2	36.4	49	5	BO101179	BO101179	i125a03.y	C 513	10	35.7	40	1	AA149946	AA149946	zo68f05.s
441	10.2	36.4	49	7	H14859	H14859	ym19c11.s1	C 514	10	35.7	40	1	AA149946	AA149946	zo68f05.s
442	10.2	36.4	49	7	W73879	W73879	zd68h10.s1	C 515	10	35.7	40	1	AA969419	AA969419	AV969419
443	10.2	36.4	49	8	AQ025828	AQ025828	1(2)10731	C 516	10	35.7	40	8	AA402839	AA402839	zu54c01.x
444	10.2	36.4	49	8	AQ025828	AQ025828	1(2)10731	C 517	10	35.7	40	8	AA402839	AA402839	zu54c01.x
445	10.2	36.4	49	8	AQ025828	AQ025828	1(2)10731	C 518	10	35.7	40	8	AA402839	AA402839	zu54c01.x
446	10.2	36.4	49	9	CG13615	CG13615	1119032F0	C 519	10	35.7	40	8	AA402839	AA402839	zu54c01.x
447	10.2	36.4	50	1	AJ672742	AJ672742	AJ672742	C 520	10	35.7	41	6	C00436	C00436	HUMGS00621
448	10.2	36.4	50	1	AJ672742	AJ672742	AJ672742	C 521	10	35.7	41	6	C00436	C00436	HUMGS00621
449	10.2	36.4	50	1	AJ672742	AJ672742	AJ672742	C 522	10	35.7	41	6	C00436	C00436	HUMGS00621
450	10.2	36.4	50	1	AJ672742	AJ672742	AJ672742	C 523	10	35.7	41	6	C00436	C00436	HUMGS00621
451	10.2	36.4	50	1	AJ672742	AJ672742	AJ672742	C 524	10	35.7	41	6	C00436	C00436	HUMGS00621
452	10.2	36.4	50	1	AJ672742	AJ672742	AJ672742	C 525	10	35.7	41	6	C00436	C00436	HUMGS00621
453	10.2	36.4	50	1	AJ672742	AJ672742	AJ672742	C 526	10	35.7	41	6	C00436	C00436	HUMGS00621
454	10.2	36.4	50	1	AJ672742	AJ672742	AJ672742	C 527	10	35.7	41	6	C00436	C00436	HUMGS00621
455	10.2	36.4	50	1	AJ672742	AJ672742	AJ672742	C 528	10	35.7	41	6	C00436	C00436	HUMGS00621
456	10.2	36.4	50	1	AJ672742	AJ672742	AJ672742	C 529	10	35.7	41	6	C00436	C00436	HUMGS00621
457	10.2	36.4	50	1	AJ672742	AJ672742	AJ672742	C 530	10	35.7	41	6	C00436	C00436	HUMGS00621
458	10.2	36.4	50	1	AJ672742	AJ672742	AJ672742	C 531	10	35.7	41	6	C00436	C00436	HUMGS00621
459	10.2	36.4	50	1	AJ672742	AJ672742	AJ672742	C 532	10	35.7	41	6	C00436	C00436	HUMGS00621
460	10.2	36.4	50	5	BX556043	BX556043	BX556043	C 533	10	35.7	42	9	AX532481	AX532481	Arabidops
461	10.2	36.4	50	5	BH412566	BH412566	1007027H1	C 534	10	35.7	42	9	AX532481	AX532481	Arabidops
462	10.2	36.4	50	9	BX949622	BX949622	Arabidops	C 535	10	35.7	43	1	AA903096	AA903096	OK46102.5

C 536	10	35.7	43	1	A1318513	A1318513	ta74d07.x	C 609	9.8	35.0	20	8	A2330662	A2330662	1M0056F15
C 537	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 610	9.8	35.0	21	8	AZ397567	AZ397567	1M0162C09
C 538	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 611	9.8	35.0	22	8	AU006620	AU006620	AU006620
C 539	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 612	9.8	35.0	22	1	AU006633	AU006633	AU006633
C 540	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 613	9.8	35.0	24	2	AU006633	AU006633	AU006633
C 541	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 614	9.8	35.0	24	8	A2505513	A2505513	A2505513
C 542	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 615	9.8	35.0	24	8	A2505513	A2505513	A2505513
C 543	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 616	9.8	35.0	25	8	A2505513	A2505513	A2505513
C 544	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 617	9.8	35.0	26	8	A2505513	A2505513	A2505513
C 545	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 618	9.8	35.0	26	8	A2505513	A2505513	A2505513
C 546	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 619	9.8	35.0	27	5	BQ588135	BQ588135	E012336-0
C 547	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 620	9.8	35.0	27	8	A2840144	A2840144	2M0136L03
C 548	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 621	9.8	35.0	28	8	BH903329	BH903329	SALK_1024
C 549	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 622	9.8	35.0	30	8	A2390145	A2390145	1M0151A24
C 550	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 623	9.8	35.0	30	8	A2390145	A2390145	1M0151A24
C 551	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 624	9.8	35.0	30	9	AL759156	AL759156	ArabiDops
C 552	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 625	9.8	35.0	31	9	DR19J3S	DR19J3S	Danio rer
C 553	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 626	9.8	35.0	31	1	AA935085	AA935085	ny3e09.s
C 554	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 627	9.8	35.0	31	1	AT120884	AT120884	ub73e03.r
C 555	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 628	9.8	35.0	31	8	A2598183	A2598183	1M0412A22
C 556	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 629	9.8	35.0	31	8	BH906192	BH906192	SALK_1094
C 557	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 630	9.8	35.0	31	8	BH906199	BH906199	SALK_1094
C 558	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 631	9.8	35.0	32	4	BG391939	BG391939	602409874
C 559	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 632	9.8	35.0	32	4	BM051667	BM051667	603638419
C 560	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 633	9.8	35.0	32	8	A2345674	A2345674	1M0080A03
C 561	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 634	9.8	35.0	32	9	CL692844	CL692844	PR1015a.F
C 562	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 635	9.8	35.0	33	8	AZ959267	AZ959267	2M0226D21
C 563	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 636	9.8	35.0	33	4	BH909395	BH909395	SALK_0533
C 564	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 637	9.8	35.0	34	1	AA961906	AA961906	or68D08.s
C 565	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 638	9.8	35.0	34	1	AL682978	AL682978	tw47h06.x
C 566	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 639	9.8	35.0	34	8	CC458626	CC458626	SALK_1214
C 567	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 640	9.8	35.0	34	9	CL437149	CL437149	PST4587-N
C 568	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 641	9.8	35.0	35	1	AV967387	AV967387	AV967387
C 569	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 642	9.8	35.0	35	2	BE782279	BE782279	601470033
C 570	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 643	9.8	35.0	35	6	CF298864	CF298864	7LEAF--02
C 571	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 644	9.8	35.0	35	8	BZ761423	BZ761423	SALK_0004
C 572	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 645	9.8	35.0	35	9	CK405374	CK405374	ArabiDops
C 573	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 646	9.8	35.0	36	1	AV851790	AV851790	AV851790
C 574	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 647	9.8	35.0	36	6	CD533247	CD533247	30M2 Arab
C 575	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 648	9.8	35.0	36	7	D44934	D44934	HUMSPY417
C 576	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 649	9.8	35.0	36	8	A2603547	A2603547	1M0422O21
C 577	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 650	9.8	35.0	36	9	AJ593292	AJ593292	ArabiDops
C 578	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 651	9.8	35.0	37	1	AA986717	AA986717	cy73e01.x
C 579	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 652	9.8	35.0	37	1	AI079739	AI079739	cy73e01.x
C 580	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 653	9.8	35.0	37	1	AA088913	AA088913	z169b11.s
C 581	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 654	9.8	35.0	37	6	CF337139	CF337139	JMT--07-H
C 582	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 655	9.8	35.0	37	9	AZ351733	AZ351733	1M0089K21
C 583	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 656	9.8	35.0	37	9	CC884512	CC884512	SALK_1134
C 584	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 657	9.8	35.0	38	8	BH812118	BH812118	SALK_0612
C 585	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 658	9.8	35.0	39	8	AZ825961	AZ825961	2M0101K20
C 586	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 659	9.8	35.0	39	8	CC057354	CC057354	SALK_1406
C 587	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 660	9.8	35.0	40	1	AA972469	AA972469	op42a04.s
C 588	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 661	9.8	35.0	40	1	AI970772	AI970772	wr13g04.x
C 589	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 662	9.8	35.0	40	1	AL039224	AL039224	DKF2p(nul
C 590	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 663	9.8	35.0	40	1	AA482490	AA482490	zv29c01.s
C 591	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 664	9.8	35.0	40	2	BE960473	BE960473	601653217
C 592	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 665	9.8	35.0	40	8	AZ760260	AZ760260	1M0553G21
C 593	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 666	9.8	35.0	40	8	BH629306	BH629306	1M0070780
C 594	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 667	9.8	35.0	40	8	BH850455	BH850455	SALK_0713
C 595	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 668	9.8	35.0	40	9	AZ217566	AZ217566	DrOgoph11
C 596	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 669	9.8	35.0	41	1	AU243521	AU243521	AU243521
C 597	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 670	9.8	35.0	41	2	BE386704	BE386704	601274126
C 598	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 671	9.8	35.0	41	6	CF304527	CF304527	ABF1--05-
C 599	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 672	9.8	35.0	41	7	H62327	H62327	Yr15f04.r1
C 600	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 673	9.8	35.0	41	8	AZ449036	AZ449036	1M0247P02
C 601	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 674	9.8	35.0	41	8	BH802322	BH802322	1008121P0
C 602	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 675	9.8	35.0	41	8	CC022435	CC022435	3591_1_2
C 603	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 676	9.8	35.0	42	6	CA966788	CA966788	CcLX06a23
C 604	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 677	9.8	35.0	42	8	BH624960	BH624960	1007091C0
C 605	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 678	9.8	35.0	42	8	BH865278	BH865278	SALK_0980
C 606	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 679	9.8	35.0	42	8	BZ356384	BZ356384	SALK_1289
C 607	10	35.7	43	1	A1540308	A1540308	ta74d07.x	C 680	9.8	35.0	42	9	AG229867	AG229867	Lotus cor
C 608	9.8	35.0	19	8	AZ351194	AZ351194	1M0089A08	C 681	9.8	35.0	43	1	AA829397	AA829397	od06d01.s

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C 682	9.8	35.0	43	1	AI917027	AI917027 tss1a12.x	C 755	9.8	35.0	50	1	AUI05353	AUI05353
C 683	9.8	35.0	43	4	BG756501	BG756501 602715642	C 756	9.8	35.0	50	1	AUI05354	AUI05354
C 684	9.8	35.0	43	4	BX001161	BX001161 BJ001161	C 757	9.8	35.0	50	1	AUI05355	AUI05355
C 685	9.8	35.0	43	5	BX553258	BX553258 BX553258	C 758	9.8	35.0	50	1	AUI05356	AUI05356
C 686	9.8	35.0	43	8	BH903418	BH903418 SALK 1025	C 759	9.8	35.0	50	1	AUI05361	AUI05361
C 687	9.8	35.0	43	9	AL764203	AL764203 Arabidops	C 760	9.8	35.0	50	1	AUI05362	AUI05362
C 688	9.8	35.0	43	9	BX546941	BX546941 Arabidops	C 761	9.8	35.0	50	1	AUI05363	AUI05363
C 689	9.8	35.0	44	4	BI645989	BI645989 603274968	C 762	9.8	35.0	50	1	AUI05364	AUI05364
C 690	9.8	35.0	45	5	BX626763	BX626763 BX626763	C 763	9.8	35.0	50	1	AUI05365	AUI05365
C 691	9.8	35.0	45	8	BH810609	BH810609 SALK 0509	C 764	9.8	35.0	50	1	AUI05367	AUI05367
C 692	9.8	35.0	45	8	BH846431	BH846431 SALK 0079	C 765	9.8	35.0	50	1	AUI05369	AUI05369
C 693	9.8	35.0	45	8	BH848090	BH848090 SALK 0674	C 766	9.8	35.0	50	1	AUI05370	AUI05370
C 694	9.8	35.0	45	9	BX153691	BX153691 DanLo ter	C 767	9.8	35.0	50	1	AUI05371	AUI05371
C 695	9.8	35.0	45	9	CR399267	CR399267 Arabidops	C 768	9.8	35.0	50	1	AUI05372	AUI05372
C 696	9.8	35.0	45	9	TA247B07Q	TA247B07Q Arabidops	C 769	9.8	35.0	50	1	AUI05373	AUI05373
C 697	9.8	35.0	45	9	AG191484	AG191484 Pan trogl	C 770	9.8	35.0	50	1	AUI05374	AUI05374
C 698	9.8	35.0	46	1	AV847044	AV847044 AV847044	C 771	9.8	35.0	50	1	AUI05375	AUI05375
C 699	9.8	35.0	46	1	C02279	C02279 HUMGS000664	C 772	9.8	35.0	50	1	AUI05376	AUI05376
C 700	9.8	35.0	46	6	AZ807543	AZ807543 2M0070021	C 773	9.8	35.0	50	1	AUI05377	AUI05377
C 701	9.8	35.0	46	8	BH901203	BH901203 SALK_0736	C 774	9.8	35.0	50	1	AUI05379	AUI05379
C 702	9.8	35.0	46	8	AZ581261	AZ581261 1M0369P06	C 775	9.8	35.0	50	1	AUI05380	AUI05380
C 703	9.8	35.0	47	8	BH801184	BH801184 1008126A0	C 776	9.8	35.0	50	1	AUI05381	AUI05381
C 704	9.8	35.0	47	8	BH903423	BH903423 SALK 1025	C 777	9.8	35.0	50	1	AUI05382	AUI05382
C 705	9.8	35.0	47	8	CNS07FDV	CNS07FDV Arabidops	C 778	9.8	35.0	50	1	AUI05383	AUI05383
C 706	9.8	35.0	47	9	CG869956	CG869956 XT0078 Sa	C 779	9.8	35.0	50	1	AUI05384	AUI05384
C 707	9.8	35.0	47	9	AA429295	AA429295 2M07a04.r	C 780	9.8	35.0	50	1	AUI05385	AUI05385
C 708	9.8	35.0	48	1	BE896146	BE896146 601438738	C 781	9.8	35.0	50	1	AUI05386	AUI05386
C 709	9.8	35.0	48	2	BH811707	BH811707 SALK_0596	C 782	9.8	35.0	50	1	AUI05387	AUI05387
C 710	9.8	35.0	48	8	DMES46992	DMES46992 Lotus cor	C 783	9.8	35.0	50	1	AUI05388	AUI05388
C 711	9.8	35.0	48	9	AG229425	AG229425 Lotu	C 784	9.8	35.0	50	1	AUI05389	AUI05389
C 712	9.8	35.0	48	9	AA903833	AA903833 ok60g11.s	C 785	9.8	35.0	50	1	AUI05390	AUI05390
C 713	9.8	35.0	49	1	AI680037	AI680037 tW80107.X	C 786	9.8	35.0	50	1	AUI05391	AUI05391
C 714	9.8	35.0	49	1	AI680037	AI680037 tW80107.X	C 787	9.8	35.0	50	1	AUI05392	AUI05392
C 715	9.8	35.0	49	1	AUI02669	AUI02669 Arabidops	C 788	9.8	35.0	50	1	AUI05393	AUI05393
C 716	9.8	35.0	49	8	AZ950523	AZ950523 2M0214G12	C 789	9.8	35.0	50	1	AUI05394	AUI05394
C 717	9.8	35.0	49	8	BZ594709	BZ594709 SALK_0851	C 790	9.8	35.0	50	1	AUI05395	AUI05395
C 718	9.8	35.0	49	8	AL758948	AL758948 Arabidops	C 791	9.8	35.0	50	1	AUI05396	AUI05396
C 719	9.8	35.0	49	9	AL943577	AL943577 Arabidops	C 792	9.8	35.0	50	1	AUI05397	AUI05397
C 720	9.8	35.0	49	9	EX161887	EX161887 Danio rer	C 793	9.8	35.0	50	1	AUI05398	AUI05398
C 721	9.8	35.0	50	1	AUI02669	AUI02669 Arabidops	C 794	9.8	35.0	50	1	AUI05399	AUI05399
C 722	9.8	35.0	50	1	AUI03372	AUI03372 Arabidops	C 795	9.8	35.0	50	1	AUI05400	AUI05400
C 723	9.8	35.0	50	1	AUI03698	AUI03698 Arabidops	C 796	9.8	35.0	50	1	AUI05401	AUI05401
C 724	9.8	35.0	50	1	AUI04010	AUI04010 Arabidops	C 797	9.8	35.0	50	1	AUI05402	AUI05402
C 725	9.8	35.0	50	1	AUI04010	AUI04010 Arabidops	C 798	9.8	35.0	50	1	AUI05403	AUI05403
C 726	9.8	35.0	50	1	AUI04010	AUI04010 Arabidops	C 799	9.8	35.0	50	1	AUI05404	AUI05404
C 727	9.8	35.0	50	1	AUI04010	AUI04010 Arabidops	C 800	9.8	35.0	50	1	AUI05405	AUI05405
C 728	9.8	35.0	50	1	AUI04010	AUI04010 Arabidops	C 801	9.8	35.0	50	1	AUI05406	AUI05406
C 729	9.8	35.0	50	1	AUI04010	AUI04010 Arabidops	C 802	9.8	35.0	50	1	AUI05407	AUI05407
C 730	9.8	35.0	50	1	AUI04010	AUI04010 Arabidops	C 803	9.8	35.0	50	1	AUI05408	AUI05408
C 731	9.8	35.0	50	1	AUI04010	AUI04010 Arabidops	C 804	9.8	35.0	50	1	AUI05409	AUI05409
C 732	9.8	35.0	50	1	AUI04010	AUI04010 Arabidops	C 805	9.8	35.0	50	1	AUI05410	AUI05410
C 733	9.8	35.0	50	1	AUI04010	AUI04010 Arabidops	C 806	9.8	35.0	50	1	AUI05411	AUI05411
C 734	9.8	35.0	50	1	AUI04010	AUI04010 Arabidops	C 807	9.8	35.0	50	1	AUI05412	AUI05412
C 735	9.8	35.0	50	1	AUI04010	AUI04010 Arabidops	C 808	9.8	35.0	50	1	AUI05413	AUI05413
C 736	9.8	35.0	50	1	AUI04010	AUI04010 Arabidops	C 809	9.8	35.0	50	1	AUI05414	AUI05414
C 737	9.8	35.0	50	1	AUI04010	AUI04010 Arabidops	C 810	9.8	35.0	50	1	AUI05415	AUI05415
C 738	9.8	35.0	50	1	AUI04010	AUI04010 Arabidops	C 811	9.8	35.0	50	1	AUI05416	AUI05416
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C 741	9.8	35.0	50	1	AUI04010	AUI04010 Arabidops	C 814	9.8	35.0	50	1	AUI05419	AUI05419
C 742	9.8	35.0	50	1	AUI04010	AUI04010 Arabidops	C 815	9.8	35.0	50	1	AUI05420	AUI05420
C 743	9.8	35.0	50	1	AUI04010	AUI04010 Arabidops	C 816	9.8	35.0	50	1	AUI05421	AUI05421
C 744	9.8	35.0	50	1	AUI04010	AUI04010 Arabidops	C 817	9.8	35.0	50	1	AUI05422	AUI05422
C 745	9.8	35.0	50	1	AUI04010	AUI04010 Arabidops	C 818	9.8	35.0	50	1	AUI05423	AUI05423
C 746	9.8	35.0	50	1	AUI04010	AUI04010 Arabidops	C 819	9.8	35.0	50	1	AUI05424	AUI05424
C 747	9.8	35.0	50	1	AUI04010	AUI04010 Arabidops	C 820	9.8	35.0	50	1	AUI05425	AUI05425
C 748	9.8	35.0	50	1	AUI04010	AUI04010 Arabidops	C 821	9.8	35.0	50	1	AUI05426	AUI05426
C 749	9.8	35.0	50	1	AUI04010	AUI04010 Arabidops	C 822	9.8	35.0	50	1	AUI05427	AUI05427
C 750	9.8	35.0	50	1	AUI04010	AUI04010 Arabidops	C 823	9.8	35.0	50	1	AUI05428	AUI05428
C 751	9.8	35.0	50	1	AUI04010	AUI04010 Arabidops	C 824	9.8	35.0	50	1	AUI05429	AUI05429
C 752	9.8	35.0	50	1	AUI04010	AUI04010 Arabidops	C 825	9.8	35.0	50	1	AUI05430	AUI05430
C 753	9.8	35.0	50	1	AUI04010	AUI04010 Arabidops	C 826	9.8	35.0	50	1	AUI05431	AUI05431
C 754	9.8	35.0	50	1	AUI04010	AUI04010 Arabidops	C 827	9.8	35.0	50	1	AUI05432	AUI05432

828	9.8	35.0	50	4	BG261065	901	9.6	34.3	38	8	AZ609074	1M0433H11
829	9.8	35.0	50	4	BI744116	c 902	9.6	34.3	38	8	BH855997	SALK_0838
830	9.8	35.0	50	6	CB277369	c 903	9.6	34.3	38	8	BZ595524	SALK_0927
831	9.8	35.0	50	7	R70221	c 904	9.6	34.3	38	9	TA241B11Q	T. brucei
832	9.8	35.0	50	7	T82774	c 905	9.6	34.3	38	9	AG019398	AG019398 Homo sapi
833	9.8	35.0	50	8	A0073798	c 906	9.6	34.3	39	1	AJ799081	AJ799081
834	9.8	35.0	50	8	AZ592619	c 907	9.6	34.3	39	2	BZ58028	BZ58028 601645348
835	9.8	35.0	50	8	AZ621023	c 908	9.6	34.3	39	8	AZ485216	1M0312F05
836	9.8	35.0	50	8	B07507	c 909	9.6	34.3	39	8	AZ595333	1M0407F23
837	9.8	35.0	50	9	AL771848	c 910	9.6	34.3	39	8	AZ832494	2M0112L21
838	9.8	35.0	50	9	AL952981	c 911	9.6	34.3	39	8	BZ354203	SALK_1233
839	9.8	35.0	50	9	EX969349	c 912	9.6	34.3	39	8	BZ354203	SALK_1233
840	9.8	35.0	50	9	TA230801Q	c 913	9.6	34.3	39	8	BZ593796	SALK_0820
841	9.6	34.3	17	9	AJ592362	c 914	9.6	34.3	39	8	CC054876	BZ593796 SALK_0801
842	9.6	34.3	20	8	AZ440002	c 915	9.6	34.3	39	9	CG427920	01S0783-0
843	9.6	34.3	21	8	AZ607204	c 916	9.6	34.3	39	9	CL517573	SAASH03 F
844	9.6	34.3	22	8	AZ607204	c 917	9.6	34.3	39	9	AG019397	Homo sapi
845	9.6	34.3	23	1	AU254061	c 918	9.6	34.3	40	1	AI049834	an37g11.x
846	9.6	34.3	24	8	AZ416129	c 919	9.6	34.3	40	1	AA160572	Zq46d11.r
847	9.6	34.3	24	8	AZ481314	c 920	9.6	34.3	40	7	H87885	Yw16d04.r1
848	9.6	34.3	27	8	BZ356916	c 921	9.6	34.3	40	8	AZ452300	AZ452300 1M0252002
849	9.6	34.3	28	1	AI006798	c 922	9.6	34.3	40	8	AZ841730	2M0139G21
850	9.6	34.3	28	1	AI168501	c 923	9.6	34.3	40	8	BH848610	SALK_0685
851	9.6	34.3	28	1	AI442950	c 924	9.6	34.3	40	8	BZ288532	SALK_0219
852	9.6	34.3	28	1	AA191808	c 925	9.6	34.3	40	8	BZ764171	SALK_1240
853	9.6	34.3	28	8	AZ591964	c 926	9.6	34.3	40	9	CG733826	1115F5960
854	9.6	34.3	29	8	AZ623171	c 927	9.6	34.3	40	9	CL212513	Gen trogl
855	9.6	34.3	30	9	CG733855	c 928	9.6	34.3	41	1	AU251358	AU251358
856	9.6	34.3	30	9	AG189187	c 929	9.6	34.3	41	2	BF569468	602185954
857	9.6	34.3	31	1	AA983092	c 930	9.6	34.3	41	7	D74277	CEK0709AXF
858	9.6	34.3	31	6	CF291819	c 931	9.6	34.3	41	7	N80572	ZD02C07.s1
859	9.6	34.3	31	9	CR359652	c 932	9.6	34.3	41	7	N90699	ZB43F04.s1
860	9.6	34.3	31	9	CL309426	c 933	9.6	34.3	41	8	AZ304505	1M0004B10
861	9.6	34.3	32	8	AZ320746	c 934	9.6	34.3	41	8	AZ330647	1M0056B15
862	9.6	34.3	32	9	DNE545736	c 935	9.6	34.3	41	8	AZ442277	1M0234P20
863	9.6	34.3	32	9	CH902610	c 936	9.6	34.3	41	8	AZ785156	2M028P13
864	9.6	34.3	33	8	BH902610	c 937	9.6	34.3	41	8	AZ992210	2M0276H13
865	9.6	34.3	33	9	AA455395	c 938	9.6	34.3	41	9	TA94F02Q	CL765427 T. brucei
866	9.6	34.3	34	1	AA959736	c 939	9.6	34.3	41	9	CT799936	01S0783-0
867	9.6	34.3	34	1	AA116347	c 940	9.6	34.3	42	1	AI191530	qe49a09.x
868	9.6	34.3	34	2	BE914450	c 941	9.6	34.3	42	8	BH847647	SALK_0551
869	9.6	34.3	34	8	AZ799773	c 942	9.6	34.3	42	9	DR1LJ38	DaniG rrr
870	9.6	34.3	34	9	AA597693	c 943	9.6	34.3	43	1	AA967042	ua39e07.r
871	9.6	34.3	34	9	CR360358	c 944	9.6	34.3	43	1	AA098967	ub99g04.r
872	9.6	34.3	35	2	AW245489	c 945	9.6	34.3	43	1	AI789878	ue65f10.r
873	9.6	34.3	35	8	AZ439115	c 946	9.6	34.3	43	1	AJ651163	AJ651163
874	9.6	34.3	35	8	AZ820699	c 947	9.6	34.3	43	1	AA231183	mw33f06.r
875	9.6	34.3	35	8	AZ821491	c 948	9.6	34.3	43	1	AV833807	AV833807
876	9.6	34.3	36	8	BH011362	c 949	9.6	34.3	43	8	AZ778245	2M0013022
877	9.6	34.3	36	8	BI651926	c 950	9.6	34.3	43	8	BZ583006	3590_1_48
878	9.6	34.3	36	8	AX936282	c 951	9.6	34.3	43	9	AL756095	Arabidops
879	9.6	34.3	36	8	AX936282	c 952	9.6	34.3	44	1	AA111655	Arabidops
880	9.6	34.3	36	8	BZ287178	c 953	9.6	34.3	44	4	BJ037636	BJ037636
881	9.6	34.3	36	4	BG765238	c 954	9.6	34.3	44	8	AZ836041	2M0130B12
882	9.6	34.3	36	4	BI651926	c 955	9.6	34.3	44	8	BZ353146	SALK_1198
883	9.6	34.3	36	8	AZ434008	c 956	9.6	34.3	44	9	AJ600107	Arabidops
884	9.6	34.3	36	8	AZ493433	c 957	9.6	34.3	44	9	TA16505Q	CL773116 T. brucei
885	9.6	34.3	36	8	AZ599432	c 958	9.6	34.3	44	9	CG783767	01S0585-0
886	9.6	34.3	36	8	BZ287178	c 959	9.6	34.3	45	8	AZ779998	2M0016122
887	9.6	34.3	36	9	AA587667	c 960	9.6	34.3	45	1	AA276118	VC36612.r
888	9.6	34.3	37	1	AA906103	c 961	9.6	34.3	45	5	BQ582321	E012305-0
889	9.6	34.3	37	1	AI634572	c 962	9.6	34.3	45	8	AZ311865	1M0027A05
890	9.6	34.3	37	1	AI647510	c 963	9.6	34.3	45	8	AZ772088	1M0574P09
891	9.6	34.3	37	1	AJ239943	c 964	9.6	34.3	45	8	AZ779998	2M0016122
892	9.6	34.3	37	1	AA519848	c 965	9.6	34.3	45	8	BH171077	SALK_0037
893	9.6	34.3	37	6	CD987913	c 966	9.6	34.3	45	8	BH813038	SALK_0636
894	9.6	34.3	37	8	AQ073641	c 967	9.6	34.3	45	8	BZ595896	SALK_0897
895	9.6	34.3	37	8	AZ817320	c 968	9.6	34.3	45	8	BZ769795	SALK_1427
896	9.6	34.3	37	9	BH812715	c 969	9.6	34.3	46	1	AV855174	AV855174
897	9.6	34.3	37	9	CL640636	c 970	9.6	34.3	46	1	AA480238	ne31d04.s
898	9.6	34.3	38	4	BM007143	c 971	9.6	34.3	46	1	AA547190	vk81d07.s
899	9.6	34.3	38	5	BQ589313	c 972	9.6	34.3	46	8	AZ429933	1M0214H10
900	9.6	34.3	38	8	AZ514073	c 973	9.6	34.3	46	8	AZ460164	1M0265G23

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C 974      9.6  34.3      46      8  AZ611861
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C 976      9.6  34.3      46      8  AZ810710
C 977      9.6  34.3      47      6  CA587715
C 978      9.6  34.3      47      7  H45354
C 979      9.6  34.3      47      8  B2355838
C 980      9.6  34.3      47      8  B2665134
C 981      9.6  34.3      47      9  AL751461
C 982      9.6  34.3      47      9  AL945750
C 983      9.6  34.3      48      5  TA122802P
C 984      9.6  34.3      48      5  BX551876
C 985      9.6  34.3      48      7  CO781458
C 986      9.6  34.3      48      7  CO781458
C 987      9.6  34.3      48      8  AZ371084
C 988      9.6  34.3      48      8  AZ810805
C 989      9.6  34.3      48      8  AZ810805
C 990      9.6  34.3      48      8  CC044288
C 991      9.6  34.3      48      9  DR15D3T
C 992      9.6  34.3      49      1  AA907765
C 993      9.6  34.3      49      1  AI003826
C 994      9.6  34.3      49      1  AI941380
C 995      9.6  34.3      49      1  AJ666269
C 996      9.6  34.3      49      2  AW041893
C 997      9.6  34.3      49      5  BQ482698
C 998      9.6  34.3      49      6  CF311120
C 999      9.6  34.3      49      7  D11989
C1000     9.6  34.3      49      8  AZ430355
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ALIGNMENTS

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RESULT 1
LOCUS      AA223130
DEFINITION 43 bp mRNA linear EST 19-FEB-1997
            cDNA clone IMAGE:650739 5' similar to TR:G984325 G984325
            PHOSPHOGLUCONATE DEHYDROGENASE. ;, mRNA sequence.
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ACCESSION  AA223130
VERSION     1
KEYWORDS    43 bp mRNA linear EST 19-FEB-1997
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 43)
            Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
            Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,
            Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
            Madis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
            Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
            Trevaaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
            and Marra, M.
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TITLE       Generation and analysis of 280,000 human expressed sequence tags
JOURNAL     Genome Res. 6 (9), 807-828 (1996)
MEDLINE     97044478
PUBMED      8889549
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LNL; contact the
            IMAGE Consortium (info@image.lnl.gov) for further information.
            Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand
            Seq primer: -28mi3 rev1 Et from Amersham
            High quality sequence stop: 1.
            Location/Qualifiers
            1..43
            /organism="Homo sapiens"
            /mol_type="mRNA"
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/db_xref="GDB:5277328"
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/clone="IMAGE:650739"
/tissue_type="neuroepithelial cells"
/dev_stage="Ntera-2 neuroepithelial cells"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene NT2 neuronal precursor 937230"
/note="Organ: brain; Vector: pBluescript SK-; Site 1:
EcORI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Uninduced, exponentially growing neuroepithelial
cells (Ntera-2/cl.D1). Average insert size: 1.0 kb;
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGCGACGAG
3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3"
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ORIGIN

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Query Match      51.4%; Score 14.4; DB 1; Length 43;
Best Local Similarity 75.0%; Pred. No. 5.4e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1  CGTTCGTGGGATGATCGTCATG 24
Db      15  CGCTGATCGGATGGCGTCATG 38

RESULT 2
LOCUS      AU104451/c
DEFINITION AU104451 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            HRC00222, mRNA sequence.
ACCESSION  AU104451
VERSION     1
KEYWORDS    50 bp mRNA linear EST 28-JAN-2004
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 50)
            Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
            Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
            Sakaki, Y., Nakamura, Y., Sugama, A. and Sugano, S.
            Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
            EMBO Rep. 2 (5), 388-393 (2001)
            21270072
            11375929
            Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
            Sugano, S. Construction and characterization of a full
            length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
            149-156 (1997).
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FEATURES

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source      1..50
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="HRC00222"
            /clone_lib="Sugano Homo sapiens cDNA library"
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ORIGIN

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Query Match      49.3%; Score 13.8; DB 1; Length 50;
Best Local Similarity 72.0%; Pred. No. 1e+05;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      2  GTTCGTGGGATGATCGTCATG 26
Db      35  GTTCGTGGGATGATCGTCATG 11
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RESULT 3





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/clone="UUGC2M0063C02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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## ORIGIN

```

Query Match      47.1%; Score 13.2; DB 8; Length 34;
Best Local Similarity 69.2%; Pred. No. 1.9e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY 3 TTCTGGGATAGTCGTCATGGTGT 28
    ||||| ||||| ||||| |||||
DB 2 TTCTGGTGTGGTGTAGGCGTGT 27
    ||||| ||||| ||||| |||||

```

```

RESULT 6
AZ770060/c
LOCUS
DEFINITION
  AZ770060 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0571F19 F, genomic survey sequence.

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ACCESSION
  AZ770060
VERSION
  AZ770060.1 GI:12890851

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KEYWORDS
  GSS.

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SOURCE
  Mus musculus (house mouse)

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ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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REFERENCE
  1 (bases 1 to 46)
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D. Weiss,R.

```

```

  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts

```

```

JOURNAL
  Unpublished (2000)

```

```

COMMENT
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah

```

```

  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu

```

```

  Insert Length: 10000 Std Error: 0.00

```

```

  Plate: 0571 row: F column: 19

```

```

  Seq primer: CGTTGTAACACGACGGCAGT

```

```

  Class: plasmid ends

```

```

  High quality sequence stop: 46.

```

```

  Location/Qualifiers

```

```

    1..46

```

```

      /organism="Mus musculus"

```

```

      /mol_type="genomic DNA"

```

```

      /strain="C57BL/6J"

```

```

      /db_xref="taxon:10090"

```

```

FEATURES
  source

```

```

/clone="UUGC1M0571F19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

## ORIGIN

```

Query Match      47.1%; Score 13.2; DB 8; Length 46;
Best Local Similarity 69.2%; Pred. No. 2e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```

```

QY 3 TTCTGGGATAGTCGTCATGGTGT 28
    ||||| ||||| ||||| |||||
DB 28 TTCTGGAACTGTAGTCAGGAGTT 3
    ||||| ||||| ||||| |||||

```

## RESULT 7

```

CB189272/c
LOCUS
DEFINITION
  CB189272 Trichuris vulpis pAMP1 v1 Trichuris vulpis cDNA 5'
  similar to contains element MER33 repetitive element ;, mRNA
  sequence.

```

```

ACCESSION
  CB189272
VERSION
  CB189272.1 GI:28252664

```

```

KEYWORDS
  EST.

```

```

SOURCE
  Trichuris vulpis

```

```

ORGANISM
  Trichuris vulpis
  Eukaryota; Metazoa; Nematoda; Enoplea; Trichocephalida;
  Trichuridae; Trichuris.

```

```

REFERENCE
  1 (bases 1 to 49)
  McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,
  Wyllie,T., Dante,W., Marra,M., Hillier,L., Kucaba,T., Theising,B.,
  Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,
  Tsagarisvili,I., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,
  Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,
  Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
  McCann,R., Waterston,R. and Wilson,R.

```

```

  The Washington Univ. Nematode EST Project, 1999
  Unpublished (1999)

```

```

  Contact: McCarter JP
  The Washington Univ. Nematode EST Project, 1999

```

```

  Washington University School of Medicine
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
  Tel: 314 286 1800
  Fax: 314 286 1810

```

```

  Email: est@watson.wustl.edu
  The library was constructed by Claire Murphy and Dr. James McCarter
  at Washington University, St. Louis. The cDNA was made by using
  Dynabead oligo-dT priming (Dyna). PCR based library using a
  modified protocol from the SMART PCR cDNA Synthesis Kit from
  Clontech. Directionally cloned into the UDG sites of pAMP1. Adult
  nematodes were collected from infected dogs by Dr. Prema Arasu of
  North Carolina State University, Raleigh.

```

```

  Seq primer: -40RP from Gibco.
  Location/Qualifiers

```

```

    1..49

```

```

      /organism="Trichuris vulpis"

```

```

      /mol_type="cDNA"

```

```

      /strain="C57BL/6J"

```

```

      /db_xref="taxon:10090"

```

```

FEATURES
  source

```



Db	34	GGCTAGTCCGTTATGAGTT 14	
RESULT 10			
AI588805/c			
LOCUS		40 bp mRNA linear EST 07-JUN-2001	
DEFINITION		fb99f01.y1 Zebrafish WashU MPIMG EST Danio rerio cDNA clone	
		IMAGE:3720025 5' similar to SW:COX1_SALTUR P29653 CYTOCHROME C	
		OXIDASE POLYPEPTIDE 1 ; mRNA sequence.	
ACCESSION		AI588805	
VERSION		AI588805.1 GI:4597852	
KEYWORDS		EST	
SOURCE		Danio rerio (zebrafish)	
ORGANISM		Danio rerio	
REFERENCE			
AUTHORS		Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,P., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson.R.	
TITLE		WashU Zebrafish EST Project 1998	
JOURNAL		Unpublished (1998)	
COMMENT		Contact: Stephen L. Johnson Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: zbrafish@watson.wustl.edu cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone Distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and RessourcenzentrumPrimatDatenbank, Berlin, Germany (web address: www.rzpd.de) Trace considered overall poor quality Possible reversed clone: similarity on wrong strand Seq primer: T3 ET from Amersham High quality sequence stop: 1 POLYA-NO.	
FEATURES		Location/Qualifiers	
source		1..40	
		/organism="Danio rerio"	
		/mol_type="mRNA"	
		/db_xref="taxon:7955"	
		/clone="IMAGE:3720025"	
		/sex="mixed"	
		/tissue_type="26 somite embryos, adult livers, shield stage embryos"	
		/lab_host="XLI-blue MRF"	
		/clone_lib="Zebrafish WashU MPIMG EST"	
		/note="vector: pSPORT1; Site 1: NotI; Site 2: SalI; 1st strand cDNA was primed with a Not I - oligo(dT)15 primer [5'pGACTAGTTCAGATCGGACGCGCCGCTTTTCTTTT3']; double-stranded cDNA was ligated to Sal I adaptors (BRL), digested with Not I and cloned into the Not I and Sal I sites of the pSPORT1 vector (BRL). Library was constructed by Matthew Clark (Lehrach lab; ICRF, London and Max Planck Institut fuer Molekulare Genetik, Berlin). cDNAs for EST analysis were selected following oligonucleotide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality	
ORIGIN			
Query Match		46.4%; Score 13; DB 1; Length 40;	
Best Local Similarity		76.2%; Pred. No. 2.4e+05;	
Matches		16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
QY	5	CGTGGGATAGTCGTCATGCT 25	
Db	38	CGTAGTATGTCACACATGCT 18	
RESULT 11			
AI649066			
LOCUS		AI649066 CSEORAN19 Sus scrofa cDNA clone C0003271_H04, mRNA	
DEFINITION		Sequence.	
ACCESSION		AI649066	
VERSION		AI649066.1 GI:49325911	
KEYWORDS		EST	
SOURCE		Sus scrofa (pig)	
ORGANISM		Sus scrofa	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.	
AUTHORS		Anderson,S.I., Finlayson,H.A. and Archibald,A.L.	
TITLE		Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle	
JOURNAL		Unpublished (2004)	
COMMENT		Contact: Anderson SI Genomics and Bioinformatics Roslin Institute Roslin, Midlothian, EH25 9PS, UNITED KINGDOM Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -minscore 20 and -mismatch 12 options. Vector:pBluescriptII (KS) R. Site1: EcoRI R. Site2: NotI 5' Seq Primer M13F Normalised library constructed from pooled ovaries. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.ark-genomics.org.	
FEATURES		Location/Qualifiers	
source		1..43	
		/organism="Sus scrofa"	
		/mol_type="mRNA"	
		/db_xref="taxon:9823"	
		/clone="C0003271_H04"	
		/tissue_type="ovary"	
		/clone_lib="CSEORAN19"	
		/note="vector: pBluescriptII (KS+); Site 1: EcoRI; Site 2: NotI; Single pass sequencing; Normalised library constructed from pooled ovaries"	
ORIGIN			
Query Match		46.4%; Score 13; DB 1; Length 43;	
Best Local Similarity		76.2%; Pred. No. 2.4e+05;	
Matches		16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
QY	6	GTGGGATAGTCGTCATGCTG 26	
Db	22	GTGGTATTCTCTCTCTGCTG 42	
RESULT 12			
BG523557/c			
LOCUS		BG523557 47 bp mRNA linear EST 16-NOV-2001	
DEFINITION		33-14 Stevia field grown leaf cDNA Stevia rebaudiana cDNA 5', mRNA sequence.	
ACCESSION		BG523557	
VERSION		BG523557.1 GI:16946975	
KEYWORDS		EST	
SOURCE		Stevia rebaudiana	
ORGANISM		Stevia rebaudiana	
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Eupatoriaceae; Stevia.

1 (bases 1 to 47)

Leaf ESTs from *Stevia rebaudiana*: A resource for gene discovery in diterpene synthesis unpublished (2001)

#### JOURNAL

##### COMMENT

Contact: Jim Brandle

Genomics and Biotechnology

Agriculture and Agri-Food Canada - SCPPRC

1391 Sandford St., London, Ontario, CANADA, N5V 4T3

Tel: 519 457 1470

Fax: 519 457 3997

Email: brandleje@agr.gc.ca

Seq primer: T3 promoter primer.

#### FEATURES

source

Location/Qualifiers

1..47

/organism="Stevia rebaudiana"

/mol\_type="mRNA"

/strain="751/1501"

/cultivar="Landrace"

/db\_xref="taxon:55670"

/tissue\_type="leaf"

/dev\_stages="field grown, mid-size"

/lab\_host="E. coli strain XLOLR"

/clone\_lib="Stevia field grown leaf cDNA"

/note="Vector: pBK-CMV; Site 1: EcoRI; Site 2: XhoI; This

cDNA library was constructed from polyA+ enriched mRNA

from field grown leaves. Mid-size actively growing leaves

were collected and pooled from several plants and frozen

immediately after harvesting in liquid nitrogen. The cDNA

was prepared using an XhoI-poly(dT) linker-primer. An

EcoRI adapter was ligated to the blunt end cDNA and the

products were digested with EcoRI and XhoI enabling

directional cloning into the lambda ZAP Express vector.

The library was amplified using the host strain XLI-Blue

MRF+. Mass excision of the library was performed to

obtain pBK-CMV phagemid clones in the host strain XLOLR.

Single pass DNA sequencing was performed using the T3

promoter primer: 5' ATTAACCTCCTCAAGGGA 3'. This library

was constructed by Alex Richman."

#### ORIGIN

##### Query Match

Best Local Similarity 46.4%; Score 13; DB 4; Length 47;

Matches 16; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

##### QY

1 CTTTCGTGGGATAGTCGTCATG 23

||||| ||||| ||||| ||||| |||||

Db 45 CTTTCGTGGGAAAGTAGGTNAG 23

##### RESULT 13

##### LOCUS

##### DEFINITION

AI581062 t197d01.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2139937 3'

similar to SW:NUIM HUMAN P03886 NADH-UBIQUINONE OXIDOREDUCTASE

CHAIN 1 ; mRNA sequence.

AI581062 49 bp mRNA linear EST 13-DEC-1999

AI581062.1 GI:4565438

EST.

KEYWORDS Homo sapiens (human)

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini, Homiidae; Homo.

1 (bases 1 to 49)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

#### FEATURES

##### COMMENT

Location/Qualifiers

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 883 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1

POLYA=No.

Location/Qualifiers

1..49

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2139937"

/tissue\_type="poorly differentiated adenocarcinoma with

signet ring cell features"

/lab\_host="DH10B"

/clone\_lib="NCI CGAP Gas4"

/note="Organ: stomach; Vector: pCMV-SPORT6; Site 1: SalI;

Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.69 kb. Life Technologies catalog #:

11549-011"

#### ORIGIN

##### Query Match

Best Local Similarity 46.4%; Score 13; DB 1; Length 49;

Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

##### QY

2 GTTCGTGGGATAGTCGTCAT 22

||||| ||||| ||||| ||||| |||||

Db 16 GTTCACGGGAGAGTCGCTAAT 36

##### RESULT 14

##### LOCUS

##### DEFINITION

AZ585210

clone UUGC1M0390B16 F, genomic survey sequence.

ACCESSION

AZ585210

KEYWORDS

GSS

SOURCE

ORGANISM

Mus musculus

(house mouse)

REFERENCE

AUTHORS

##### TITLE

##### JOURNAL

##### COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical

Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0390 row: B column: 16

Seq primer: CGTTGTAACGACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 33.

Location/Qualifiers

1. 33  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUC1M033322"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

source

ORIGIN

Query Match 45.7%; Score 12.8; DB 8; Length 35;  
Best Local Similarity 87.5%; Pred.No. 2.9e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TCGTGGGATAGTCGCT 19  
|||||  
DB 30 TCGTGGGATAGTCCT 15

RESULT 16

BH791451 47 bp DNA linear GSS 02-APR-2002  
LOCUS  
DEFINITION  
SALK 059978.40.35.x Arabidopsis thaliana TDNA insertion lines  
Arabidopsis thaliana genomic clone SALK\_059978.40.35.x, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE

Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE

1 (bases 1 to 47)  
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,  
Shinn,P., Zimmerman,J. and Ecker,J.R.  
A Sequence-Indexed Library of Insertion Mutations in the  
Arabidopsis Genome  
Unpublished (2001)

JOURNAL

COMMENT  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
This is single pass sequence recovered from the left border of  
TDNA.  
Class: TDNA tagged.  
Location/Qualifiers  
1..47  
/organism="Arabidopsis thaliana"

FEATURES

source

1. 33  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUC1M0390B16"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

source

ORIGIN

Query Match 45.7%; Score 12.8; DB 8; Length 33;  
Best Local Similarity 87.5%; Pred.No. 2.9e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTTCGTGGGATAGTCC 17  
|||||  
DB 2 GTTCGTGGGATAGTCC 17

RESULT 15

AZ497161/c 35 bp DNA linear GSS 05-OCT-2000  
LOCUS  
DEFINITION  
IM033322R Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M033322 R, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 35)  
Dunn,D., Aoyagi,A., Barber,M., Bescorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D. Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)

JOURNAL

COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0333 row: G column: 22  
Seq primer: CACACGAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 35.  
Location/Qualifiers

FEATURES

```

/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match          45.7%; Score 12.8; DB 8; Length 47;
Best Local Similarity 70.8%; Pred. No. 3e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0

QY  2  GTTCGTGGGATAGTCCGTCATGGT 25
    ||||| | | ||||| |||||
DB  15  GGTGAGGGGTCCCGCTCGTGGT 38

RESULT 17
CL234325/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 48)
Latshaw,S., Tan,B.-C., Settles,A.M. and McCarty,D.R.
Sequence tagged transposon insertions from the UniformMu maize
population
Unpublished (2003)
Contact: Donald R. McCarty
Plant Molecular and Cellular Biology Program
University of Florida
PO 110690 Gainesville, FL 32611-0690, USA
Tel: 352-392-1928 x322
Email: drmc@fl.edu
Sequence flanking probable Mu insertion site in UniformMu line:
02S0422-02, Primer set: A
Class: transposon insertion site.
FEATURES
source
1..48
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="W22 (ACR, bz1-m9)"
/cultivar="UniformMu"
/db_xref="taxon:4577"
/clone_lib="UniformMu MuTAIL Library"
/note="Vector: TOPO-PCR4; DNA flanking Mu transposon
insertions in Mu inactive lines were extracted from the
UniformMu maize population by the thermo asymmetric
intercalated PCR (TAIL) protocol using primers specific for
the Mu terminal inverted repeat and a set of 16 arbitrary
primers. Amplicons were size enriched using Sepharose 400
spin columns and cloned into the TOPO PCR4 vector."

ORIGIN

Query Match          45.7%; Score 12.8; DB 9; Length 48;
Best Local Similarity 70.8%; Pred. No. 3e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0

QY  3  TTCTGCGGATAGTCCGTCATGGT 26
    ||||| | | ||||| |||||

```



```

ACCESSION      BH802890
VERSION        BH802890.1  GI:20317479
KEYWORDS       GSS.
SOURCE         Zea mays
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
               clade; Panicoideae; Andropogoneae; Zea.
REFERENCE      1 (bases 1 to 49)
AUTHORS        Walbot,V.
TITLE          Maize genomic sequences found using engineered RescueMu transposon
JOURNAL        Unpublished (2001)
COMMENT        Department of Biological Sciences
               Stanford University
               855 California Ave, Palo Alto, CA 94304, USA
               Tel: 650 723 2227
               Fax: 650 725 8221
               Email: walbot@stanford.edu
               Possible ligation site of ends cut by 2 different endonucleases.
               Reverse complemented post-ligation sequence from source sequence.
               Plate: 1008097 row: 13
               Class: transposon-tagged.
               Location/Qualifiers
                 source            1..49
                 /organism="Zea mays"
                 /mol_type="genomic DNA"
                 /cultivar="mixed background W23/A188/B73"
                 /db_xref="taxon:4577"
                 /tissue_type="leaf"
                 /dev_stage="adult"
                 /lab_host="DH10B"
                 /clone_lib="1008 - RescueMu Grid I"
                 /note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site www.zmldb.iastate.edu and follow the links for 'RescueMu.' Grid I was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN
Query Match           45.7%; Score 12.8; DB 8; Length 49;
Best Local Similarity 70.8%; Pred. No.3e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY    2 GTTCGTGGGATAGTCCGTCATGGT 25
      ||| |||| | ||| ||| ||| |||
DB    9 GTTCGTGGGTCAGTTGCCAGGCT 32

RESULT 20
BZ769405
LOCUS      SALK_142144.44.90.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_142144.44.90.x, genomic survey sequence.
ACCESSION  BZ769405
VERSION    BZ769405
KEYWORDS   BZ769405.1 GI:28943089
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM  Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE  1 (bases 1 to 49)
AUTHORS    Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Castiblanco,C., Teske,A., Karnes,M., Kim,C.J., Parker,H., Prednisi,L.,

```

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source
1..42
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="242a07"

ORIGIN
Query Match 45.0%; Score 12.6; DB 9; Length 42;
Best Local Similarity 78.9%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GTTCGTGGGATAGTCGGTC 20
   ||| ||| ||| ||| |||
Db 42 GTTACTGTGAAGTCGGTC 24

RESULT 22
CC886211 46 bp DNA linear GSS 31-JUL-2003
LOCUS SALK_148336.25.55.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_148336.25.55.x, genomic
survey sequence.
ACCESSION CC886211
VERSION CC886211.1 GI:33362567
SOURCE GSS.
ORGANISM Arabidopsis thaliana (thale cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 46)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE A sequence-indexed library of insertion mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
The Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At4g28980.
Class: TDNA tagged.
FEATURES
Location/Qualifiers
source
1..46
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/scotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_148336.25.55.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match 45.0%; Score 12.6; DB 9; Length 46;
Best Local Similarity 66.7%; Pred. No. 3.7e+05;
Matches 18; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 GTTCGTGGGATAGTCGGTCATGGTGT 28
   ||| ||| ||| ||| ||| |||
Db 6 GTTCGCTGTTCTCAATCTTGCTT 32

RESULT 23
AZ436588
LOCUS iM0224H20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0224H20 F, genomic survey sequence.
ACCESSION AZ436588
VERSION AZ436588.1 GI:10560601
SOURCE GSS.
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 24)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0224 row: H column: 20
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
FEATURES
Location/Qualifiers
source
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0224H20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 Kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 44.3%; Score 12.4; DB 8; Length 24;
Best Local Similarity 72.7%; Pred. No. 4.2e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 CGTGGGATAGTCGGTCATGGTGT 26
   ||| ||| ||| ||| |||
Db 3 CGTGGACGGTCGGGAGGGTG 24

```





Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus; 1 (bases 1 to 46)

**REFERENCE**  
**AUTHORS** Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tinge, A., von Niederhausern, A. and Wright, D., Weiss, R.  
**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
**JOURNAL** Unpublished (2000)  
**COMMENT** Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0030 row: K column: 06  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 46.  
 Location/Qualifiers  
 1. 46  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0030R06"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed into adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

**ORIGIN**  
 Query Match 44.3%; Score 12.4; DB 8; Length 46;  
 Best Local Similarity 92.9%; Pred. No. 4.6e+05;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 8 GGGTAGTCCGTC A 21  
 |||||  
 DB 20 GGGTAGTCCGTC A 7

**RESULT 29**  
**LOCUS** CL213822/c  
**DEFINITION** M046F03 Ggnc Gene Trap Library GV05C04 Mus musculus cDNA clone  
**ACCESSION** M046F03, mRNA sequence.  
**VERSION** CL213822  
**KEYWORDS** CL213822.2 GI:49489749  
**SOURCE** GSS.  
**ORGANISM** Mus musculus (house mouse)  
 Mus musculus

This is single pass sequence recovered from the left border of

```

TDNA.
Class: TDNA tagged.
Location/Qualifiers
1..50
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_062036.27.05.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/notes="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match 44.3%; Score 12.4; DB 8; Length 50;
Best Local Similarity 72.7%; Pred. No. 4.6e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 7 TGGGATAGTCGTCATGTT 28
|||||
Db 21 TGAATAATCTGTCGTGAT 42
|||||

RESULT 31
AZ341655/c
LOCUS AZ341655 32 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0074J07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0074J07 F, genomic survey sequence.
ACCESSION AZ341655
VERSION AZ341655.1 GI:10418123
KEYWORDS GSS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 32)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0074 row: J column: 07
Seq primer: CGTTGTAACACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 32.
Location/Qualifiers
1..32
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0074J07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

FEATURES
source
1..32
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0074J07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
Location/Qualifiers
1..50
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_062036.27.05.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/notes="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match 44.3%; Score 12.4; DB 8; Length 50;
Best Local Similarity 72.7%; Pred. No. 4.6e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 7 TGGGATAGTCGTCATGTT 28
|||||
Db 21 TGAATAATCTGTCGTGAT 42
|||||

RESULT 31
AZ341655/c
LOCUS AZ341655 32 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0074J07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0074J07 F, genomic survey sequence.
ACCESSION AZ341655
VERSION AZ341655.1 GI:10418123
KEYWORDS GSS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 32)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0074 row: J column: 07
Seq primer: CGTTGTAACACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 32.
Location/Qualifiers
1..32
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0074J07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

FEATURES
source
1..32
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0074J07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

```

Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 43.6%; Score 12.2; DB 8; Length 32;  
Best Local Similarity 82.4%; Pred. No. 5.4e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 12 TAGTCCGTCATGTT 28  
|||||  
Db 29 TAGTCATTCATGGTGT 13  
|||||

## RESULT 32

AZ852234  
LOCUS AZ852234 38 bp DNA linear GSS 21-FEB-2001  
DEFINITION 2M0154D24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0154D24 R, genomic survey sequence.  
ACCESSION AZ852234  
VERSION AZ852234.1 GI:13039094  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 38)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0154 row: D column: 24  
Seq primer: CACACAGGAAACAGCATGACC  
Class: plasmid ends  
High quality sequence stop: 38.  
Location/Qualifiers  
1..38  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0154D24"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson

## FEATURES

source

1..38  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0154D24"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson

FEATURES	source
Location/Qualifiers	
1..46	
/organism="Mus musculus"	
/mol_type="mRNA"	
/strain="C57BL/6J"	
/db_xref="taxon:10090"	
/clone="IMAGE:1314214"	
/sex="male"	
/tissue type="mammary gland"	
/dev stage="4 weeks"	

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FEATURES
source
Class: insertion
Location/Qualifiers
1..46
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_087693.32.05.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna\_protocols.html"

```

ORIGIN	Query Match	Score 12.2;	DB 9;	Length 46;
		43.6%		



Best Local Similarity 82.4%; Pred. No. 5.7e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	10	GATAGTCCGTCATG	26
Db	12	GATAGTGCCTCAAG	28

RESULT 35					
B2661004/c					
LOCUS	B2661004	48 bp	DNA	linear	GSS 31-JAN-2003
DEFINITION	SALK_024466.34.10.x Arabidopsis thaliana TDNA insertion lines.				

ACCESSION	B2661.004	
VERSION	B2661.004.1	GI:28174151
KEYWORDS	SSS	
SOURCE	Arabidopsis thaliana (thale cress)	
ORGANISM	Arabidopsis thaliana	

REFERENCE  
AUTHORS

1 (bases 1 to 48)  
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,  
Gedrinab, C., Jesse, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,  
Shim, P., Zimmerman, J. and Eckert, J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the  
JOURNAL Arabidopsis Genome  
COMMENT Unpublished (2001)  
Contact: Joseph R. Ecker

This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of At4g03270.  
Class: TDNA tagged.

FEATURES	Location/Qualifiers
source	1. .48

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1..48
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_024466.34.10.x"
/clone.lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/cdna\_protocols.html"

```

Query Match	43.6%	Score 12.2	DB 8	Length 48
Best Local Similarity	68.0%	Pred. No. 5.7e+05		
Matches 17, Conservative	0	Mismatches 8	Indels 0	Gaps 0

Oy 4 TCGTGGATAGTCCGTCATGCTT 28  
 | | | | | | | | | |  
 Db 39 TTGTGAGATAGAGAGAGATGTTTT 15

RESULT	36
AUI04471	
LOCUS	50 bp mRNA linear EST 28-JAN-2004
DEFINITION	AUI04471 Saguano Homo sapiens cDNA library Homo sapiens CDNA clone
KATO5864,	mRNA sequence.
AUI04471	
ACCESSION	AUI04471.1 GI:13553992
VERSION	
KEYWORDS	EST.

SOURCE ORGANISM	
Homo sapiens (human)	
Homo sapiens	

REFERENCE  
AUTHORS  
1 (bases 1 to 50)  
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,

TITLE	Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
JOURNAL	EMBO Rep. 2 (5), 388-393 (2001)

COMMENT Contact: Yutaka Suzuki

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Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and  
Sugano, S. Construction and characterization of a full  
length-enriched and a 5'-end-enriched cDNA library. *Gene* 200 (1-2)  
149-156 (1997).

FEATURES	Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="KAT05864"
/clone_lib="Sugano Homo sapiens cDNA library"
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Best Local Similarity	82.4%	Pred. NO.	5.7e+05						
Matches	14	Conservative	0	Mismatches	3	Indels	0	Gaps	0

QY 10 GATAGTCGTCATGGTG 26  
| | | | | | | | | |  
Db 9 GTTAGTACGACATGGTG 25

RESULT 37					
BZ356733/c					
LOCUS					
DEFINITION					
BZ356733	27 bp	DNA	linear	GSS 14-NOV-2002	
SALK_129645.42..60.x	Arabidopsis thaliana TDNA insertion lines				
Arabidopsis thaliana genomic clone SALK_129645.42.60.x,					
survey sequence.					

ACCESSION	B2356733
VERSION	B2356733.1
KEYWORDS	GI:24948373
SOURCE	GSS.
ORGANISM	Arabidopsis thaliana (thale cress) Arabidopsis thaliana

REFERENCE 1 (bases 1 to 27

Gadriab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,  
Shinn, P., Zimmerman, J. and Ecker, J.R.  
A Sequence-Indexed Library of Insertion Mutations in the

FEATURES

Email: ecker@sal.k.edu

This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of Ac490255.

Class: TDNA tagged

Location/Qualifiers

### FEATURES

Location/Qualifiers





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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:50:22 ; Search time 378.157 Seconds  
(without alignments)  
2626.113 Million cell updates/sec

Title: US-10-087-631B-17  
Perfect score: 21  
Sequence: 1 cgcgcattagaccgtagcgca 21

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 1785872

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : GenEmbl:  
1: gb ba:\*  
2: gb hcg:\*  
3: gb in:\*  
4: gb om:\*  
5: gb ov:\*  
6: gb pat:\*  
7: gb ph:\*  
8: gb pl:\*  
9: gb pr:\*  
10: gb ro:\*  
11: gb sts:\*  
12: gb sy:\*  
13: gb un:\*  
14: gb vl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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C 2	100.0	21	6	BD181378	BD181378 A method
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C 4	100.0	21	6	AX524841	AX524841 Sequence
C 5	100.0	21	6	AX524856	AX524856 Sequence
C 6	13.6	64.8	29	BD227377	BD227377 Secreted
C 7	12.8	61.0	30	AX752106	AX752106 Sequence
C 8	12.6	60.0	20	AX295474	AX295474 Sequence
C 9	12.6	60.0	24	AX290841	AX290841 Sequence
C 10	12.6	60.0	26	BD260345	BD260345 Methods
C 11	12.6	60.0	26	AX044290	AX044290 Sequence
C 12	12.6	60.0	31	AR168721	AR168721 Sequence
C 13	12.6	60.0	33	AR047950	AR047950 Sequence
C 14	12.6	60.0	38	AR334533	AR334533 Sequence
C 15	12.6	60.0	38	AR335779	AR335779 Sequence
C 16	12.6	60.0	38	AR336409	AR336409 Sequence
C 17	12.6	60.0	38	AR455837	AR455837 Sequence
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C 19	12.6	60.0	38	AX219231	AX219231 Sequence

C 20	12.6	60.0	38	6	AX351248	AX351248 Sequence
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311	11	52.4	38	6	AX219543	AX219543	Sequence	384	11	52.4	38	6	AX581093	AX581093	Sequence



385	11	52.4	38	6	AX581157	AX581157 Sequence	458	10.6	50.5	18	6	BD250577	BD250577 Identific
386	11	52.4	38	6	AX581200	AX581200 Sequence	459	10.6	50.5	18	6	AR215579	AR215579 Sequence
387	11	52.4	38	6	AX581242	AX581242 Sequence	460	10.6	50.5	18	6	AR293681	AR293681 Sequence
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390	11	52.4	38	6	AX581302	AX581302 Sequence	463	10.6	50.5	20	6	AX295232	AX295232 Sequence
391	11	52.4	38	6	AX581352	AX581352 Sequence	464	10.6	50.5	20	6	AX296546	AX296546 Sequence
392	11	52.4	38	6	AX581365	AX581365 Sequence	465	10.6	50.5	21	6	AX963392	AX963392 Sequence
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394	11	52.4	38	6	AX581544	AX581544 Sequence	467	10.6	50.5	24	6	AE6684	AE6684 Sequence 3
395	11	52.4	40	6	AR095875	AR095875 Sequence	468	10.6	50.5	24	6	BD260387	BD260387 Method.
396	11	52.4	40	6	AR157230	AR157230 Sequence	469	10.6	50.5	24	6	AR261951	AR261951 Sequence
397	11	52.4	40	6	AR3611054	AR3611054 Sequence	470	10.6	50.5	24	6	AX044332	AX044332 Sequence
398	11	52.4	40	6	AR767184	AR767184 Sequence	471	10.6	50.5	24	6	AX181781	AX181781 Sequence
399	11	52.4	42	6	AR007099	AR007099 Sequence	472	10.6	50.5	24	6	AX290523	AX290523 Sequence
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401	11	52.4	42	6	AR034923	AR034923 Sequence	474	10.6	50.5	24	6	AX291913	AX291913 Sequence
402	11	52.4	42	6	AR111123	AR111123 Sequence	475	10.6	50.5	24	6	BD077184	BD077184 Method an
403	11	52.4	42	6	AR111123	AR111123 Sequence	476	10.6	50.5	26	6	BD260268	BD260268 Method.
404	11	52.4	42	6	BD086796	BD086796 Nucleic a	477	10.6	50.5	26	6	BD260289	BD260289 Method.
405	11	52.4	44	6	AX752645	AX752645 Sequence	478	10.6	50.5	26	6	BD260331	BD260331 Method.
406	11	52.4	44	6	AX752646	AX752646 Sequence	479	10.6	50.5	26	6	BD260385	BD260385 Method.
407	11	52.4	50	6	AX951984	AX951984 Sequence	480	10.6	50.5	26	6	BD260395	BD260395 Method.
408	11	52.4	50	6	AX952578	AX952578 Sequence	481	10.6	50.5	26	6	BD260396	BD260396 Method.
409	10.8	51.4	17	6	BD199105	BD199105 Method an	482	10.6	50.5	26	6	BD260397	BD260397 Method.
410	10.8	51.4	19	6	AR096607	AR096607 Sequence	483	10.6	50.5	26	6	BD260398	BD260398 Method.
411	10.8	51.4	20	6	AR065350	AR065350 Sequence	484	10.6	50.5	26	6	BD260399	BD260399 Method.
412	10.8	51.4	23	6	AX935258	AX935258 Sequence	485	10.6	50.5	26	6	BD260401	BD260401 Method.
413	10.8	51.4	24	6	AX443621	AX443621 Sequence	486	10.6	50.5	26	6	BD260402	BD260402 Method.
414	10.8	51.4	24	6	AX443691	AX443691 Sequence	487	10.6	50.5	26	6	BD260404	BD260404 Method.
415	10.8	51.4	25	6	C0797626	C0797626 Sequence	488	10.6	50.5	26	6	BD260405	BD260405 Method.
416	10.8	51.4	25	6	AX447603	AX447603 Sequence	489	10.6	50.5	26	6	BD260406	BD260406 Method.
417	10.8	51.4	27	6	BD177071	BD177071 Strandard	490	10.6	50.5	26	6	AX044213	AX044213 Sequence
418	10.8	51.4	27	6	BD207836	BD207836 Enzymatic	491	10.6	50.5	26	6	AX044213	AX044213 Sequence
419	10.8	51.4	27	6	BD208021	BD208021 Enzymatic	492	10.6	50.5	26	6	AX044276	AX044276 Sequence
420	10.8	51.4	27	6	AR185827	AR185827 Sequence	493	10.6	50.5	26	6	AX044330	AX044330 Sequence
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422	10.8	51.4	27	6	AR191317	AR191317 Sequence	495	10.6	50.5	26	6	AX044347	AX044347 Sequence
423	10.8	51.4	29	6	BD199461	BD199461 Method an	496	10.6	50.5	26	6	AX044348	AX044348 Sequence
424	10.8	51.4	29	6	BD200040	BD200040 Method an	497	10.6	50.5	26	6	AX044341	AX044341 Sequence
425	10.8	51.4	30	6	BD252904	BD252904 Regulatio	498	10.6	50.5	26	6	AX044342	AX044342 Sequence
426	10.8	51.4	31	6	AR117368	AR117368 Sequence	499	10.6	50.5	26	6	AX044343	AX044343 Sequence
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436	10.8	51.4	36	6	AX058554	AX058554 Sequence	509	10.6	50.5	30	6	AR456133	AR456133 Sequence
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441	10.8	51.4	38	6	IS2894	IS2894 Sequence 63	514	10.6	50.5	31	6	AX117931	AX117931 Sequence
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443	10.8	51.4	38	6	AR333074	AR333074 Sequence	516	10.6	50.5	31	6	AX248288	AX248288 Sequence
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446	10.8	51.4	38	6	AX246444	AX246444 Sequence	519	10.6	50.5	34	6	AR256995	AR256995 Sequence
447	10.8	51.4	39	6	AR080416	AR080416 Sequence	520	10.6	50.5	35	6	AR256995	AR256995 Sequence
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450	10.8	51.4	39	6	AR123550	AR123550 Sequence	523	10.6	50.5	36	6	BD259738	BD259738 Regulatio
451	10.8	51.4	39	6	AR148367	AR148367 Sequence	524	10.6	50.5	36	6	BD259739	BD259739 Regulatio
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453	10.8	51.4	43	6	AX484526	AX484526 Sequence	526	10.6	50.5	36	6	BD259773	BD259773 Regulatio
454	10.8	51.4	45	6	A05538	A05538 Oligonucleo	527	10.6	50.5	36	6	BD259834	BD259834 Regulatio
455	10.8	51.4	45	6	AR001631	AR001631 Sequence	528	10.6	50.5	36	6	BD259835	BD259835 Regulatio
456	10.8	51.4	45	6	I09088	I09088 Sequence 3	529	10.6	50.5	36	6	BD259864	BD259864 Regulatio
457	10.8	51.4	45	6	AR65316	AR65316 Sequence	530	10.6	50.5	36	6	BD259869	BD259869 Regulatio

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532	10.6	50.5	37	6	I69247	I69247	Sequence	605	10.6	50.5	38	6	AR336243	AR336243	Sequence
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537	10.6	50.5	38	6	AR333837	AR333837	Sequence	610	10.6	50.5	38	6	AR336282	AR336282	Sequence
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541	10.6	50.5	38	6	AR334016	AR334016	Sequence	614	10.6	50.5	38	6	AR336362	AR336362	Sequence
542	10.6	50.5	38	6	AR334046	AR334046	Sequence	615	10.6	50.5	38	6	AR336436	AR336436	Sequence
543	10.6	50.5	38	6	AR334112	AR334112	Sequence	616	10.6	50.5	38	6	AR336574	AR336574	Sequence
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545	10.6	50.5	38	6	AR334245	AR334245	Sequence	618	10.6	50.5	38	6	AR336505	AR336505	Sequence
546	10.6	50.5	38	6	AR334248	AR334248	Sequence	619	10.6	50.5	38	6	AR336532	AR336532	Sequence
547	10.6	50.5	38	6	AR334287	AR334287	Sequence	620	10.6	50.5	38	6	AR336568	AR336568	Sequence
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551	10.6	50.5	38	6	AR334394	AR334394	Sequence	624	10.6	50.5	38	6	AX044050	AX044050	Sequence
552	10.6	50.5	38	6	AR334396	AR334396	Sequence	625	10.6	50.5	38	6	AX044104	AX044104	Sequence
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554	10.6	50.5	38	6	AR334422	AR334422	Sequence	627	10.6	50.5	38	6	AX219088	AX219088	Sequence
555	10.6	50.5	38	6	AR334445	AR334445	Sequence	628	10.6	50.5	38	6	AX219091	AX219091	Sequence
556	10.6	50.5	38	6	AR334447	AR334447	Sequence	629	10.6	50.5	38	6	AX219111	AX219111	Sequence
557	10.6	50.5	38	6	AR334449	AR334449	Sequence	630	10.6	50.5	38	6	AX219131	AX219131	Sequence
558	10.6	50.5	38	6	AR334469	AR334469	Sequence	631	10.6	50.5	38	6	AX219145	AX219145	Sequence
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571	10.6	50.5	38	6	AR334782	AR334782	Sequence	644	10.6	50.5	38	6	AX219266	AX219266	Sequence
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994	10.4	49.5	38	6	AX227918	AX227918 Sequence
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## ALIGNMENTS

RESULT 1  
BD181363/c 21 bp DNA linear PAT 15-MAY-2003  
LOCUS A method for determination of a nucleic acid using a control.

DEFINITION BD181363  
ACCESSION BD181363.1 GI:30792281  
VERSION JP 2002335981-A/2.

KEYWORDS synthetic construct

SOURCE artificial sequences.

ORGANISM 1 (bases 1 to 21)

REFERENCE Jaeger, S.  
A method for determination of a nucleic acid using a control

AUTHORS Patent: JP 2002335981-A 2 26-NOV-2002;

JOURNAL F. HOFFMANN LA ROCHE AG

COMMENT OS Artificial Sequence

PN JP 2002335981-A/2

PD 26-NOV-2002

PR 04-MAR-2002 JP 2002057515

PT 02-MAR-2001 EP 01105172.9

PC STEPHAN JAEGER

PC C12N15/09, C12Q1/68, G01N33/50, G01N33/53, G01N33/566, G01N33/58,

CC Description of Artificial Sequence: artificial sequence to CC

CC exemplify

CC principle

CC key

CC source

CC location/Qualifiers

CC location/Qualifiers

CC location/Qualifiers

CC location/Qualifiers

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CC location/Qualifiers

Query Match 100.0%; Score 21; DB 6; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGTCATTAGACCGTACGCGA 21

DB 21 CGGTCATTAGACCGTACGCGA 1

RESULT 2  
BD181378 21 bp DNA linear PAT 15-MAY-2003

LOCUS A method for determination of a nucleic acid using a control.

DEFINITION BD181378

ACCESSION BD181378.1 GI:30792296

VERSION JP 2002335981-A/17.

KEYWORDS synthetic construct

SOURCE artificial sequences.

ORGANISM 1 (bases 1 to 21)

REFERENCE Jaeger, S.  
A method for determination of a nucleic acid using a control

AUTHORS Patent: JP 2002335981-A 17 26-NOV-2002;

JOURNAL F. HOFFMANN LA ROCHE AG

COMMENT OS Artificial Sequence

PN JP 2002335981-A/17

PD 26-NOV-2002

PR 04-MAR-2002 JP 2002057515

PT 02-MAR-2001 EP 01105172.9

PC STEPHAN JAEGER

PC C12N15/09, C12Q1/68, G01N33/50, G01N33/53, G01N33/566, G01N33/58,

PC C12N15/00

CC Description of Artificial Sequence: artificial sequence to CC

CC exemplify

CC principle

CC key

CC source

CC location/Qualifiers

CC location/Qualifiers

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CC location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGGTCAATAGACCGTACGCGA 21  
DB 21 CGGTCAATAGACCGTACGCGA 1

RESULT 4  
AX524841/c  
LOCUS AX524841 21 bp DNA linear PAT 21-NOV-2002  
DEFINITION Sequence 2 from Patent EP1236805.  
ACCESSION AX524841  
VERSION AX524841.1 GI:25169935  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM artificial sequences.

REFERENCE 1  
AUTHORS Jaeger, S.  
TITLE A method for the determination of a nucleic acid using a control  
JOURNAL Patent: EP 1236805-A 2 04-SEP-2002;  
Roche Diagnostics GmbH (DE) ; F. HOFMANN-LA ROCHE AG (CH)  
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Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGGTCAATAGACCGTACGCGA 21  
DB 21 CGGTCAATAGACCGTACGCGA 1

RESULT 5  
AX524856  
LOCUS AX524856 21 bp DNA linear PAT 21-NOV-2002  
DEFINITION Sequence 17 from Patent EP1236805.  
ACCESSION AX524856  
VERSION AX524856.1 GI:25169950  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM artificial sequences.

REFERENCE 1  
AUTHORS Jaeger, S.  
TITLE A method for the determination of a nucleic acid using a control  
JOURNAL Patent: EP 1236805-A 17 04-SEP-2002;  
Roche Diagnostics GmbH (DE) ; F. HOFMANN-LA ROCHE AG (CH)  
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OY 1 CGGTCAATAGACCGTACGCGA 21  
DB 21 CGGTCAATAGACCGTACGCGA 1

DB 1 CGGTCAATAGACCGTACGCGA 21  
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RESULT 6  
BD227377 29 bp DNA linear PAT 17-JUL-2003  
LOCUS BD227377  
DEFINITION Secreted proteins and polynucleotides encoding them.  
ACCESSION BD227377  
VERSION BD227377.1 GI:33037147  
KEYWORDS JP 2002522062-A/138.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 29)  
AUTHORS Jacob, K., McCoy, J.M., Lavallie, E.R., Racie, L.A.C., Evans, C.,  
Weber, D., Treacy, M., Agostino, M.J., II, R.J.S., Spaulding, V.,  
Wong, G.G., Clark, H.F., and Fechtel, K.  
TITLE Secreted proteins and polynucleotides encoding them  
JOURNAL Patent: JP 2002522062-A 138 23-JUL-2002;  
GENETICS INSTITUTE INC  
COMMENT OS Artificial Sequence  
PN JP 2002522062-A/138  
PD 23-JUL-2002  
PF 13-AUG-1999 JP 2000565001  
PR 14-AUG-1998 US 60/096622, 17-AUG-1998 US 60/096815 PR  
04-SEP-1998 US 60/099229, 23-OCT-1998 US 60/105368 PR  
08-JAN-1999 US 60/115234, 12-FEB-1999 US 60/119931 PR  
18-FEB-1999 US 60/120575, 30-APR-1999 US 60/132020 PR  
11-AUG-1999 US 60/148424  
PI KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A COLLINS  
PI RACIE,  
PI CHERYL EVANS, DAVID MERBERG, MAURICE TREACY, MICHAEL J AGOSTINO,  
PI ROBERT J STEININGER II, YIKKI SRAULDING, GORDON G WONG, HILARY F  
PI CLARK,  
PI KIM FECHTEL  
PC C12N15/09, A61K38/00, A61K39/395, A61K45/00, A61K48/00,  
PC A61P7/00,  
PC A61P7/02, A61P7/04, A61P7/06, A61P13/00, A61P29/00, A61P35/00, PC  
A61P37/02,  
PC A61P43/00, A61P43/00, C07K14/47, C12N5/10, C12P21/02, G01N33/15, PC  
G01N33/50,  
PC C12N15/00, C12N5/00, A61K37/02  
CC oligonucleotide  
CC biotinylated phosphoramidite residue  
FH key Location/Qualifiers  
FT misc\_feature (2).  
Location/Qualifiers  
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OY 2 GGTCAATAGACCGTACGCGA 21  
DB 5 GGTCAATAGACCGTACGCGA 24

RESULT 7  
AX752106/c  
LOCUS AX752106 30 bp DNA linear PAT 20-JUN-2003  
DEFINITION Sequence 5 from Patent WO03035876.  
ACCESSION AX752106  
VERSION AX752106.1 GI:32134216  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

REFERENCE Hepacivirus.  
 AUTHORS Krebs, A., John, M., Schuppan, D., Limmer, S. and Kreutzler, R.  
 TITLE Use of a double strand ribonucleic acid for treating an infection  
 JOURNAL with a positive-strand RNA-virus  
 Patent: WO 03035876-A 5 01-MAY-2003;  
 Ribopharma AG (DE)  
 FEATURES Location/Qualifiers  
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 30 GTCATTAGACCGTCCG 15  
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 RESULT 8  
 AX295474 20 bp DNA linear PAT 21-NOV-2001  
 LOCUS Sequence 7236 from Patent WO0179548.  
 DEFINITION AX295474  
 ACCESSION AX295474  
 VERSION AX295474.1 GI:17057163  
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 ORGANISM synthetic construct  
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 Best Local Similarity 78.9%; Pred. No. 1.1e+05;  
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 QY 1 CGGTCATTAGACCGTACG 19  
 20 CCGTACTAGACCGACGCG 2  
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 RESULT 9  
 AX290841 24 bp DNA linear PAT 21-NOV-2001  
 LOCUS Sequence 2603 from Patent WO0179548.  
 DEFINITION AX290841  
 ACCESSION AX290841  
 VERSION AX290841.1 GI:17052524  
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 ORGANISM synthetic construct  
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 Best Local Similarity 78.9%; Pred. No. 1.1e+05;  
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 QY 1 CGGTCATTAGACCGTACG 19  
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 RESULT 11  
 AX044290 26 bp DNA linear PAT 24-NOV-2000  
 LOCUS Sequence 102 from Patent WO0066773.  
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 ACCESSION AX044290.1 GI:11343168  
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 Best Local Similarity 78.9%; Pred. No. 1.1e+05;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
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 Db  
 RESULT 10  
 BD260345 26 bp DNA linear PAT 17-JUL-2003  
 LOCUS Methods.  
 DEFINITION BD260345  
 ACCESSION BD260345.1 GI:33070115  
 VERSION UP 2002542803-A/102.  
 KEYWORDS  
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 ORGANISM synthetic construct  
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 Best Local Similarity 78.9%; Pred. No. 1.1e+05;  
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 QY 2 GGTCAATTAGACCGTACG 20  
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 Db  
 RESULT 11  
 AX044290 26 bp DNA linear PAT 24-NOV-2000  
 LOCUS Sequence 102 from Patent WO0066773.  
 DEFINITION AX044290  
 ACCESSION AX044290.1 GI:11343168  
 VERSION AX044290.1 GI:11343168  
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 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 FEATURES Location/Qualifiers  
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 Best Local Similarity 78.9%; Pred. No. 1.1e+05;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 2 GGTCAATTAGACCGTACG 20  
 20 GTCATTAGACCGTACG 2  
 Db  
 RESULT 11  
 AX044290 26 bp DNA linear PAT 24-NOV-2000  
 LOCUS Sequence 102 from Patent WO0066773.  
 DEFINITION AX044290  
 ACCESSION AX044290.1 GI:11343168  
 VERSION AX044290.1 GI:11343168  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 FEATURES Location/Qualifiers  
 source 1..26  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="Hypothetical Probe Sequence"



REFERENCE 1  
AUTHORS Windase,J.D., Heaney,S.P., Renwick,A., Whitcombe,D.M., Little,S.,  
Gibson,N.J., Theaker,J. and Stranger,C.P.  
TITLE Method of detection of cytochrome b mutations in fungi leading to  
JOURNAL resistance against anti-fungal agents  
ZENBCA LIMITED (GB)  
Patent: WO 006773-A 102 09-NOV-2000;  
FEATURES Location/Qualifiers  
SOURCE 1..26  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

ORIGIN  
Query Match 60.0%; Score 12.6; DB 6; Length 26;  
Best Local Similarity 78.9%; Pred.No.1e+05;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGTCAATTAGACCGTACGCG 20  
DB 20 GGTCAATTGACCATACAGC 2

RESULT 12  
LOCUS AR168721 31 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 17 from patent US 6287866.  
ACCESSION AR168721  
VERSION AR168721.1 GI:17904788  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 31)  
AUTHORS Mukerji,P., Lemmel,S.A., Leonard,A.Eun.-Yeong. and Chaudhary,S.  
TITLE beta-casein expressing constructs  
JOURNAL Patent: US 6287866-A 17 11-SEP-2001;  
FEATURES Location/Qualifiers  
SOURCE 1..31  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 60.0%; Score 12.6; DB 6; Length 31;  
Best Local Similarity 78.9%; Pred.No.1e+05;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGGTCAATTAGACCGTACGC 19  
DB 30 CGGTCAATGACAGTACTC 12

RESULT 13  
LOCUS AR047950 33 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 29 from patent US 5820866.  
ACCESSION AR047950  
VERSION AR047950.1 GI:5970293  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 33)  
AUTHORS Kappler,J.W. and Marrack,P.  
TITLE Product and process for T cell regulation  
JOURNAL Patent: US 5820866-A 29 13-OCT-1998;  
FEATURES Location/Qualifiers  
SOURCE 1..33  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 60.0%; Score 12.6; DB 6; Length 33;  
Best Local Similarity 78.9%; Pred.No.1e+05;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGGTCAATTAGACCGTACGC 19  
DB 20 GGTCAATCGTTCGTACGC 2

RESULT 14  
LOCUS AR334533 38 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 11935 from patent US 6566127.  
ACCESSION AR334533  
VERSION AR334533.1 GI:33720341  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 38)  
AUTHORS Payco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions  
JOURNAL related to levels of vascular endothelial growth factor receptor  
Patent: US 6566127-A 11935 20-MAY-2003;  
FEATURES Location/Qualifiers  
SOURCE 1..38  
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/mol\_type="unassigned RNA"

ORIGIN  
Query Match 60.0%; Score 12.6; DB 6; Length 38;  
Best Local Similarity 75.0%; Pred.No.1e+05;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 GGTCAATTAGACCGTACGCGA 21  
DB 16 GGCGGTAGGCCGANGCGA 35

RESULT 15  
LOCUS AR335779 38 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 13181 from patent US 6566127.  
ACCESSION AR335779  
VERSION AR335779.1 GI:33721587  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 38)  
AUTHORS Payco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
TITLE Method and reagent for the treatment of diseases or conditions  
JOURNAL related to levels of vascular endothelial growth factor receptor  
Patent: US 6566127-A 13181 20-MAY-2003;  
FEATURES Location/Qualifiers  
SOURCE 1..38  
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/mol\_type="unassigned RNA"

ORIGIN  
Query Match 60.0%; Score 12.6; DB 6; Length 38;  
Best Local Similarity 75.0%; Pred.No.1e+05;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 GGTCAATTAGACCGTACGCGA 21  
DB 16 GGCGGTAGGCCGANGCGA 35

RESULT 16  
LOCUS AR336409 38 bp RNA linear PAT 17-AUG-2003  
DEFINITION Sequence 13811 from patent US 6566127.

Accession	Version	KeyWords	Source	Organism	Reference	Authors	Title	Journal	Features	Source	Origin	Query Match	Best Local Similarity	Matches	Score	DB	Length	Indels	Gaps	
AR336409	1	GI:33722217	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 38)	Pavco, P., Meswigen, J. A., Stinchcomb, D. T. and Escobedo, J.	Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor	Patent: US 6566127 A 13811 20-MAY-2003;	Location/Qualifiers	1. 38	/organism="unknown"	/mol_type="unassigned RNA"		60.0%;	Score 12.6;	DB 6;	Length 38;		
AR455837/c	1	GI:42690729	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 38)	Nock, S. and Kassner, P. D.	Screening of phage displayed peptides without clearing of the cell culture	Patent: US 6686154-A 83 03-FEB-2004;	Location/Qualifiers	1. 38	/organism="unknown"	/mol_type="genomic DNA"		60.0%;	Score 12.6;	DB 6;	Length 38;		
AR455837	1	GI:42690729	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 38)	Nock, S. and Kassner, P. D.	Screening of phage displayed peptides without clearing of the cell culture	Patent: US 6686154-A 83 03-FEB-2004;	Location/Qualifiers	1. 38	/organism="unknown"	/mol_type="genomic DNA"		60.0%;	Score 12.6;	DB 6;	Length 38;		
AR455837	1	GI:42690729	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 38)	Nock, S. and Kassner, P. D.	Screening of phage displayed peptides without clearing of the cell culture	Patent: US 6686154-A 83 03-FEB-2004;	Location/Qualifiers	1. 38	/organism="unknown"	/mol_type="genomic DNA"		60.0%;	Score 12.6;	DB 6;	Length 38;		
AR455837	1	GI:42690729	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 38)	Nock, S. and Kassner, P. D.	Screening of phage displayed peptides without clearing of the cell culture	Patent: US 6686154-A 83 03-FEB-2004;	Location/Qualifiers	1. 38	/organism="unknown"	/mol_type="genomic DNA"		60.0%;	Score 12.6;	DB 6;	Length 38;		
AR455837	1	GI:42690729	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 38)	Nock, S. and Kassner, P. D.	Screening of phage displayed peptides without clearing of the cell culture	Patent: US 6686154-A 83 03-FEB-2004;	Location/Qualifiers	1. 38	/organism="unknown"	/mol_type="genomic DNA"		60.0%;	Score 12.6;	DB 6;	Length 38;		
AR455837	1	GI:42690729	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 38)	Nock, S. and Kassner, P. D.	Screening of phage displayed peptides without clearing of the cell culture	Patent: US 6686154-A 83 03-FEB-2004;	Location/Qualifiers	1. 38	/organism="unknown"	/mol_type="genomic DNA"		60.0%;	Score 12.6;	DB 6;	Length 38;		
AR455837	1	GI:42690729	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 38)	Nock, S. and Kassner, P. D.	Screening of phage displayed peptides without clearing of the cell culture	Patent: US 6686154-A 83 03-FEB-2004;	Location/Qualifiers	1. 38	/organism="unknown"	/mol_type="genomic DNA"		60.0%;	Score 12.6;	DB 6;	Length 38;		
AR455837	1	GI:42690729	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 38)	Nock, S. and Kassner, P. D.	Screening of phage displayed peptides without clearing of the cell culture	Patent: US 6686154-A 83 03-FEB-2004;	Location/Qualifiers	1. 38	/organism="unknown"	/mol_type="genomic DNA"		60.0%;	Score 12.6;	DB 6;	Length 38;		
AR455837	1	GI:42690729	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 38)	Nock, S. and Kassner, P. D.	Screening of phage displayed peptides without clearing of the cell culture	Patent: US 6686154-A 83 03-FEB-2004;	Location/Qualifiers	1. 38	/organism="unknown"	/mol_type="genomic DNA"		60.0%;	Score 12.6;	DB 6;	Length 38;		
AR455837	1	GI:42690729	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 38)	Nock, S. and Kassner, P. D.	Screening of phage displayed peptides without clearing of the cell culture	Patent: US 6686154-A 83 03-FEB-2004;	Location/Qualifiers	1. 38	/organism="unknown"	/mol_type="genomic DNA"		60.0%;	Score 12.6;	DB 6;	Length 38;		
AR455837	1	GI:42690729	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 38)	Nock, S. and Kassner, P. D.	Screening of phage displayed peptides without clearing of the cell culture	Patent: US 6686154-A 83 03-FEB-2004;	Location/Qualifiers	1. 38	/organism="unknown"	/mol_type="genomic DNA"		60.0%;	Score 12.6;	DB 6;	Length 38;		
AR455837	1	GI:42690729	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 38)	Nock, S. and Kassner, P. D.	Screening of phage displayed peptides without clearing of the cell culture	Patent: US 6686154-A 83 03-FEB-2004;	Location/Qualifiers	1. 38	/organism="unknown"	/mol_type="genomic DNA"		60.0%;	Score 12.6;	DB 6;	Length 38;		
AR455837	1	GI:42690729	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 38)	Nock, S. and Kassner, P. D.	Screening of phage displayed peptides without clearing of the cell culture	Patent: US 6686154-A 83 03-FEB-2004;	Location/Qualifiers	1. 38	/organism="unknown"	/mol_type="genomic DNA"		60.0%;	Score 12.6;	DB 6;	Length 38;		
AR455837	1	GI:42690729	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 38)	Nock, S. and Kassner, P. D.	Screening of phage displayed peptides without clearing of the cell culture	Patent: US 6686154-A 83 03-FEB-2004;	Location/Qualifiers	1. 38	/organism="unknown"	/mol_type="genomic DNA"		60.0%;	Score 12.6;	DB 6;	Length 38;		
AR455837	1	GI:42690729	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 38)	Nock, S. and Kassner, P. D.	Screening of phage displayed peptides without clearing of the cell culture	Patent: US 6686154-A 83 03-FEB-2004;	Location/Qualifiers	1. 38</									

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/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="WVK24 primer"

ORIGIN

Query Match 60.0%; Score 12.6; DB 6; Length 38;  
Best Local Similarity 78.9%; Pred. No. 1e+05;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 GGTCAATTGACCGTACGCG 20  
|||||  
30 GGTCAATTACATGTCGCG 12

Db

RESULT 21  
AX424618 38 bp RNA linear PAT 18-JUN-2002  
LOCUS  
DEFINITION Sequence 2954 from Patent WO0188124.  
ACCESSION AX424618  
VERSION AX424618.1 GI:21528000  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Jarvis, T., von Carlowitz, I., Mewswigen, J.A., McLaughlin, F.G. and Randi, A.M.  
JOURNAL Method and reagent for the inhibition of erg  
PATENT: WO 0188124-A 2954 22-NOV-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)

FEATURES  
source 1..38  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Enzymatic Nucleic Acid"

misc\_feature 31

ORIGIN

Query Match 60.0%; Score 12.6; DB 6; Length 38;  
Best Local Similarity 75.0%; Pred. No. 1e+05;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 GGTCAATTGACCGTACGCG 21  
|||||  
16 GGCCGTTAGCCGCGANGCGA 35

Db

RESULT 22  
AX424731 38 bp RNA linear PAT 18-JUN-2002  
LOCUS  
DEFINITION Sequence 3067 from Patent WO0188124.  
ACCESSION AX424731  
VERSION AX424731.1 GI:21528113  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Jarvis, T., von Carlowitz, I., Mewswigen, J.A., McLaughlin, F.G. and Randi, A.M.  
JOURNAL Method and reagent for the inhibition of erg  
PATENT: WO 0188124-A 3067 22-NOV-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)

FEATURES  
source 1..38  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Enzymatic Nucleic Acid"

misc\_feature 31

/note="n strands for inosine"

ORIGIN

Query Match 60.0%; Score 12.6; DB 6; Length 38;  
Best Local Similarity 75.0%; Pred. No. 1e+05;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 GGTCAATTGACCGTACGCG 21  
|||||  
16 GGCCGTTAGCCGCGANGCGA 35

Db

RESULT 23  
AX581188 38 bp RNA linear PAT 10-JAN-2003  
LOCUS  
DEFINITION Sequence 3026 from Patent WO0211674.  
ACCESSION AX581188  
VERSION AX581188.1 GI:27652998  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Thompson, J., Mewswigen, J., McKenzie, T., Ayers, D., Szymkowski, D.E. and Grube, A.  
JOURNAL Method and reagent for the inhibition of calcium activated chloride channel-1 (CICa-1)  
PATENT: WO 0211674-A 3026 14-FEB-2002;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ; Thompson, James (US)

FEATURES  
source 1..38  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Enzymatic Nucleic Acid"

modified\_base 31  
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ORIGIN

Query Match 60.0%; Score 12.6; DB 6; Length 38;  
Best Local Similarity 75.0%; Pred. No. 1e+05;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 GGTCAATTGACCGTACGCG 21  
|||||  
16 GGCCGTTAGCCGCGANGCGA 35

Db

RESULT 24  
AX581359 38 bp RNA linear PAT 10-JAN-2003  
LOCUS  
DEFINITION Sequence 3197 from Patent WO0211674.  
ACCESSION AX581359  
VERSION AX581359.1 GI:27653169  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Thompson, J., Mewswigen, J., McKenzie, T., Ayers, D., Szymkowski, D.E. and Grube, A.  
JOURNAL Method and reagent for the inhibition of calcium activated chloride channel-1 (CICa-1)  
PATENT: WO 0211674-A 3197 14-FEB-2002;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ; Thompson, James (US)

FEATURES  
source 1..38  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Enzymatic Nucleic Acid"

modified\_base 31  
/mod\_base=1

## ORIGIN

Query Match 60.0%; Score 12.6; DB 6; Length 38;  
Best Local Similarity 75.0%; Pred. No. 1e+05;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 GGTGATTAGACCGTAGCGGA 21  
16 GGGCGGTAGCGCGAANGCGA 35  
Db

## RESULT 25

A65234 42 bp DNA linear PAT 29-MAR-1999  
LOCUS Sequence 5 from Patent WO9735011.  
DEFINITION A65234  
ACCESSION A65234  
VERSION A65234.1 GI:4531029  
KEYWORDS  
SOURCE  
ORGANISM

unidentified  
unidentified  
unclassified.

REFERENCE 1 Silvestrini, M.C., Cutruzzola, F., Ciabatti, Iliaria, Zennaro, E.,  
AUTHORS Visco, C., Discepolo and Massimo.  
TITLE RECOMBINANT PROCESS FOR THE PRODUCTION IN PSEUDOMONAS PUTIDA OF THE  
JOURNAL CYTOCHROME C551 OF PSEUDOMONAS AERUGINOSA  
Patent: WO 9735011-A 5 25-SEP-1997;  
COMMENT MINI RICERCA SCIENT TECNOLOG (17)  
FEATURES Other publication IT MI960515 19970915.  
source location/Qualifiers

1..42  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

## ORIGIN

Query Match 60.0%; Score 12.6; DB 6; Length 42;  
Best Local Similarity 78.9%; Pred. No. 1e+05;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CGGTCTTAGACCGTAGCGC 19  
19 CCGTGATGAACCGTAGCGC 37  
Db

## RESULT 26

AX295733/c 20 bp DNA linear PAT 21-NOV-2001  
LOCUS AX295733  
DEFINITION Sequence 7495 from Patent WO0179548.  
ACCESSION AX295733  
VERSION AX295733.1 GI:17057422  
KEYWORDS  
SOURCE  
ORGANISM

synthetic construct  
synthetic construct  
artificial sequences.

REFERENCE 1 Barany, F., Zivvi, M., Gerry, N.P., Favis, R. and Kliman, R.  
AUTHORS Method of designing addressable array for detection of nucleic acid  
TITLE sequence differences using ligase detection reaction  
JOURNAL Patent: WO 0179548-A 7495 25-OCT-2001;  
CORNELL RESEARCH FOUNDATION, INC. (US)  
FEATURES location/Qualifiers

1..20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Hypothetical Probe Sequence"

## ORIGIN

Query Match 59.0%; Score 12.4; DB 6; Length 20;  
Best Local Similarity 92.9%; Pred. No. 1.4e+05;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 ATTAGACCGTAGCGC 19  
15 ATTAGACCGTAGCGC 2  
Db

## RESULT 27

AX291100/c 24 bp DNA linear PAT 21-NOV-2001  
LOCUS AX291100  
DEFINITION Sequence 2862 from Patent WO0179548.  
ACCESSION AX291100  
VERSION AX291100.1 GI:17052783  
KEYWORDS  
SOURCE  
ORGANISM

synthetic construct  
synthetic construct  
artificial sequences.

REFERENCE 1 Barany, F., Zivvi, M., Gerry, N.P., Favis, R. and Kliman, R.  
AUTHORS Method of designing addressable array for detection of nucleic acid  
TITLE sequence differences using ligase detection reaction  
JOURNAL Patent: WO 0179548-A 2862 25-OCT-2001;  
CORNELL RESEARCH FOUNDATION, INC. (US)  
FEATURES location/Qualifiers

1..24  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Hypothetical Probe Sequence"

## ORIGIN

Query Match 59.0%; Score 12.4; DB 6; Length 24;  
Best Local Similarity 92.9%; Pred. No. 1.4e+05;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 ATTAGACCGTAGCGC 19  
15 ATTAGACCGTAGCGC 2  
Db

## RESULT 28

AX464504/c 34 bp DNA linear PAT 16-JUL-2002  
LOCUS AX464504  
DEFINITION Sequence 39 from Patent EP1219635.  
ACCESSION AX464504  
VERSION AX464504.1 GI:21899300  
KEYWORDS  
SOURCE  
ORGANISM

synthetic construct  
synthetic construct  
artificial sequences.

REFERENCE 1 Couture, F., Hamel, J., Brodeur, B.R. and Martin, D.  
AUTHORS Chlamydia pneumoniae antigens  
TITLE Patent: EP 1219635-A 39 03-JUL-2002;  
JOURNAL SHIRE BIOCHEM INC. (CA)  
FEATURES location/Qualifiers

1..34  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="oligonucleotide primer"

## ORIGIN

Query Match 59.0%; Score 12.4; DB 6; Length 34;  
Best Local Similarity 92.9%; Pred. No. 1.3e+05;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 CATTAGACCGTAGC 18  
34 CATTAGACCGTAGC 21  
Db

## RESULT 29

CC ABI97546 represent oligonucleotide sequences used in the exemplification  
CC of the present invention  
XX  
SQ Sequence 24 BP; 7 A; 10 C; 5 G; 2 T; 0 U; 0 Other;  
Query Match 60.0%; Score 12.6; DB 6; Length 24;  
Best Local Similarity 78.9%; Pred. No. 4.1e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 1 CGGTCAATGACCGTACGC 19  
|||  
Db 5 CGGTCAATGACCGTACGC 23  
|||  
RESULT 15  
ACI25753  
ID ACI25753 standard; DNA; 25 BP.  
XX  
ACI25753;  
XX  
DT 13-OCT-2003 (first entry)  
XX  
DE Human microarray DNA oligonucleotide SEQ ID NO 25744.  
XX  
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;  
KW genetic variation; biallelic marker; polymorphism; human;  
KW cross-species comparison.  
XX  
OS Homo sapiens.  
XX  
PN US2003104410-A1.  
XX  
PD 05-JUN-2003.  
XX  
PF 15-MAR-2002; 2002US-00098263.  
XX  
PR 16-MAR-2001; 2001US-0276759P.  
XX  
PA (AFFY-) AFFYMETRIX INC.  
XX  
PI Miltmann MP;  
XX  
DR WPI; 2003-567953/53.  
XX  
PT New array of nucleic acid probes, useful for in situ hybridization, in  
PT Southern, Northern or dot-blot hybridization to identify or detect the  
PT sequence or specific mutations of any gene.  
XX  
PS Claim 1; SEQ ID NO 25744; 9pp; English.  
XX  
CC The invention discloses a microarray comprising a plurality of nucleic  
CC acid probes including one of 2,018,500 fully defined sequences, or its  
CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
CC Also disclosed is a method of gene expression analysis. The array is used  
CC in monitoring gene expression levels by hybridisation to a DNA library,  
CC in analysis of genetic variation or in hybridisation of tag-labelled  
CC compounds. The nucleic acid probes are specifically designed for analysis  
CC of at least one target sequence. The method of analysis comprises  
CC hybridising at least one or more nucleic acids to at least two or more  
CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
CC probes are attached to a solid support. The analysis comprises monitoring  
CC gene expression levels, identifying biallelic markers or polymorphisms,  
CC or family members of a gene and a cross-species comparison. Each of the  
CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-  
CC blot hybridisation to identify or detect the sequence or specific  
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
CC primer extensions or in screening cDNA or genomic libraries or subclones  
CC for additional subclones containing segments of DNA that have been  
CC isolated and previously sequenced. The sequence presented is one of the  
CC nucleic acid probes incorporated in the microarray. Note: The sequence  
CC data for this patent can also be obtained in electronic format directly  
CC from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)

XX  
SQ Sequence 25 BP; 5 A; 9 C; 7 G; 4 T; 0 U; 0 Other;  
Query Match 60.0%; Score 12.6; DB 9; Length 25;  
Best Local Similarity 78.9%; Pred. No. 4.1e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 1 CGGTCAATGACCGTACGC 19  
|||  
Db 7 CGTCCCTTACCGTACGC 25  
|||  
RESULT 16  
ACK18838/C  
ID ACK18838 standard; DNA; 25 BP.  
XX  
ACK18838;  
XX  
DT 14-OCT-2003 (first entry)  
XX  
DE Human microarray DNA oligonucleotide SEQ ID NO 118819.  
XX  
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;  
KW genetic variation; biallelic marker; polymorphism; human;  
KW cross-species comparison.  
XX  
OS Homo sapiens.  
XX  
PN US2003104410-A1.  
XX  
PD 05-JUN-2003.  
XX  
PF 15-MAR-2002; 2002US-00098263.  
XX  
PR 16-MAR-2001; 2001US-0276759P.  
XX  
PA (AFFY-) AFFYMETRIX INC.  
XX  
PI Miltmann MP;  
XX  
DR WPI; 2003-567953/53.  
XX  
PT New array of nucleic acid probes, useful for in situ hybridization, in  
PT Southern, Northern or dot-blot hybridization to identify or detect the  
PT sequence or specific mutations of any gene.  
XX  
PS Claim 1; SEQ ID NO 118819; 9pp; English.  
XX  
CC The invention discloses a microarray comprising a plurality of nucleic  
CC acid probes including one of 2,018,500 fully defined sequences, or its  
CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
CC Also disclosed is a method of gene expression analysis. The array is used  
CC in monitoring gene expression levels by hybridisation to a DNA library,  
CC in analysis of genetic variation or in hybridisation of tag-labelled  
CC compounds. The nucleic acid probes are specifically designed for analysis  
CC of at least one target sequence. The method of analysis comprises  
CC hybridising at least one or more nucleic acids to at least two or more  
CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
CC probes are attached to a solid support. The analysis comprises monitoring  
CC gene expression levels, identifying biallelic markers or polymorphisms,  
CC or family members of a gene and a cross-species comparison. Each of the  
CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-  
CC blot hybridisation to identify or detect the sequence or specific  
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
CC primer extensions or in screening cDNA or genomic libraries or subclones  
CC for additional subclones containing segments of DNA that have been  
CC isolated and previously sequenced. The sequence presented is one of the  
CC nucleic acid probes incorporated in the microarray. Note: The sequence  
CC data for this patent can also be obtained in electronic format directly  
CC from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)

Query Match 60.0%; Score 12.6; DB 9; Length 25;  
Best Local Similarity 78.9%; Pred. No. 4.1e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGGTGATTAGACCGTAGCG 19  
21 CTGTGATTGACCGACGACAC 3

Db

RESULT 17  
AC156057  
ID AC156057 standard; DNA; 25 BP.  
XX AC156057;  
XX  
XX 13-OCT-2003 (first entry)  
XX  
XX Human microarray DNA oligonucleotide SEQ ID NO 56048.  
XX  
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;  
XX genetic variation; diallelic marker; polymorphism; human;  
XX cross-species comparison.  
XX  
XX Homo sapiens.  
XX  
XX US2003104410-A1.  
XX  
XX 05-JUN-2003.  
XX  
XX 15-MAR-2002; 2002US-00098263.  
XX  
XX 16-MAR-2001; 2001US-0276759P.  
XX  
XX (AFY-) AFFYMETRIX INC.  
XX  
XX Mitmann MP;  
XX  
XX WPI; 2003-567953/53.  
XX  
XX New array of nucleic acid probes, useful for in situ hybridization, in  
XX Southern, Northern or dot-blot hybridization to identify or detect the  
XX sequence or specific mutations of any gene.  
XX  
XX Claim 1; SEQ ID NO 56048; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic  
XX acid probes including one of 2,018,500 fully defined sequences, or its  
XX perfect match, perfect mismatch, antisense match or antisense mismatch.  
XX Also disclosed is a method of gene expression analysis. The array is used  
XX in monitoring gene expression levels by hybridization to a DNA library,  
XX in analysis of genetic variation or in hybridization of tag-labelled  
XX compounds. The nucleic acid probes are specifically designed for analysis  
XX of at least one target sequence. The method of analysis comprises  
XX hybridizing at least one or more nucleic acids to at least two or more  
XX nucleic acid probes and detecting the hybridization. The nucleic acid  
XX probes are attached to a solid support. The analysis comprises monitoring  
XX gene expression levels, identifying diallelic markers or polymorphisms,  
XX or family members of a gene and a cross-species comparison. Each of the  
XX nucleic acids further comprises a tag sequence. The array of nucleic acid  
XX probes is useful in situ hybridization, in Southern, Northern or dot-  
XX blot hybridization to identify or detect the sequence or specific  
XX mutations of any gene, in mapping the 5' termini of mRNA molecules by  
XX primer extensions or in screening cDNA or genomic libraries or subclones  
XX for additional subclones containing segments of DNA that have been  
XX isolated and previously sequenced. The sequence presented is one of the  
XX nucleic acid probes incorporated in the microarray. Note: The sequence  
XX data for this patent can also be obtained in electronic format directly  
XX from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)

XX Sequence 25 BP; 7 A; 5 C; 4 G; 9 T; 0 U; 0 Other;  
XX  
XX Query Match 60.0%; Score 12.6; DB 9; Length 25;

Best Local Similarity 78.9%; Pred. No. 4.1e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GTGATTAGACCGTAGCGGA 21  
6 GTGATTACACCGTGTGGA 24

Db

RESULT 18  
AC18839/C  
ID AC18839 standard; DNA; 25 BP.  
XX AC18839;  
XX  
XX 14-OCT-2003 (first entry)  
XX  
XX Human microarray DNA oligonucleotide SEQ ID NO 118820.  
XX  
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;  
XX genetic variation; diallelic marker; polymorphism; human;  
XX cross-species comparison.  
XX  
XX Homo sapiens.  
XX  
XX US2003104410-A1.  
XX  
XX 05-JUN-2003.  
XX  
XX 15-MAR-2002; 2002US-00098263.  
XX  
XX 16-MAR-2001; 2001US-0276759P.  
XX  
XX (AFY-) AFFYMETRIX INC.  
XX  
XX Mitmann MP;  
XX  
XX WPI; 2003-567953/53.  
XX  
XX New array of nucleic acid probes, useful for in situ hybridization, in  
XX Southern, Northern or dot-blot hybridization to identify or detect the  
XX sequence or specific mutations of any gene.  
XX  
XX Claim 1; SEQ ID NO 118820; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic  
XX acid probes including one of 2,018,500 fully defined sequences, or its  
XX perfect match, perfect mismatch, antisense match or antisense mismatch.  
XX Also disclosed is a method of gene expression analysis. The array is used  
XX in monitoring gene expression levels by hybridization to a DNA library,  
XX in analysis of genetic variation or in hybridization of tag-labelled  
XX compounds. The nucleic acid probes are specifically designed for analysis  
XX of at least one target sequence. The method of analysis comprises  
XX hybridizing at least one or more nucleic acids to at least two or more  
XX nucleic acid probes and detecting the hybridization. The nucleic acid  
XX probes are attached to a solid support. The analysis comprises monitoring  
XX gene expression levels, identifying diallelic markers or polymorphisms,  
XX or family members of a gene and a cross-species comparison. Each of the  
XX nucleic acids further comprises a tag sequence. The array of nucleic acid  
XX probes is useful in situ hybridization, in Southern, Northern or dot-  
XX blot hybridization to identify or detect the sequence or specific  
XX mutations of any gene, in mapping the 5' termini of mRNA molecules by  
XX primer extensions or in screening cDNA or genomic libraries or subclones  
XX for additional subclones containing segments of DNA that have been  
XX isolated and previously sequenced. The sequence presented is one of the  
XX nucleic acid probes incorporated in the microarray. Note: The sequence  
XX data for this patent can also be obtained in electronic format directly  
XX from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)

XX Sequence 25 BP; 6 A; 5 C; 7 G; 7 T; 0 U; 0 Other;  
XX  
XX Query Match 60.0%; Score 12.6; DB 9; Length 25;  
XX Best Local Similarity 78.9%; Pred. No. 4.1e+03;  
XX Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CC ABI97546 represent oligonucleotide sequences used in the exemplification  
CC of the present invention

XX Sequence 20 BP, 2 A, 4 C, 8 G, 6 T, 0 U, 0 Other;

Query Match 60.0%; Score 12.6; DB 6; Length 20;

Best Local Similarity 78.9%; Pred. No. 4e+03;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGGTCTTAGACCGTAGC 19

DB 20 CCGTCACTAGACCGAGCGC 2

RESULT 13

ABI87602/C

ID ABI87602 standard; DNA; 24 BP.

XX ABI87602;

DT 15-FEB-2002 (first entry)

DE Capture oligonucleotide Zip ID#2603 oligo #1.

XX Human; K-ras; PCR primer; probe; capture probe; mutation detection;  
XX ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;  
XX infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;  
XX oncogene; tumour suppressor; human papillomavirus; forensic;  
XX environmental monitoring; food industry; feed industry; ss.

OS Synthetic.

PN WO200179548-A2.

PD 25-OCT-2001.

PF 04-APR-2001; 2001WO-US010958.

PR 14-APR-2000; 2000US-0197271P.

(CORR ) CORNELL RES FOUND INC.

PI Barany F, Zivri M, Gerry NP, Favis R, Kliman R;

DR WPI; 2002-034366/04.

PT Designing capture oligonucleotide probes for use on a support to which  
PT complementary oligonucleotides hybridize with little mismatch.

PS Example 5; Fig 25; 300pp; English.

XX The present invention describes a method (M1) for designing capture  
XX oligonucleotide probes (I) for use on a support to which complementary  
XX oligonucleotide probes (II) will hybridize with little mismatch, where  
XX (I) have melting temperatures within a narrow range. The method is useful  
XX for detecting infectious diseases caused by bacterial infectious agents  
XX e.g. Salmonella, listeria monocytogenes and Haemophilus influenza, fungal  
XX infectious agents e.g. Cryptococcus neoformans, Candida albicans and  
XX Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,  
XX Epstein-Barr virus and polio virus, and parasitic infectious agents  
XX selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus  
XX medialis. The method is also useful for detecting genetic diseases such  
XX as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.  
XX Detecting cancer involving oncogenes, tumour suppressor genes, or genes  
XX involved in DNA amplification, replication, recombination or repair, the  
XX cancer is specifically associated with a gene selected from BRCA1 gene,  
XX p53 gene, human papillomavirus types 16 and 18 and liver cancers. The  
XX method is also used for environmental monitoring, forensics and the food  
XX and feed industry, detecting comprises scanning (using e.g. a scanning  
XX electron microscope and infrared microscope) the support at the  
XX particular sites and identifying if ligation of the oligonucleotide probe  
XX sets occurred and correlating (using a computer) identified ligation to a  
XX presence or absence of the target nucleotide sequences. ABI82074 to

CC ABI97546 represent oligonucleotide sequences used in the exemplification  
CC of the present invention

XX Sequence 24 BP, 2 A, 5 C, 10 G, 7 T, 0 U, 0 Other;

Query Match 60.0%; Score 12.6; DB 6; Length 24;

Best Local Similarity 78.9%; Pred. No. 4.1e+03;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGGTCTTAGACCGTAGC 19

DB 20 CCGTCACTAGACCGAGCGC 2

RESULT 14

ABI87603

ID ABI87603 standard; DNA; 24 BP.

XX ABI87603;

DT 15-FEB-2002 (first entry)

DE Capture oligonucleotide Zip ID#2603 oligo #2.

XX Human; K-ras; PCR primer; probe; capture probe; mutation detection;  
XX ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;  
XX infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;  
XX oncogene; tumour suppressor; human papillomavirus; forensic;  
XX environmental monitoring; food industry; feed industry; ss.

OS Synthetic.

PN WO200179548-A2.

PD 25-OCT-2001.

PF 04-APR-2001; 2001WO-US010958.

PR 14-APR-2000; 2000US-0197271P.

(CORR ) CORNELL RES FOUND INC.

PI Barany F, Zivri M, Gerry NP, Favis R, Kliman R;

DR WPI; 2002-034366/04.

PT Designing capture oligonucleotide probes for use on a support to which  
PT complementary oligonucleotides hybridize with little mismatch.

PS Example 5; Fig 25; 300pp; English.

XX The present invention describes a method (M1) for designing capture  
XX oligonucleotide probes (I) for use on a support to which complementary  
XX oligonucleotide probes (II) will hybridize with little mismatch, where  
XX (I) have melting temperatures within a narrow range. The method is useful  
XX for detecting infectious diseases caused by bacterial infectious agents  
XX e.g. Salmonella, listeria monocytogenes and Haemophilus influenza, fungal  
XX infectious agents e.g. Cryptococcus neoformans, Candida albicans and  
XX Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,  
XX Epstein-Barr virus and polio virus, and parasitic infectious agents  
XX selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus  
XX medialis. The method is also useful for detecting genetic diseases such  
XX as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.  
XX Detecting cancer involving oncogenes, tumour suppressor genes, or genes  
XX involved in DNA amplification, replication, recombination or repair, the  
XX cancer is specifically associated with a gene selected from BRCA1 gene,  
XX p53 gene, human papillomavirus types 16 and 18 and liver cancers. The  
XX method is also used for environmental monitoring, forensics and the food  
XX and feed industry, detecting comprises scanning (using e.g. a scanning  
XX electron microscope and infrared microscope) the support at the  
XX particular sites and identifying if ligation of the oligonucleotide probe  
XX sets occurred and correlating (using a computer) identified ligation to a  
XX presence or absence of the target nucleotide sequences. ABI82074 to



AC	ADD12949;
XX	
DT	01-JAN-2004 (first entry)
DE	HCV NS3 probe.
XX	
KW	double-stranded RNA; dsRNA; infection; NS3 helicase; vironuclide;
KW	antiinflammatory; hepatotropic; hepatitis C virus infection; ss; probe.
XX	
OS	Hepatitis C virus.
XX	
FT	Key
FT	Location/Qualifiers
FT	modified_base
FT	1
FT	/tag= a
FT	/mod_base= OTHER
FT	/note= "FAM labelled"
FT	
FT	modified_base
FT	30
FT	/tag= b
FT	/mod_base= OTHER
FT	/note= "TAMRA labelled"
XX	
PN	WO2003035876-A1.
XX	
FD	01-MAY-2003.
ED	
XX	
PE	25-OCT-2002; 2002WO-EP011973.
XX	
PR	26-OCT-2001; 2001DE-01055280.
PR	29-NOV-2001; 2001DE-01058411.
PR	07-DEC-2001; 2001DE-01060151.
PR	09-JAN-2002; 2002WO-EP000151.
PR	09-JAN-2002; 2002WO-EP000152.
PR	02-AUG-2002; 2002DE-01035621.
XX	
PA	(RIBO-) RIBOPHARMA AG.
PI	
XX	
PI	Krebs A, John M, Schuppan D, Limmer S, Kreuzer R;
XX	
DR	WPI; 2003-430419/40.
XX	
PT	New double-stranded RNA for treating viral infections, useful especially
PT	for hepatitis C infection, is complementary to a region of a positive-
PT	strand RNA viral genome.
XX	
PS	Disclosure; SEQ ID NO 5; 35pp; German.
XX	
XX	
CC	This invention describes a novel use of a double-stranded RNA for
CC	treating infections by a (+)-strand RNA virus, where one strand (S1) of
CC	dsRNA includes a segment that is at least partly complementary to the
CC	translatable region of the viral genome. dsRNA is directed against
CC	hepatitis C virus (HCV) and inhibits expression of a polypeptide encoded
CC	by the viral genome, preferably a protease or helicase and most
CC	particularly the NS3 helicase, with the complementary region, in the
CC	reading direction of viral RNA, being upstream of, or within, the
CC	helicase coding region. dsRNA has, at least one end, an overhang of 1-4,
CC	preferably 2-3 nucleotides particularly at the 3'-end of S1. The second
CC	strand (S2) of dsRNA contains a 2-nucleotide overhang at the 3'-end of S1
CC	but no overhang at the other end (blunt). A single overhang increases
CC	inhibitory activity without causing significant loss of in vivo
CC	stability. dsRNA is formulated with a conventional solvent (especially
CC	phosphate-buffered saline) or it is incorporated into a micellar
CC	structure, particularly a liposome, viral capsid, capsid or a polymeric
CC	nanor- or micro-capsule (or it is bound to such capsules). The products of
CC	the invention have virucide, antiinflammatory and hepatotropic activity.
CC	dsRNA is administered by inhalation, infusion or injection, or orally,
CC	especially by intravenous or intraperitoneal injection or infusion. dsRNA
CC	is specifically used for treatment of hepatitis C virus infections. dsRNA
CC	permanently destroys the integrity of the viral genome. HuH-7 cells were
CC	transfected with double-stranded RNA (dsRNA), directed against the NS3
CC	coding region of the hepatitis C virus (HCV) genome and a fragment of the
CC	HCV genome that replicated stably without formation of infectious
CC	particles. Transfection with dsRNA resulted in a 60-fold inhibition of

**SQ** Sequence 30 BP; 8 A; 8 C; 7 G; 7 T; 0 U; 0 Other;

**Query Match** 61.0%; Score 12.8; DB 10; Length 30;  
**Best Local Similarity** 87.5%; Pred. No. 3.2e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0

**Dy** 3 GTCAATGACCGTACG 18  
|||||  
30 GTCAATTAGAGCCTCCG 15

**Db**

**RESULT 12**  
**ID** ABI95516/c  
**XX** ABI95516 standard; DNA; 20 BP.  
**XX AC** ABI95516;  
**DT** 16-FEB-2002 (first entry)  
**DE** Capture oligonucleotide Zlip ID#2603 oligo #9.

**KM** Human; K-Ras; PCR primer; probe; capture probe; mutation detection;  
**KW** ligase detection reaction; JDP; p53; BRCA1; BRCA2; infectious disease;  
**RN** infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;  
**KV** oncogene; tumour suppressor; human papillomavirus; forensic;  
**KW** environmental monitoring; food industry; feed industry; ss.  
**XX OS** Synthetic.  
**FN** WO200179548-A2.  
**PD** 25-OCT-2001.  
**Pf** 04-APR-2001; 2001WO-US010958.  
**PR** 14-APR-2000; 2000US-0197271P.  
**PA** (CORR ) CORNELI RES FOUND INC.  
**PI** Barany F, Zilvi M, Gerry NP, Pavis R, Kilman R;  
**DR** WPI; 2002-034366/04.

**Abstract:** Designing capture oligonucleotide probes for use on a support to which complementary oligonucleotides hybridize with little mismatch.

**Example 5; Fig 29; 30pp; English.**

The present invention describes a method (M1) for designing capture oligonucleotide probes (I) for use on a support to which complementary oligonucleotide probes (II) will hybridise with little mismatch, where (i) have melting temperatures within a narrow range. The method is useful for detecting infectious diseases caused by bacterial infectious agents e.g. Salmonella, bacteria monocytogenes and Haemophilus influenza, fungal infectious agents e.g. Cryptococcus neoformans, Candida albicans and Aspergillus fumigatus, viruses e.g. T-cell lymphocyctrophis citrus, Epstein-Barr virus and polio virus, and parasitic infectious agents selected from Onchovovera volvulus, Entamoeba histolytica and Dracunculus medinensis. The method is also useful for detecting genetic diseases such as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.

Detecting cancer involving oncogenes, tumour suppressor genes, or genes involved in DNA amplification, replication, recombination or repair, the cancer is specifically associated with a gene selected from BRCA1 gene, p53 gene, human papillomavirus types 16 and 18 and liver cancers. The method is also used for environmental monitoring, forensics and the food and feed industry, detecting comprises scanning (using e.g. a scanning electron microscope and infrared microscope) the support at the particular sites and identifying if ligation of the oligonucleotide probe sets occurred and correlating (using a computer) identified ligation to a presence or absence of the target nucleotide sequences. AB182074 to

DR WPI; 1998-523164/45.

XX Determination of gene expression levels - using combinations of different

PT cDNA samples tagged with different PCR adaptors.

XX Example 2; Page 10; 22pp; English.

XX The present sequence represents an adaptor which was used in the method

CC of the invention to determine the amount ratio between a cDNA coding for

CC mouse liver-derived Apolipoprotein and a cDNA coding for the mouse kidney

CC -derived Apolipoprotein by using Adaptor-tagged Competitive PCR (ATAC-PCR).

CC This method allows gene expression to be quantitatively determined,

CC and because internal standards are not required to prepare a calibration

CC curve, it is a quicker and less laborious process

XX

XX Sequence 35 BP; 8 A; 9 C; 9 G; 9 T; 0 U; 0 Other;

QY Query Match 62.9%; Score 13.2; DB 2; Length 35;

Best Local Similarity 83.3%; Pred. No. 1.9e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 3 GTCATTGACCGTACGCG 20

10 GTCGTTGAAACGACGCG 27

RESULT 7

ACN31831/C

ID ACN31831 standard; RNA; 37 BP.

XX ACN31831;

XX

DT 22-APR-2004 (first entry)

XX

DE WNV minus strand Zinzyme SEQ ID NO 31847.

XX

XX WNV; West Nile Virus; antiinflammatory; cytosolic; hepatotropic;

KW viruslike; neuroprotective; antibacterial; replication; pancreatitis;

KW encephalitis; myocarditis; meningitis; infection; hepatitis;

KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;

XX Amberzyme; Zinzyme; ss.

XX

XX West Nile Virus.

OS

PN WO200268637-A2.

XX

PD 06-SEP-2002.

XX

PF 19-OCT-2001; 2001WO-US048350.

XX

PR 20-OCT-2000; 2000US-0242411P.

XX

PA (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGEN J A.

XX

PI Blact L, Mcswiggen JA;

XX

XX WPI; 2002-706994/76.

XX

PT New nucleic acid molecule that modulates replication of West Nile Virus

PT (WNV), useful for treating a condition related to WNV infection e.g.

PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX

XX Claim 24; SEQ ID NO 31847; 495bp; English.

XX

XX The invention relates to nucleic acid molecules that modulate replication

CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for

CC treating a condition related to WNV infection e.g. pancreatitis,

CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,

CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid

CC molecule is selected from the group of ribozymes consisting of

CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The

CC nucleic acid molecules further comprise at least five ribose residues, at

CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at

CC least three of the 5' terminal nucleotides and a 3' end modification of a

CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080

CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given

CC in the specification. The present sequence is that of a nucleic acid

CC molecule of the invention

XX

XX Sequence 37 BP; 13 A; 7 C; 12 G; 0 T; 5 U; 0 Other;

QY Query Match 62.9%; Score 13.2; DB 6; Length 37;

Best Local Similarity 83.3%; Pred. No. 1.9e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 3 GTCATTGACCGTACGCG 20

35 GTCATTGACCTACTCG 18

RESULT 8

AAV61560/C

ID AAV61560 standard; DNA; 39 BP.

XX AAV61560;

XX

DT 08-DEC-1998 (first entry)

XX

DE Adaptor NNNN-CIGSR (- strand).

XX

XX Adaptor; quantitate; amount ratio; liver; kidney; apolipoprotein;

KW ATAC-PCR; Adaptor-tagged Competitive PCR; gene expression;

KW internal standard; calibration curve; ss.

XX

XX Synthetic.

OS

OS Mus sp.

XX

XX EP870842-A2.

XX

PD 14-OCT-1998.

XX

PF 07-APR-1998; 98EP-00302726.

XX

PR 07-APR-1997; 97JP-00088495.

XX

PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX

XX Kato K;

XX

XX WPI; 1998-523164/45.

XX

PT Determination of gene expression levels - using combinations of different

PT cDNA samples tagged with different PCR adaptors.

XX

XX Example 2; Page 10; 22pp; English.

XX

XX The present sequence represents an adaptor which was used in the method

CC of the invention to determine the amount ratio between a cDNA coding for

CC mouse liver-derived Apolipoprotein and a cDNA coding for the mouse kidney

CC -derived Apolipoprotein by using Adaptor-tagged Competitive PCR (ATAC-PCR).

CC This method allows gene expression to be quantitatively determined,

CC and because internal standards are not required to prepare a calibration

CC curve, it is a quicker and less laborious process

XX

XX Sequence 39 BP; 9 A; 9 C; 9 G; 8 T; 0 U; 4 Other;

QY Query Match 62.9%; Score 13.2; DB 2; Length 39;

Best Local Similarity 83.3%; Pred. No. 2e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 3 GTCATTGACCGTACGCG 20

30 GTCGTTGAAACGACGCG 13



XX Miltmann MP;  
 PI  
 XX  
 DR MPI; 2003-567953/53.  
 XX  
 PT New array of nucleic acid probes, useful for in situ hybridization, in  
 PT Southern, Northern or dot-blot hybridization to identify or detect the  
 PT sequence or specific mutations of any gene.  
 XX  
 PS Claim 1, SEQ ID NO 88853; 9pp, English.  
 XX  
 CC The invention discloses a microarray comprising a plurality of nucleic  
 CC acid probes including one of 2,018,500 fully defined sequences, or its  
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
 CC Also disclosed is a method of gene expression analysis. The array is used  
 CC in monitoring gene expression levels by hybridisation to a DNA library,  
 CC in analysis of genetic variation or in hybridisation of tag-labelled  
 CC compounds. The nucleic acid probes are specifically designed for analysis  
 CC of at least one target sequence. The method of analysis comprises  
 CC hybridising at least one or more nucleic acids to at least two or more  
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
 CC probes are attached to a solid support. The analysis comprises monitoring  
 CC gene expression levels, identifying allelic markers or polymorphisms,  
 CC or family members of a gene and a cross-species comparison. Each of the  
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-  
 CC blot hybridisation to identify or detect the sequence or specific  
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
 CC primer extensions or in screening cDNA or genomic libraries or subclones  
 CC for additional subclones containing segments of DNA that have been  
 CC isolated and previously sequenced. The sequence presented is one of the  
 CC nucleic acid probes incorporated in the microarray. Note: The sequence  
 CC data for this patent can also be obtained in electronic format directly  
 CC from USPTO at seqdata.uspto.gov/sequence.html  
 XX  
 SQ Sequence 25 BP; 7 A; 7 C; 5 G; 6 T; 0 U; 0 Other;  
 XX  
 Query Match 62.9%; Score 13.2; DB 9; Length 25;  
 Best Local Similarity 83.3%; Pred. No. 1.9e+03;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 TCATTAGACCGTAGCGGA 21  
 Db |||||  
 8 TCATATGACCTTACGGGA 25  
 RESULT 5  
 ACI88244  
 ID ACI88244 standard; DNA; 25 BP.  
 XX  
 AC ACI88244;  
 XX  
 DT 14-OCT-2003 (first entry)  
 XX  
 DE Human microarray DNA oligonucleotide SEQ ID NO 88235.  
 XX  
 KW EST; ss; probe; expressed sequence tag; microarray; gene expression;  
 KW genetic variation; biallelic marker; polymorphism; human;  
 KW cross-species comparison.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003104410-A1.  
 XX  
 PD 05-JUN-2003.  
 XX  
 PF 15-MAR-2002; 2002US-00098263.  
 XX  
 PR 16-MAR-2001; 2001US-0276759P.  
 XX  
 PA (AFPY-) AFFYMETRIX INC.  
 XX  
 PI Miltmann MP;

XX MPI; 2003-567953/53.  
 DR  
 XX  
 PT New array of nucleic acid probes, useful for in situ hybridization, in  
 PT Southern, Northern or dot-blot hybridization to identify or detect the  
 PT sequence or specific mutations of any gene.  
 XX  
 PS Claim 1, SEQ ID NO 88235; 9pp, English.  
 XX  
 CC The invention discloses a microarray comprising a plurality of nucleic  
 CC acid probes including one of 2,018,500 fully defined sequences, or its  
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
 CC Also disclosed is a method of gene expression analysis. The array is used  
 CC in monitoring gene expression levels by hybridisation to a DNA library,  
 CC in analysis of genetic variation or in hybridisation of tag-labelled  
 CC compounds. The nucleic acid probes are specifically designed for analysis  
 CC of at least one target sequence. The method of analysis comprises  
 CC hybridising at least one or more nucleic acids to at least two or more  
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
 CC probes are attached to a solid support. The analysis comprises monitoring  
 CC gene expression levels, identifying allelic markers or polymorphisms,  
 CC or family members of a gene and a cross-species comparison. Each of the  
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-  
 CC blot hybridisation to identify or detect the sequence or specific  
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
 CC primer extensions or in screening cDNA or genomic libraries or subclones  
 CC for additional subclones containing segments of DNA that have been  
 CC isolated and previously sequenced. The sequence presented is one of the  
 CC nucleic acid probes incorporated in the microarray. Note: The sequence  
 CC data for this patent can also be obtained in electronic format directly  
 CC from USPTO at seqdata.uspto.gov/sequence.html  
 XX  
 SQ Sequence 25 BP; 7 A; 7 C; 5 G; 6 T; 0 U; 0 Other;  
 XX  
 Query Match 62.9%; Score 13.2; DB 9; Length 25;  
 Best Local Similarity 83.3%; Pred. No. 1.9e+03;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 TCATTAGACCGTAGCGGA 21  
 Db |||||  
 7 TCATATGACCTTACGGGA 24  
 RESULT 6  
 AAV61559  
 ID AAV61559 standard; DNA; 35 BP.  
 XX  
 AC AAV61559;  
 XX  
 DT 08-DEC-1998 (first entry)  
 XX  
 DE Adaptor NNNN-C1GSR (+ strand).  
 XX  
 KW Adaptor; quantitate; amount ratio; liver; kidney; apolipoprotein;  
 KW ATAC-PCR; Adaptor-tagged Competitive PCR; gene expression;  
 KW internal standard; calibration curve; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN Mus sp.  
 XX  
 PD EP870842-A2.  
 XX  
 PF 14-OCT-1998.  
 XX  
 PF 07-APR-1998; 98EP-00302726.  
 XX  
 PR 07-APR-1997; 97JP-00088495.  
 XX  
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
 XX  
 PI Kato K;

XX Jacobs K, McCoy JM, Lavallie ER, Collins-Racie JA, Evans C;  
 PI Meberg D, Treacy M, Agostino MJ, Steininger RJ, Spaulding V;  
 PI Wong GG, Clark HF, Reichel K;  
 DR WPI; 2000-205979/18.  
 XX  
 PT New polynucleotides encoding secreted proteins, which may have e.g.  
 PT nutritional, chemokine, immune stimulating or suppressing, hematopoiesis  
 PT regulating, tissue growth, activin/inhibin antiinflammatory or tumor  
 PT inhibition activity.  
 PS  
 PS Disclosure; Page 631, 641pp; English.  
 XX  
 XX AAA16618 to AAA16697 encode the human secreted proteins given in AA94898  
 CC to AA94980, isolated from human adult brain, adult thyroid, adult  
 CC retina, foetal carcinoma, adult blood, adult neural, foetal kidney, adult  
 CC placenta, adult testis, whole embryo, adult cartilage, kidney, foetal  
 CC brain, adult thymus, foetal placenta, adult uterus, adult tumour, and  
 CC adult bladder, cDNA libraries. The polynucleotides and proteins are  
 CC predicted to have biological activities which would make them suitable  
 CC for treating, preventing or ameliorating medical conditions in humans and  
 CC animals. The polynucleotides can be used as markers for tissues in which  
 CC the protein is preferentially expressed, as molecular weight markers on  
 CC Southern gels, and as chromosome markers or tags to identify chromosomes  
 CC or to map gene positions. The proteins can be used in the treatment of  
 CC immune deficiencies and disorders, such as severe combined  
 CC immunodeficiency (SCID), as well as viral, bacterial, fungal and other  
 CC infections. These infections include human immunodeficiency virus (HIV),  
 CC hepatitis, herpesviruses, mycobacteria, Leishmania spp., malaria and  
 CC candidiasis. The proteins can be used to treat autoimmune disorders such  
 CC as connective tissue disease, multiple sclerosis, systemic lupus  
 CC erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation,  
 CC Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent  
 CC diabetes mellitus, myasthenia gravis, graft-versus-host disease and  
 CC autoimmune inflammatory eye disease. The proteins can also be used to  
 CC treat allergic conditions, such as asthma. AAA16698 to AAA16774 represent  
 CC probes for the human secreted proteins from the present invention  
 CC  
 SQ Sequence 29 BP; 7 A; 9 C; 6 G; 6 T; 0 U; 1 Other;  
 XX  
 XX Query Match 64.8%; Score 13.6; DB 3; Length 29;  
 XX Best Local Similarity 80.0%; Pred. No. 1.1e+03;  
 XX Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 2 GGTCAATTAGACCGTAGCGGA 21  
 DB 5 GGTCAATAGACAGTACTCCA 24  
 XX  
 XX RESULT 3  
 XX AC109445/c  
 XX ID AC109445 standard; DNA; 25 BP.  
 XX AC AC109445;  
 XX  
 XX 13-OCT-2003 (first entry)  
 XX  
 XX Human microarray DNA oligonucleotide SEQ ID NO 9436.  
 XX  
 XX EST; ss; probe; expressed sequence tag; microarray; gene expression;  
 XX genetic variation; diallelic marker; polymorphism; human;  
 XX cross-species comparison.  
 XX  
 XX Homo sapiens.  
 XX OS  
 XX US2003104410-A1.  
 XX PN  
 XX 05-JUN-2003.  
 XX  
 XX 15-MAR-2002; 2002US-00098263.  
 XX PF  
 XX 16-MAR-2001; 2001US-0276759P.  
 XX PR

XX (AFFY-) AFFYMETRIX INC.  
 PA  
 XX Miltmann MP;  
 PI  
 XX WPI; 2003-567953/53.  
 DR  
 XX  
 PT New array of nucleic acid probes, useful for in situ hybridization, in  
 PT Southern, Northern or dot-blot hybridization to identify or detect the  
 PT sequence or specific mutations of any gene.  
 PT  
 PS Claim 1; SEQ ID NO 9436; 9pp; English.  
 XX  
 XX The invention discloses a microarray comprising a plurality of nucleic  
 CC acid probes including one of 2,018,500 fully defined sequences, or its  
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
 CC Also disclosed is a method of gene expression analysis. The array is used  
 CC in monitoring gene expression levels by hybridization to a DNA library,  
 CC in analysis of genetic variation or in hybridization of tag-labelled  
 CC compounds. The nucleic acid probes are specifically designed for analysis  
 CC of at least one target sequence. The method of analysis comprises  
 CC hybridizing at least one or more nucleic acids to at least two or more  
 CC nucleic acid probes and detecting the hybridization. The nucleic acid  
 CC probes are attached to a solid support. The analysis comprises monitoring  
 CC gene expression levels, identifying diallelic markers or polymorphisms,  
 CC or family members of a gene and a cross-species comparison. Each of the  
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
 CC probes is useful in in situ hybridization, in Southern, Northern or dot-  
 CC blot hybridization to identify or detect the sequence or specific  
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
 CC primer extensions or in screening cDNA or genomic libraries or subclones  
 CC for additional subclones containing segments of DNA that have been  
 CC isolated and previously sequenced. The sequence presented is one of the  
 CC nucleic acid probes incorporated in the microarray. Note: The sequence  
 CC data for this patent can also be obtained in electronic format directly  
 CC from USPTO at seqdata.uspto.gov/sequence.html  
 CC  
 SQ Sequence 25 BP; 11 A; 3 C; 3 G; 8 T; 0 U; 0 Other;  
 XX  
 XX Query Match 63.8%; Score 13.4; DB 9; Length 25;  
 XX Best Local Similarity 93.3%; Pred. No. 1.4e+03;  
 XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 GTCATTAGACCGTAGAC 17  
 DB 18 GTCATTAGACTGTAC 4  
 XX  
 XX RESULT 4  
 XX AC188862  
 XX ID AC188862 standard; DNA; 25 BP.  
 XX AC AC188862;  
 XX  
 XX 14-OCT-2003 (first entry)  
 XX  
 XX Human microarray DNA oligonucleotide SEQ ID NO 88853.  
 XX  
 XX EST; ss; probe; expressed sequence tag; microarray; gene expression;  
 XX genetic variation; diallelic marker; polymorphism; human;  
 XX cross-species comparison.  
 XX  
 XX Homo sapiens.  
 XX OS  
 XX US2003104410-A1.  
 XX PN  
 XX 05-JUN-2003.  
 XX  
 XX 15-MAR-2002; 2002US-00098263.  
 XX PF  
 XX 16-MAR-2001; 2001US-0276759P.  
 XX PR  
 XX (AFFY-) AFFYMETRIX INC.

533	11	52.4	36	6	ABX02836	Abx02836 HCV hamme	606	11	52.4	38	4	ABK05210	Abk05210 Human NOG
534	11	52.4	36	6	ABX02270	Abx02270 HCV hamme	607	11	52.4	38	4	ABK04785	Abk04785 Human NOG
535	11	52.4	36	6	ABX02731	Abx02731 HCV hamme	608	11	52.4	38	4	ABK04953	Abk04953 Human NOG
536	11	52.4	36	6	ABX02408	Abx02408 HCV hamme	609	11	52.4	38	4	ABK05212	Abk05212 Human NOG
537	11	52.4	36	6	ABX02198	Abx02198 HCV hamme	610	11	52.4	38	4	ABK03884	Abk03884 Human NOG
538	11	52.4	36	6	ABX02402	Abx02402 HCV hamme	611	11	52.4	38	4	ABK05178	Abk05178 Human NOG
539	11	52.4	36	6	ABX02026	Abx02026 HCV hamme	612	11	52.4	38	4	ABK08311	Abk08311 Human CD2
540	11	52.4	36	6	ABX02602	Abx02602 HCV hamme	613	11	52.4	38	4	ABK03825	Abk03825 Human NOG
541	11	52.4	36	6	ABX02319	Abx02319 HCV hamme	614	11	52.4	38	4	ABK04543	Abk04543 Human NOG
542	11	52.4	36	6	ABX01863	Abx01863 HCV hamme	615	11	52.4	38	4	ABK05160	Abk05160 Human NOG
543	11	52.4	36	6	ABX02404	Abx02404 HCV hamme	616	11	52.4	38	4	ABK08344	Abk08344 Human CD2
544	11	52.4	36	6	ABX02705	Abx02705 HCV hamme	617	11	52.4	38	4	ABK04527	Abk04527 Human NOG
545	11	52.4	36	6	ABX02219	Abx02219 HCV hamme	618	11	52.4	38	4	ABK04580	Abk04580 Human NOG
546	11	52.4	36	8	ACD56262	AcD56262 HBV enzym	619	11	52.4	38	4	ABK04691	Abk04691 Human NOG
547	11	52.4	36	8	ACD56358	AcD56358 HBV enzym	620	11	52.4	38	4	ABK04765	Abk04765 Human NOG
548	11	52.4	36	12	AD159388	Ad159388 Inozyme s	621	11	52.4	38	4	ABK08356	Abk08356 Human CD2
549	11	52.4	36	12	AD159408	Ad159408 Inozyme s	622	11	52.4	38	4	ABK04566	Abk04566 Human NOG
550	11	52.4	36	12	AD159410	Ad159410 Inozyme s	623	11	52.4	38	4	ABK04583	Abk04583 Human NOG
551	11	52.4	36	12	AD159425	Ad159425 Inozyme s	624	11	52.4	38	4	ABK04646	Abk04646 Human NOG
552	11	52.4	36	12	AD159437	Ad159437 Inozyme s	625	11	52.4	38	4	ABK08260	Abk08260 Human CD2
553	11	52.4	36	12	AD159396	Ad159396 Inozyme s	626	11	52.4	38	4	ABK08382	Abk08382 Human CD2
554	11	52.4	36	12	AD159457	Ad159457 Inozyme s	627	11	52.4	38	4	ABK05112	Abk05112 Human NOG
555	11	52.4	37	3	AA264928	AA264928 RPI motif	628	11	52.4	38	4	ABK07994	Abk07994 Human CD2
556	11	52.4	37	6	ABX03427	Abx03427 Ribozyme	629	11	52.4	38	4	ABK08174	Abk08174 Human CD2
557	11	52.4	37	6	ABK59352	AbK59352 Human CLC	630	11	52.4	38	4	ABK08243	Abk08243 Human CD2
558	11	52.4	37	6	ABK59388	AbK59388 Human CLC	631	11	52.4	38	4	ABK04529	Abk04529 Human NOG
559	11	52.4	37	6	ABK59340	AbK59340 Human CLC	632	11	52.4	38	4	ABK04985	Abk04985 Human NOG
560	11	52.4	37	6	ACN18895	Acn18895 MNV Zinz	633	11	52.4	38	4	ABK05127	Abk05127 Human CD2
561	11	52.4	37	6	ACN18992	Acn18992 MNV Zinz	634	11	52.4	38	4	ABK08277	Abk08277 Human CD2
562	11	52.4	37	6	ACN13108	Acn13108 MNV minus	635	11	52.4	38	4	ABK08316	Abk08316 Human CD2
563	11	52.4	37	6	ACN19493	Acn19493 MNV Zinz	636	11	52.4	38	4	ABK03855	Abk03855 Human NOG
564	11	52.4	37	6	ACN19321	Acn19321 MNV Zinz	637	11	52.4	38	4	ABK04698	Abk04698 Human NOG
565	11	52.4	37	6	ACN19329	Acn19329 MNV minus	638	11	52.4	38	4	ABK04824	Abk04824 Human NOG
566	11	52.4	37	6	ACN19323	Acn19323 MNV Zinz	639	11	52.4	38	4	ABK05306	Abk05306 Human NOG
567	11	52.4	37	6	ACN19355	Acn19355 MNV Zinz	640	11	52.4	38	4	ABK08435	Abk08435 Human CD2
568	11	52.4	37	6	ACN19418	Acn19418 MNV Zinz	641	11	52.4	38	4	ABK04862	Abk04862 Human NOG
569	11	52.4	37	6	ACN19889	Acn19889 MNV Zinz	642	11	52.4	38	4	ABK04963	Abk04963 Human NOG
570	11	52.4	37	6	ACN19339	Acn19339 MNV minus	643	11	52.4	38	4	ABK05042	Abk05042 Human NOG
571	11	52.4	37	6	ACN19246	Acn19246 MNV Zinz	644	11	52.4	38	4	ABK08305	Abk08305 Human CD2
572	11	52.4	37	6	ACN19519	Acn19519 MNV Zinz	645	11	52.4	38	4	AB147584	Ab147584 Human GRI
573	11	52.4	37	6	ACN37010	Acn37010 MNV enzym	646	11	52.4	38	4	AB147630	Ab147630 Human GRI
574	11	52.4	37	6	ACN31978	Acn31978 MNV minus	647	11	52.4	38	4	AB147555	Ab147555 Human GRI
575	11	52.4	37	6	ACN31928	Acn31928 MNV minus	648	11	52.4	38	4	AB147620	Ab147620 Human GRI
576	11	52.4	37	6	ACN31151	Acn31151 MNV minus	649	11	52.4	38	4	AB147500	Ab147500 Human GRI
577	11	52.4	37	6	ACN31700	Acn31700 MNV minus	650	11	52.4	38	4	AB147479	Ab147479 Human GRI
578	11	52.4	37	6	ACN30899	Acn30899 MNV minus	651	11	52.4	38	4	AB147551	Ab147551 Human GRI
579	11	52.4	37	8	ACA10034	ACA10034 Necrosis	652	11	52.4	38	4	AB147475	Ab147475 Human GRI
580	11	52.4	37	8	ACA08160	ACA08160 Necrosis	653	11	52.4	38	4	AB147530	Ab147530 Human GRI
581	11	52.4	37	8	ACA08072	ACA08072 Necrosis	654	11	52.4	38	6	ABQ72443	AbQ72443 PCR prime
582	11	52.4	37	8	ACA10010	ACA10010 Necrosis	655	11	52.4	38	6	ABQ72448	AbQ72448 PCR prime
583	11	52.4	37	8	ACA07927	ACA07927 Necrosis	656	11	52.4	38	6	ABQ72439	AbQ72439 PCR prime
584	11	52.4	37	11	ADL75687	Adl75687 Human PTG	657	11	52.4	38	6	ABK19546	Abk19546 Human ERG
585	11	52.4	37	11	ADL52737	Adl52737 Human NOG	658	11	52.4	38	6	ABK20611	Abk20611 Human ERG
586	11	52.4	37	11	ADL54427	Adl54427 Human NOG	659	11	52.4	38	6	ABK20602	Abk20602 Human ERG
587	11	52.4	37	11	ADL75730	Adl75730 Human PTG	660	11	52.4	38	6	ABK20586	Abk20586 Human ERG
588	11	52.4	37	11	ADL54222	Adl54222 Human IXX	661	11	52.4	38	6	ABK20090	Abk20090 Human ERG
589	11	52.4	37	11	ADL73674	Adl73674 Human PKR	662	11	52.4	38	6	ABK20145	Abk20145 Human ERG
590	11	52.4	37	11	ADL75675	Adl75675 Human PTG	663	11	52.4	38	6	ABK20161	Abk20161 Human ERG
591	11	52.4	37	12	ADM64143	Adm64143 Hepaticlis	664	11	52.4	38	6	ABK20303	Abk20303 Human ERG
592	11	52.4	37	12	AD192342	AD192342 Anti-HCV	665	11	52.4	38	6	ABK19639	Abk19639 Human ERG
593	11	52.4	38	4	AAH96508	Aah96508 Human CHK	666	11	52.4	38	6	ABK20081	Abk20081 Human ERG
594	11	52.4	38	4	AAH96651	Aah96651 Human CHK	667	11	52.4	38	6	ABK20415	Abk20415 Human ERG
595	11	52.4	38	4	AAH96621	Aah96621 Human CHK	668	11	52.4	38	6	ABK20181	Abk20181 Human ERG
596	11	52.4	38	4	AAH96621	Aah96621 Human CHK	669	11	52.4	38	6	ABK20216	Abk20216 Human ERG
597	11	52.4	38	4	AAH96520	Aah96520 Human CHK	670	11	52.4	38	6	ABK20559	Abk20559 Human ERG
598	11	52.4	38	4	AAH96453	Aah96453 Human CHK	671	11	52.4	38	6	ABK19485	Abk19485 Human ERG
599	11	52.4	38	4	ABK04658	Abk04658 Human NOG	672	11	52.4	38	6	ABK20075	Abk20075 Human ERG
600	11	52.4	38	4	ABK04965	Abk04965 Human NOG	673	11	52.4	38	6	ABK20275	Abk20275 Human ERG
601	11	52.4	38	4	ABK05131	Abk05131 Human NOG	674	11	52.4	38	6	ABK20379	Abk20379 Human ERG
602	11	52.4	38	4	ABK05154	Abk05154 Human NOG	675	11	52.4	38	6	ABK20563	Abk20563 Human ERG
603	11	52.4	38	4	ABK05066	Abk05066 Human NOG	676	11	52.4	38	6	ABK20267	Abk20267 Human ERG
604	11	52.4	38	4	ABK05101	Abk05101 Human NOG	677	11	52.4	38	6	ABK20126	Abk20126 Human ERG
605	11	52.4	38	4	ABK04871	Human NOG	678	11	52.4	38	6	ABK20391	Abk20391 Human ERG

679	11	52.4	38	6	ABK20483	Human	ERG	752	11	52.4	38	6	ACN18335	5	ACN18355	INV	Inozy
680	11	52.4	38	6	ABK20593	Human	ERG	753	11	52.4	38	6	ACN29005	3	ACN29055	INV	minus
681	11	52.4	38	6	ABK20087	Human	ERG	754	11	52.4	38	6	ACN29142	3	ACN29142	INV	minus
682	11	52.4	38	6	ABK20244	Human	ERG	755	11	52.4	38	6	ACN30123	3	ACN30123	INV	minus
683	11	52.4	38	6	ABK58122	Human	CLC	756	11	52.4	38	6	ACN30260	3	ACN30260	INV	minus
684	11	52.4	38	6	ABK58769	Human	CLC	757	11	52.4	38	6	ACN30315	3	ACN30315	INV	minus
685	11	52.4	38	6	ABK58847	Human	CLC	758	11	52.4	38	6	ACN16816	3	ACN16816	INV	Inozy
686	11	52.4	38	6	ABK58849	Human	CLC	759	11	52.4	38	6	ACN17288	3	ACN17288	INV	Inozy
687	11	52.4	38	6	ABK58841	Human	CLC	760	11	52.4	38	6	ACN18040	3	ACN18040	INV	Inozy
688	11	52.4	38	6	ABK58709	Human	CLC	761	11	52.4	38	6	ACN27900	3	ACN27900	INV	minus
689	11	52.4	38	6	ABK59011	Human	CLC	762	11	52.4	38	6	ACN27910	3	ACN27910	INV	minus
690	11	52.4	38	6	ABK58560	Human	CLC	763	11	52.4	38	6	ACN28758	3	ACN28758	INV	minus
691	11	52.4	38	6	ABK58624	Human	CLC	764	11	52.4	38	6	ACN29274	3	ACN29274	INV	minus
692	11	52.4	38	6	ABK58913	Human	CLC	765	11	52.4	38	6	ACN29354	3	ACN29354	INV	minus
693	11	52.4	38	6	ABK58753	Human	CLC	766	11	52.4	38	6	ACN29399	3	ACN29399	INV	minus
694	11	52.4	38	6	ABK58832	Human	CLC	767	11	52.4	38	6	ACN29677	3	ACN29677	INV	minus
695	11	52.4	38	6	ABK58745	Human	CLC	768	11	52.4	38	6	ACN30104	3	ACN30104	INV	minus
696	11	52.4	38	6	ABK58462	Human	CLC	769	11	52.4	38	6	ACN30273	3	ACN30273	INV	minus
697	11	52.4	38	6	ABK58485	Human	CLC	770	11	52.4	38	6	ACN16820	3	ACN16820	INV	Inozy
698	11	52.4	38	6	ABK58667	Human	CLC	771	11	52.4	38	6	ACN17460	3	ACN17460	INV	Inozy
699	11	52.4	38	6	ABK58657	Human	CLC	772	11	52.4	38	6	ACN26565	3	ACN26565	INV	minus
700	11	52.4	38	6	ACN16957	INV	Inozy	773	11	52.4	38	6	ACN27006	3	ACN27006	INV	minus
701	11	52.4	38	6	ACN17961	INV	Inozy	774	11	52.4	38	6	ACN28084	3	ACN28084	INV	minus
702	11	52.4	38	6	ACN18702	INV	Inozy	775	11	52.4	38	6	ACN28733	3	ACN28733	INV	minus
703	11	52.4	38	6	ACN26995	INV	minus	776	11	52.4	38	6	ACN28773	3	ACN28773	INV	minus
704	11	52.4	38	6	ACN28105	INV	minus	777	11	52.4	38	6	ACN28773	3	ACN28773	INV	minus
705	11	52.4	38	6	ACN28136	INV	minus	778	11	52.4	38	6	ACN29740	3	ACN29740	INV	minus
706	11	52.4	38	6	ACN28157	INV	minus	779	11	52.4	38	6	ACN30517	3	ACN30517	INV	minus
707	11	52.4	38	6	ACN28240	INV	minus	780	11	52.4	38	6	ACN30517	3	ACN30517	INV	minus
708	11	52.4	38	6	ACN28476	INV	minus	781	11	52.4	38	6	ACN30588	3	ACN30588	INV	minus
709	11	52.4	38	6	ACN28689	INV	minus	782	11	52.4	38	6	ACN15616	3	ACN15616	INV	Hamme
710	11	52.4	38	6	ACN29388	INV	minus	783	11	52.4	38	6	ACN15956	3	ACN15956	INV	Hamme
711	11	52.4	38	6	ACN29477	INV	Inozy	784	11	52.4	38	6	ACN17088	3	ACN17088	INV	Inozy
712	11	52.4	38	6	ACN29477	INV	Inozy	785	11	52.4	38	6	ACN17550	3	ACN17550	INV	Inozy
713	11	52.4	38	6	ACN18460	INV	Inozy	786	11	52.4	38	6	ACN18481	3	ACN18481	INV	Inozy
714	11	52.4	38	6	ACN18571	INV	Inozy	787	11	52.4	38	6	ACN28044	3	ACN28044	INV	minus
715	11	52.4	38	6	ACN26491	INV	minus	788	11	52.4	38	6	ACN28074	3	ACN28074	INV	minus
716	11	52.4	38	6	ACN28227	INV	minus	789	11	52.4	38	6	ACN28260	3	ACN28260	INV	minus
717	11	52.4	38	6	ACN28248	INV	minus	790	11	52.4	38	6	ACN28612	3	ACN28612	INV	minus
718	11	52.4	38	6	ACN28336	INV	minus	791	11	52.4	38	6	ACN29159	3	ACN29159	INV	minus
719	11	52.4	38	6	ACN28714	INV	minus	792	11	52.4	38	6	ACN30301	3	ACN30301	INV	minus
720	11	52.4	38	6	ACN28832	INV	minus	793	11	52.4	38	6	ACN15754	3	ACN15754	INV	Hamme
721	11	52.4	38	6	ACN28890	INV	minus	794	11	52.4	38	6	ACN15808	3	ACN15808	INV	Hamme
722	11	52.4	38	6	ACN28896	INV	minus	795	11	52.4	38	6	ACN17155	3	ACN17155	INV	Inozy
723	11	52.4	38	6	ACN29186	INV	minus	796	11	52.4	38	6	ACN27460	3	ACN27460	INV	minus
724	11	52.4	38	6	ACN29258	INV	minus	797	11	52.4	38	6	ACN27977	3	ACN27977	INV	minus
725	11	52.4	38	6	ACN30266	INV	minus	798	11	52.4	38	6	ACN28190	3	ACN28190	INV	minus
726	11	52.4	38	6	ACN15287	INV	Hamme	799	11	52.4	38	6	ACN28200	3	ACN28200	INV	minus
727	11	52.4	38	6	ACN15916	INV	Inozy	800	11	52.4	38	6	ACN28828	3	ACN28828	INV	minus
728	11	52.4	38	6	ACN18442	INV	Inozy	801	11	52.4	38	6	ACN29056	3	ACN29056	INV	minus
729	11	52.4	38	6	ACN18442	INV	Inozy	802	11	52.4	38	6	ACN29656	3	ACN29656	INV	minus
730	11	52.4	38	6	ACN28317	INV	minus	803	11	52.4	38	6	ACN29365	3	ACN29365	INV	minus
731	11	52.4	38	6	ACN28845	INV	minus	804	11	52.4	38	6	ACN29395	3	ACN29395	INV	minus
732	11	52.4	38	6	ACN29129	INV	minus	805	11	52.4	38	6	ACN30263	3	ACN30263	INV	minus
733	11	52.4	38	6	ACN15795	INV	Hamme	806	11	52.4	38	6	ACN17108	3	ACN17108	INV	Inozy
734	11	52.4	38	6	ACN16946	INV	Inozy	807	11	52.4	38	6	ACN17324	3	ACN17324	INV	Inozy
735	11	52.4	38	6	ACN25710	INV	minus	808	11	52.4	38	6	ACN17380	3	ACN17380	INV	Inozy
736	11	52.4	38	6	ACN27240	INV	minus	809	11	52.4	38	6	ACN17711	3	ACN17711	INV	Inozy
737	11	52.4	38	6	ACN27690	INV	minus	810	11	52.4	38	6	ACN17894	3	ACN17894	INV	minus
738	11	52.4	38	6	ACN27940	INV	minus	811	11	52.4	38	6	ACN17937	3	ACN17937	INV	minus
739	11	52.4	38	6	ACN28391	INV	minus	812	11	52.4	38	6	ACN18041	3	ACN18041	INV	minus
740	11	52.4	38	6	ACN28563	INV	minus	813	11	52.4	38	6	ACN27959	3	ACN27959	INV	minus
741	11	52.4	38	6	ACN28588	INV	minus	814	11	52.4	38	6	ACN29957	3	ACN29957	INV	minus
742	11	52.4	38	6	ACN28599	INV	minus	815	11	52.4	38	6	ACN17485	3	ACN17485	INV	Inozy
743	11	52.4	38	6	ACN29103	INV	minus	816	11	52.4	38	6	ACN17578	3	ACN17578	INV	minus
744	11	52.4	38	6	ACN29501	INV	minus	817	11	52.4	38	6	ACN17764	3	ACN17764	INV	minus
745	11	52.4	38	6	ACN30440	INV	minus	818	11	52.4	38	6	ACN17937	3	ACN17937	INV	minus
746	11	52.4	38	6	ACN16780	INV	Inozy	819	11	52.4	38	6	ACN18052	3	ACN18052	INV	minus
747	11	52.4	38	6	ACN16875	INV	Inozy	820	11	52.4	38	6	ACN18201	3	ACN18201	INV	minus
748	11	52.4	38	6	ACN17072	INV	Inozy	821	11	52.4	38	6	ACN18216	3	ACN18216	INV	minus
749	11	52.4	38	6	ACN17627	INV	Inozy	822	11	52.4	38	6	ACN26930	3	ACN26930	INV	minus
750	11	52.4	38	6	ACN17717	INV	Inozy	823	11	52.4	38	6	ACN28373	3	ACN28373	INV	minus
751	11	52.4	38	6	ACN17925	INV	Inozy	824	11	52.4	38	6	ACN28406	3	ACN28406	INV	minus
					ACN18329	INV	Inozy										



825	11	52.4	38	6	ACN28443	898	11	52.4	38	8	ACA07471	ACA07471	Necrosis
826	11	52.4	38	6	ACN28810	899	11	52.4	38	8	ACA07599	ACA07599	Necrosis
827	11	52.4	38	6	ACN28885	900	11	52.4	38	8	ACA07377	ACA07377	Necrosis
828	11	52.4	38	6	ACN29256	901	11	52.4	38	8	ACA07332	ACA07332	Necrosis
829	11	52.4	38	6	ACN29922	902	11	52.4	38	8	ACA07457	ACA07457	Necrosis
830	11	52.4	38	6	ACN29953	903	11	52.4	38	8	ACA07558	ACA07558	Necrosis
831	11	52.4	38	6	ACN30579	904	11	52.4	38	8	ACA06952	ACA06952	Necrosis
832	11	52.4	38	6	ACN17136	905	11	52.4	38	8	ACA06968	ACA06968	Necrosis
833	11	52.4	38	6	ACN17634	906	11	52.4	38	8	ACA07582	ACA07582	Necrosis
834	11	52.4	38	6	ACN17918	907	11	52.4	38	8	ACA07274	ACA07274	Necrosis
835	11	52.4	38	6	ACN18044	908	11	52.4	38	8	ACA07171	ACA07171	Necrosis
836	11	52.4	38	6	ACN18084	909	11	52.4	38	8	ACA06902	ACA06902	Necrosis
837	11	52.4	38	6	ACN28708	910	11	52.4	38	8	ACA07132	ACA07132	Necrosis
838	11	52.4	38	6	ACN28738	911	11	52.4	38	8	ACA07486	ACA07486	Necrosis
839	11	52.4	38	6	ACN28907	912	11	52.4	38	8	ACA07208	ACA07208	Necrosis
840	11	52.4	38	6	ACN29169	913	11	52.4	38	8	ACA07211	ACA07211	Necrosis
841	11	52.4	38	6	ACN29180	914	11	52.4	38	8	ACA07386	ACA07386	Necrosis
842	11	52.4	38	6	ACN29563	915	11	52.4	38	8	ACA07091	ACA07091	Necrosis
843	11	52.4	38	6	ACN30084	916	11	52.4	38	8	ACA07247	ACA07247	Necrosis
844	11	52.4	38	6	ACN16310	917	11	52.4	38	8	ACA07263	ACA07263	Necrosis
845	11	52.4	38	6	ACN17199	918	11	52.4	38	8	ACA07568	ACA07568	Necrosis
846	11	52.4	38	6	ACN17556	919	11	52.4	38	8	ACD52556	ACD52556	HBV ino
847	11	52.4	38	6	ACN17661	920	11	52.4	38	8	ACD52259	ACD52259	HBV ino
848	11	52.4	38	6	ACN18473	921	11	52.4	38	8	ACD52146	ACD52146	HBV ino
849	11	52.4	38	6	ACN29017	922	11	52.4	38	8	ACD52647	ACD52647	HBV ino
850	11	52.4	38	6	ACN29109	923	11	52.4	38	8	ACD51846	ACD51846	HBV ino
851	11	52.4	38	6	ACN29662	924	11	52.4	38	8	ACD51853	ACD51853	HBV ino
852	11	52.4	38	6	ACN29849	925	11	52.4	38	8	ACD52059	ACD52059	HBV ino
853	11	52.4	38	6	ACN30114	926	11	52.4	38	8	ACD52884	ACD52884	HBV ino
854	11	52.4	38	6	ACN30291	927	11	52.4	38	8	ACD53068	ACD53068	HBV ino
855	11	52.4	38	6	ACN30347	928	11	52.4	38	8	ACD51000	ACD51000	HBV ino
856	11	52.4	38	6	ACN15696	929	11	52.4	38	8	ACD52977	ACD52977	HBV ino
857	11	52.4	38	6	ACN16680	930	11	52.4	38	8	ACD50914	ACD50914	HBV ino
858	11	52.4	38	6	ACN17566	931	11	52.4	38	8	ACD51754	ACD51754	HBV ino
859	11	52.4	38	6	ACN17785	932	11	52.4	38	8	ACD52661	ACD52661	HBV ino
860	11	52.4	38	6	ACN18063	933	11	52.4	38	8	ACD50997	ACD50997	HBV ino
861	11	52.4	38	6	ACN18465	934	11	52.4	38	8	ACD51642	ACD51642	HBV ino
862	11	52.4	38	6	ACN28121	935	11	52.4	38	8	ACD52243	ACD52243	HBV ino
863	11	52.4	38	6	ACN28284	936	11	52.4	38	8	ACD52637	ACD52637	HBV ino
864	11	52.4	38	6	ACN28574	937	11	52.4	38	8	ACD52664	ACD52664	HBV ino
865	11	52.4	38	6	ACN29324	938	11	52.4	38	8	ACD52673	ACD52673	HBV ino
866	11	52.4	38	6	ACN29616	939	11	52.4	38	8	ACD52981	ACD52981	HBV ino
867	11	52.4	38	6	ACN29697	940	11	52.4	38	8	ACD51940	ACD51940	HBV ino
868	11	52.4	38	6	ACN29765	941	11	52.4	38	8	ACD53074	ACD53074	HBV ino
869	11	52.4	38	6	ACN30340	942	11	52.4	38	8	ACD52268	ACD52268	HBV ino
870	11	52.4	38	6	ACN15599	943	11	52.4	38	8	ACD52343	ACD52343	HBV ino
871	11	52.4	38	6	ACN17500	944	11	52.4	38	8	ACD52959	ACD52959	HBV ino
872	11	52.4	38	6	ACN17782	945	11	52.4	38	8	ACD52460	ACD52460	HBV ino
873	11	52.4	38	6	ACN26162	946	11	52.4	38	8	ACD52646	ACD52646	HBV ino
874	11	52.4	38	6	ACN28211	947	11	52.4	38	8	ACD53152	ACD53152	HBV ino
875	11	52.4	38	6	ACN28291	948	11	52.4	38	8	ACD52548	ACD52548	HBV ino
876	11	52.4	38	6	ACN29165	949	11	52.4	38	8	ACD52775	ACD52775	HBV ino
877	11	52.4	38	6	ACN30093	950	11	52.4	38	8	ACD51858	ACD51858	HBV ino
878	11	52.4	38	6	ACN30562	951	11	52.4	38	8	ACD53141	ACD53141	HBV ino
879	11	52.4	38	6	ACN15580	952	11	52.4	38	11	ADL52282	ADL52282	Human NOG
880	11	52.4	38	6	ACN17255	953	11	52.4	38	11	ADL53719	ADL53719	Human IKK
881	11	52.4	38	6	ACN17935	954	11	52.4	38	11	ADL53750	ADL53750	Human IKK
882	11	52.4	38	6	ACN18449	955	11	52.4	38	11	ADL53761	ADL53761	Human IKK
883	11	52.4	38	6	ACN18450	956	11	52.4	38	11	ADL53913	ADL53913	Human IKK
884	11	52.4	38	6	ACN18506	957	11	52.4	38	11	ADL54077	ADL54077	Human IKK
885	11	52.4	38	6	ACN28560	958	11	52.4	38	11	ADL75070	ADL75070	Human PTG
886	11	52.4	38	6	ACN28668	959	11	52.4	38	11	ADL52399	ADL52399	Human NOG
887	11	52.4	38	6	ACN28716	960	11	52.4	38	11	ADL74977	ADL74977	Human PTG
888	11	52.4	38	6	ACN29218	961	11	52.4	38	11	ADL75375	ADL75375	Human PTG
889	11	52.4	38	6	ACN29811	962	11	52.4	38	11	ADL52036	ADL52036	Human NOG
890	11	52.4	38	6	ACN29811	963	11	52.4	38	11	ADL52435	ADL52435	Human NOG
891	11	52.4	38	8	ACA07476	964	11	52.4	38	11	ADL53838	ADL53838	Human IKK
892	11	52.4	38	8	ACA07410	965	11	52.4	38	11	ADL75222	ADL75222	Human PTG
893	11	52.4	38	8	ACA07570	966	11	52.4	38	11	ADL52135	ADL52135	Human NOG
894	11	52.4	38	8	ACA07379	967	11	52.4	38	11	ADL52228	ADL52228	Human NOG
895	11	52.4	38	8	ACA06956	968	11	52.4	38	11	ADL52407	ADL52407	Human NOG
896	11	52.4	38	8	ACA07113	969	11	52.4	38	11	ADL53997	ADL53997	Human IKK
897	11	52.4	38	8	ACA07319	970	11	52.4	38	11	ADL54011	ADL54011	Human IKK

971	11	52.4	38	11	ADL54087	Human	IKK
972	11	52.4	38	11	ADL53909	Human	IKK
973	11	52.4	38	11	ADL53943	Human	IKK
974	11	52.4	38	11	ADL54018	Human	IKK
975	11	52.4	38	11	ADL54083	Human	IKK
976	11	52.4	38	11	ADL54136	Human	IKK
977	11	52.4	38	11	ADL56310	Human	PKR
978	11	52.4	38	11	ADL52242	Human	NOG
979	11	52.4	38	11	ADL52269	Human	NOG
980	11	52.4	38	11	ADL53552	Human	IKK
981	11	52.4	38	11	ADL54014	Human	IKK
982	11	52.4	38	11	ADL52346	Human	NOG
983	11	52.4	38	11	ADL52246	Human	PKR
984	11	52.4	38	11	ADL56617	Human	PKR
985	11	52.4	38	11	ADL75194	Human	PTG
986	11	52.4	38	11	ADL75403	Human	PTG
987	11	52.4	38	11	ADL52249	Human	NOG
988	11	52.4	38	11	ADL53782	Human	IKK
989	11	52.4	38	11	ADL54164	Human	IKK
990	11	52.4	38	11	ADL54199	Human	IKK
991	11	52.4	38	11	ADL55733	Human	PKR
992	11	52.4	38	11	ADL56599	Human	PKR
993	11	52.4	38	11	ADL75335	Human	PTG
994	11	52.4	38	11	ADL75390	Human	PTG
995	11	52.4	38	11	ADL52144	Human	NOG
996	11	52.4	38	11	ADL53775	Human	IKK
997	11	52.4	38	11	ADL75487	Human	PTG
998	11	52.4	38	11	ADL54016	Human	IKK
999	11	52.4	38	11	ADL56557	Human	PKR
1000	11	52.4	38	11	ADL56601	Human	PKR

## ALIGNMENTS

## RESULT 1

AC156056

ID AC156056 standard; DNA; 25 BP.

AC AC156056;

DT 13-OCT-2003 (first entry)

DE Human microarray DNA oligonucleotide SEQ ID NO 56047.

XX EST; ss; probe; expressed sequence tag; microarray; gene expression;

XX genetic variation; diallelic marker; polymorphism; human;

XX cross-species comparison.

XX Homo sapiens.

XX US2003104410-A1.

XX 05-JUN-2003.

XX 15-MAR-2002; 2002US-00098263.

XX 16-MAR-2001; 2001US-0276759P.

XX (AFFY-) AFFYMETRIX INC.

XX Mitmann MP;

XX WPI; 2003-567953/53.

XX New array of nucleic acid probes, useful for in situ hybridization, in

XX Southern, Northern or dot-blot hybridization to identify or detect the

XX sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 56047; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic

XX acid probes including one of 2,018,500 fully defined sequences, or its

perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying diallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)

SQ Sequence 25 BP; 7 A; 4 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 67.6%; Score 14.2; DB 9; Length 25;

Best local Similarity 84.2%; Pred. No. 5.1e+02; Mismatches 0; Gaps 0;

Matches 16; Conservative 0; Indels 3; Indels 0; Gaps 0;

QY 3 GTCATTAGACCGTACGCCA 21

Db 6 GTCATTAGACCGTACGCCA 24

## RESULT 2

AAAL6755

ID AAAL6755 standard; DNA; 29 BP.

AC AAAL6755;

DT 16-JUN-2000 (first entry)

DE Human secreted protein clone LL89\_3 probe SEQ ID NO:218.

XX Human; secreted protein; immunostimulant; immunosuppressant; vitruide;

XX antibacterial; antifungal; cytostatic; antiinflammatory; dermatological;

XX antidiabetic; antiaesthetic; antiarthritic; antirheumatic; protozoicide;

XX antithyroid; immune deficiency; severe combined immunodeficiency; SCID;

XX infection; HIV; hepatitis; malaria; autoimmune disorder; systemic lupus;

XX connective tissue disease; multiple sclerosis; erythematosis;

XX rheumatoid arthritis; autoimmune pulmonary inflammation; asthma;

XX Guillain-Barre syndrome; autoimmune thyroiditis; myasthenia gravis;

XX insulin dependent diabetes mellitus; graft-versus-host-disease;

XX autoimmune inflammatory eye disease; allergy; hybridisation; probe; ss.

XX Homo sapiens.

XX WO200009552-A1.

XX 24-FEB-2000.

XX 13-AUG-1999; 99WO-US018298.

XX 14-AUG-1998; 98US-0096622P.

XX 17-AUG-1998; 98US-0096815P.

XX 04-SEP-1998; 98US-0099229P.

XX 23-OCT-1998; 98US-0105368P.

XX 08-JAN-1999; 99US-0115234P.

XX 12-FEB-1999; 99US-0119931P.

XX 18-FEB-1999; 99US-0120575P.

XX 30-APR-1999; 99US-0132020P.

XX 11-AUG-1999; 99US-0148424P.

XX (GEM) GENETICS INST INC.

C 387	11.2	53.3	25	9	ACH60892	ACH60892 DNA large	C 460	11	52.4	24	10	ADC57939	ADC57939 Human PRO
C 388	11.2	53.3	25	10	ABE284510	ABE284510 Toxilog	C 461	11	52.4	24	10	ADC55303	ADC55303 Human PRO
C 389	11.2	53.3	28	12	AAT73081	Aat73081 ui snRNA	C 462	11	52.4	24	10	ADCI2170	ADCI2170 Human PRO
C 390	11.2	53.3	28	12	ADO11376	Ado11376 Single mu	C 463	11	52.4	24	10	ADC55592	ADC55592 Human PRO
C 391	11.2	53.3	28	12	ADO11426	Ado11426 Single mu	C 464	11	52.4	24	10	ADCO7647	ADCO7647 Human PRO
C 392	11.2	53.3	29	6	ABO82513	Abq82513 Promoter	C 465	11	52.4	24	10	ADCI1637	ADCI1637 Human PRO
C 393	11.2	53.3	30	10	ADC83961	Adc83961 Human pap	C 466	11	52.4	24	10	ADCI14759	ADCI14759 Novel hum
C 394	11.2	53.3	30	10	ADFA3834	Adf43834 HPV 39 de	C 467	11	52.4	24	10	ADDO8291	ADDO8291 Human sec
C 395	11.2	53.3	31	2	AAT35700	Aat35700 3' VK pri	C 468	11	52.4	24	10	ADCB2116	ADCB2116 Human PRO
C 396	11.2	53.3	31	2	AAK62513	Aak62513 Granule ol	C 469	11	52.4	24	10	ADDO7758	ADDO7758 Human sec
C 397	11.2	53.3	34	3	AAK6282	Aak6282 Sample ol	C 470	11	52.4	24	10	ADCB2649	ADCB2649 Human PRO
C 398	11.2	53.3	37	6	ABK59294	Abk59294 Human CLC	C 471	11	52.4	24	10	ADDO8829	ADDO8829 Human sec
C 399	11.2	53.3	37	6	ACN19390	Acn19390 WNV Zinzy	C 472	11	52.4	24	10	ADDO7078	ADDO7078 Human sec
C 400	11.2	53.3	37	6	ACN30875	Acn30875 WNV minus	C 473	11	52.4	24	10	ADCB3325	ADCB3325 Human PRO
C 401	11.2	53.3	37	6	ACN19673	Acn19673 WNV Zinzy	C 474	11	52.4	24	10	ADCB2014	ADCB2014 Human PRO
C 402	11.2	53.3	37	6	ACN18820	Acn18820 WNV Zinzy	C 475	11	52.4	24	10	ADCB2015	ADCB2015 Human PRO
C 403	11.2	53.3	37	6	ACN30634	Acn30634 WNV minus	C 476	11	52.4	24	10	ADDO55432	ADDO55432 Human PRO
C 404	11.2	53.3	37	6	ACN31064	Acn31064 WNV minus	C 477	11	52.4	24	10	ADDO56390	ADDO56390 Human PRO
C 405	11.2	53.3	37	6	ACN31914	Acn31914 WNV minus	C 478	11	52.4	24	10	ADDO54828	ADDO54828 Human PRO
C 406	11.2	53.3	37	6	ACN30941	Acn30941 WNV minus	C 479	11	52.4	24	10	ADDE26982	ADDE26982 Novel hum
C 407	11.2	53.3	37	6	ACN31346	Acn31346 WNV minus	C 480	11	52.4	24	10	ADDE26449	ADDE26449 Novel hum
C 408	11.2	53.3	37	8	ACA08020	ACA08020 Necrosis	C 481	11	52.4	24	10	ADFB7386	ADFB7386 Human CDN
C 409	11.2	53.3	37	8	ACA08100	ACA08100 Necrosis	C 482	11	52.4	24	10	ADIB35640	ADIB35640 Human PRO
C 410	11.2	53.3	38	6	ABQ72429	Abq72429 PCR prime	C 483	11	52.4	24	10	ADIB00133	ADIB00133 Novel hum
C 411	11.2	53.3	39	10	ADC46944	Adc46944 Primer fo	C 484	11	52.4	24	10	ABX78017	ABX78017 Human PRO
C 412	11.2	53.3	40	2	AAT87214	Aat87214 Interleuk	C 485	11	52.4	24	10	ABX80429	ABX80429 Human sec
C 413	11.2	53.3	40	6	ABZ21788	Abz21788 Human ery	C 486	11	52.4	24	10	ACA69335	ACA69335 Human sec
C 414	11.2	53.3	40	6	ABZ21789	Abz21789 Human ery	C 487	11	52.4	24	10	ABX90406	ABX90406 Human sec
C 415	11.2	53.3	45	4	AA513391	Aa513391 Alantine s	C 488	11	52.4	24	10	ABX64252	ABX64252 Human PRO
C 416	11.2	53.3	50	6	ABZ06239	Abz06239 Human leu	C 489	11	52.4	24	12	ADFB35585	ADFB35585 Human PRO
C 417	11.2	52.4	16	3	AAZ47286	Aaz47286 C-myc pro	C 490	11	52.4	24	12	ADGI1835	ADGI1835 Human PRO
C 418	11.2	52.4	17	2	AAZ75296	Aaz75296 Mouse flt	C 491	11	52.4	24	12	ADHI19705	ADHI19705 Human PRO
C 419	11.2	52.4	17	2	AAZ75297	Aaz75297 Mouse flt	C 492	11	52.4	24	12	ADH21198	ADH21198 Human PRO
C 420	11.2	52.4	20	3	AAZ72519	Aaz72519 PCR prime	C 493	11	52.4	24	12	ADH20238	ADH20238 Human PRO
C 421	11.2	52.4	20	3	AAZ72519	Aaz72519 Human bia	C 494	11	52.4	24	12	ADIB37421	ADIB37421 M. tuberc
C 422	11.2	52.4	21	12	ADM92428	Adm92428 Pancreat	C 495	11	52.4	25	9	ACI74364	ACI74364 Human m1c
C 423	11.2	52.4	21	6	ABU59233	Abu59233 Antisense	C 496	11	52.4	25	9	ACI31851	ACI31851 Human m1c
C 424	11.2	52.4	22	12	ADPB6451	Adpb6451 Mouse GAP	C 497	11	52.4	25	9	ACI14671	ACI14671 Human m1c
C 425	11.2	52.4	23	4	AAO07923	Aao07923 Human G-P	C 498	11	52.4	25	9	ACI90851	ACI90851 Human m1c
C 426	11.2	52.4	24	2	AAO92089	Aao92089 Human rec	C 499	11	52.4	25	9	ACI28866	ACI28866 Human m1c
C 427	11.2	52.4	24	2	AAK35264	Aak35264 PCR prime	C 500	11	52.4	25	9	ACI04993	ACI04993 Human m1c
C 428	11.2	52.4	24	3	AAK58316	Aak58316 Human PRO	C 501	11	52.4	25	9	ACI86887	ACI86887 Human m1c
C 429	11.2	52.4	24	5	AA517470	Aa517470 P. viwax	C 502	11	52.4	25	9	ACI16965	ACI16965 Human m1c
C 430	11.2	52.4	24	5	AA544420	Aa544420 Human PRO	C 503	11	52.4	25	9	ACKO0553	ACKO0553 Human m1c
C 431	11.2	52.4	24	6	ABK87485	Abk87485 Synthetic	C 504	11	52.4	25	9	ACI28682	ACI28682 Human m1c
C 432	11.2	52.4	24	6	ABK87486	Abk87486 Synthetic	C 505	11	52.4	25	9	ACI94261	ACI94261 Human m1c
C 433	11.2	52.4	24	6	ABQ03239	Abq03239 Oligonuc	C 506	11	52.4	25	9	ACT19780	ACT19780 Human m1c
C 434	11.2	52.4	24	6	ABQ79141	Abq79141 Primer #1	C 507	11	52.4	25	9	ACKI2417	ACKI2417 Human m1c
C 435	11.2	52.4	24	8	ACA64474	Ac644474 Novel hum	C 508	11	52.4	25	9	ACT15267	ACT15267 Human m1c
C 436	11.2	52.4	24	8	ABX80933	Abx80933 Human sec	C 509	11	52.4	25	9	ACT125752	ACT125752 Human m1c
C 437	11.2	52.4	24	8	ACD04442	Ac444442 Human PRO	C 510	11	52.4	25	9	ACT196369	ACT196369 Human m1c
C 438	11.2	52.4	24	8	ABX79613	Abx79613 Human sec	C 511	11	52.4	25	9	ACH64101	ACH64101 Human m1c
C 439	11.2	52.4	24	8	ACA93634	Ac93634 Novel hum	C 512	11	52.4	25	9	ACH64227	ACH64227 DNA large
C 440	11.2	52.4	24	8	ABX81316	Abx81316 Human sec	C 513	11	52.4	25	12	ADK72525	ADK72525 Streptom
C 441	11.2	52.4	24	8	ACA93132	Ac93132 Novel hum	C 514	11	52.4	28	2	ADL71141	ADL71141 Streptom
C 442	11.2	52.4	24	8	ABX17216	Abx17216 Human PRO	C 515	11	52.4	28	2	AAQ46856	AAQ46856 Interleuk
C 443	11.2	52.4	24	9	ACA88071	Ac88071 Novel hum	C 516	11	52.4	28	6	ABR91518	ABR91518 Chlamydia
C 444	11.2	52.4	24	9	ACA88520	Ac88520 Human sec	C 517	11	52.4	31	4	AAI29879	AAI29879 Human bin
C 445	11.2	52.4	24	9	ACD82027	Ac82027 Human PRO	C 518	11	52.4	32	3	AAA99084	AAA99084 UBQ10 gen
C 446	11.2	52.4	24	9	ADA21656	Ada21656 Human sec	C 519	11	52.4	33	3	AA64927	AA64927 Control R
C 447	11.2	52.4	24	9	ADA10443	Ada10443 Human PRO	C 520	11	52.4	33	6	ABX03349	ABX03349 Ribozyme
C 448	11.2	52.4	24	9	ADA10443	Ada10443 Human PRO	C 521	11	52.4	33	12	ADPB4085	ADPB4085 Small nuc
C 449	11.2	52.4	24	9	ADA17987	Ada17987 Human PRO	C 522	11	52.4	34	10	ADFI3553	ADFI3553 Gpi1 gene
C 450	11.2	52.4	24	9	ADA28095	Ada28095 Human PRO	C 523	11	52.4	35	6	ABK54214	ABK54214 Pantocin
C 451	11.2	52.4	24	9	ADA34675	Ada34675 Human PRO	C 524	11	52.4	35	8	ACH10009	ACH10009 Necrosis
C 452	11.2	52.4	24	9	ADA38900	Ada38900 Human PRO	C 525	11	52.4	35	8	ACH10011	ACH10011 Necrosis
C 453	11.2	52.4	24	9	ADA93021	Ada93021 Human PRO	C 526	11	52.4	36	2	AAV11874	AAV11874 Synthetic
C 454	11.2	52.4	24	9	ACH65588	ACH65588 Human PRO	C 527	11	52.4	36	2	AAV19025	AAV19025 Plasmid p
C 455	11.2	52.4	24	9	ADA22582	Ada22582 Human sec	C 528	11	52.4	36	6	ABX01900	ABX01900 HCV hamme
C 456	11.2	52.4	24	9	ACD39578	Ac39578 Human PRO	C 529	11	52.4	36	6	ABX02596	ABX02596 HCV hamme
C 457	11.2	52.4	24	9	ADA06748	Ada06748 Human sec	C 530	11	52.4	36	6	ABX02112	ABX02112 HCV hamme
C 458	11.2	52.4	24	9	ADA39441	Ada39441 Human PRO	C 531	11	52.4	36	6	ABX02392	ABX02392 HCV hamme
C 459	11.2	52.4	24	9	ADB96467	Adb96467 Human PRO	C 532	11	52.4	36	6	ABX02676	ABX02676 HCV hamme

241	11.6	55.2	38	6	ACN16944	WNV	Inozy	C 314	11.4	54.3	20	2	AAQ45350	AdG45350 PCR prime
242	11.6	55.2	38	6	ACN18309	WNV	Inozy	315	11.4	54.3	22	6	ABL31902	ABL31902 Human CYP
243	11.6	55.2	38	6	ACN18573	WNV	Inozy	C 316	11.4	54.3	23	6	ABV75861	ABV75861 Arabidops
244	11.6	55.2	38	6	ACN17194	WNV	Inozy	C 317	11.4	54.3	23	10	ABZ81234	ABZ81234 Arabidops
245	11.6	55.2	38	6	ACN28445	WNV	minus	C 318	11.4	54.3	23	10	ADH55553	AdH55553 H+ -ATPas
246	11.6	55.2	38	6	ACN30165	WNV	minus	C 319	11.4	54.3	23	10	ADL18214	AdL18214 H+-ATPas
247	11.6	55.2	38	6	ACN18467	WNV	Inozy	C 320	11.4	54.3	24	6	ABO08710	ABO08710 Oligonuc
248	11.6	55.2	38	6	ACN18695	WNV	Inozy	C 321	11.4	54.3	24	6	ABO08669	ABO08669 Capture o
249	11.6	55.2	38	6	ACN28523	WNV	minus	C 322	11.4	54.3	24	6	AB1844227	AB1844227 Capture o
250	11.6	55.2	38	6	ACN29692	WNV	minus	C 323	11.4	54.3	24	6	AB1844226	AB1844226 Capture o
251	11.6	55.2	38	6	ACN29037	WNV	minus	C 324	11.4	54.3	25	9	ACK156633	ACK156633 Human mic
252	11.6	55.2	38	6	ACN28657	WNV	minus	C 325	11.4	54.3	25	9	ACK10586	ACK10586 Human mic
253	11.6	55.2	38	6	ACN29459	WNV	minus	C 326	11.4	54.3	25	9	ACK10586	ACK10586 Human mic
254	11.6	55.2	38	6	ACN29448	WNV	minus	C 327	11.4	54.3	25	9	ACK189574	ACK189574 Human mic
255	11.6	55.2	38	6	ACN30357	WNV	minus	C 328	11.4	54.3	25	9	ACK189574	ACK189574 Human mic
256	11.6	55.2	38	6	ACN29655	WNV	minus	C 329	11.4	54.3	25	9	ACK169299	ACK169299 Human mic
257	11.6	55.2	38	6	ACN29671	WNV	minus	C 330	11.4	54.3	25	9	ACK21465	ACK21465 Human mic
258	11.6	55.2	38	6	ACN29661	WNV	minus	C 331	11.4	54.3	25	9	ACK21465	ACK21465 Human mic
259	11.6	55.2	38	6	ACN17594	WNV	minus	C 332	11.4	54.3	25	9	ACK21465	ACK21465 Human mic
260	11.6	55.2	38	6	ACN29252	WNV	minus	C 333	11.4	54.3	25	9	ACK21465	ACK21465 Human mic
261	11.6	55.2	38	6	ACN17438	WNV	Inozy	C 334	11.4	54.3	25	9	ACK21465	ACK21465 Human mic
262	11.6	55.2	38	6	ACN17890	WNV	Inozy	C 335	11.4	54.3	25	9	ACK21465	ACK21465 Human mic
263	11.6	55.2	38	6	ACN16983	WNV	Inozy	C 336	11.4	54.3	25	9	ACK21465	ACK21465 Human mic
264	11.6	55.2	38	8	ACA07508	Necrosis	337	11.4	54.3	25	9	ACK56738	ACK56738 DNA targe	
265	11.6	55.2	38	8	ACA07508	Necrosis	C 338	11.4	54.3	25	9	ACK56738	ACK56738 DNA targe	
266	11.6	55.2	38	8	ACA07040	Necrosis	C 339	11.4	54.3	25	9	ABT11741	ABT11741 Drosophil	
267	11.6	55.2	38	8	ACA07037	Necrosis	C 340	11.4	54.3	25	8	ABT11785	ABT11785 Transcrip	
268	11.6	55.2	38	8	ABA26597	Human HIV	C 341	11.4	54.3	27	8	ABT11784	ABT11784 Transcrip	
269	11.6	55.2	38	8	ACD52161	HBV Inozy	C 342	11.4	54.3	27	10	ADC660797	ADC660797 C1s eleme	
270	11.6	55.2	38	8	ACD52955	HBV Inozy	C 343	11.4	54.3	27	10	ADC660796	ADC660796 C1s eleme	
271	11.6	55.2	38	8	ACD52428	HBV Inozy	C 344	11.4	54.3	27	10	ADF48566	ADF48566 C1s-eleme	
272	11.6	55.2	38	8	ACD52428	HBV Inozy	C 345	11.4	54.3	27	10	ADF48567	ADF48567 C1s-eleme	
273	11.6	55.2	38	8	ACD52433	HBV Inozy	C 346	11.4	54.3	27	10	ADP44550	ADP44550 PCR prime	
274	11.6	55.2	38	8	ACD52468	HBV Inozy	C 347	11.4	54.3	28	3	AAH91910	AAH91910 Porphorym	
275	11.6	55.2	38	8	ACD53061	HBV Inozy	C 348	11.4	54.3	36	2	AAH91910	AAH91910 Porphorym	
276	11.6	55.2	38	11	ADL53906	Human IKK	C 349	11.4	54.3	37	2	AAH91910	AAH91910 Porphorym	
277	11.6	55.2	38	11	ADL52422	Human PTG	C 350	11.4	54.3	38	2	AAH91910	AAH91910 Porphorym	
278	11.6	55.2	38	11	ADL75357	Human PTG	C 351	11.4	54.3	42	2	AAH91910	AAH91910 Porphorym	
279	11.6	55.2	38	11	ADL52170	Human NOG	C 352	11.4	54.3	43	2	AAH91910	AAH91910 Porphorym	
280	11.6	55.2	38	11	ADL53903	Human IKK	C 353	11.2	53.3	43	2	AAH91910	AAH91910 Porphorym	
281	11.6	55.2	38	11	ADL54002	Human IKK	C 354	11.2	53.3	43	2	AAH91910	AAH91910 Porphorym	
282	11.6	55.2	38	11	ADL5463	Human PTG	C 355	11.2	53.3	43	2	AAH91910	AAH91910 Porphorym	
283	11.6	55.2	38	11	ADL54079	Human IKK	C 356	11.2	53.3	43	2	AAH91910	AAH91910 Porphorym	
284	11.6	55.2	38	11	ADL75285	Human PTG	C 357	11.2	53.3	43	2	AAH91910	AAH91910 Porphorym	
285	11.6	55.2	38	11	ADL75413	Human NOG	C 358	11.2	53.3	43	2	AAH91910	AAH91910 Porphorym	
286	11.6	55.2	38	11	ADL754329	Human NOG	C 359	11.2	53.3	43	2	AAH91910	AAH91910 Porphorym	
287	11.6	55.2	38	11	ADL52336	Human NOG	C 360	11.2	53.3	43	2	AAH91910	AAH91910 Porphorym	
288	11.6	55.2	38	11	ADL52336	Human NOG	C 361	11.2	53.3	43	2	AAH91910	AAH91910 Porphorym	
289	11.6	55.2	38	11	ADL75406	Human PTG	C 362	11.2	53.3	43	2	AAH91910	AAH91910 Porphorym	
290	11.6	55.2	38	11	ADL52232	Human NOG	C 363	11.2	53.3	43	2	AAH91910	AAH91910 Porphorym	
291	11.6	55.2	38	11	ADL52232	Human NOG	C 364	11.2	53.3	43	2	AAH91910	AAH91910 Porphorym	
292	11.6	55.2	38	11	ADL56628	Human PKR	C 365	11.2	53.3	43	2	AAH91910	AAH91910 Porphorym	
293	11.6	55.2	38	11	ADL75325	Human PTG	C 366	11.2	53.3	43	2	AAH91910	AAH91910 Porphorym	
294	11.6	55.2	38	11	ADL54181	Human IKK	C 367	11.2	53.3	43	2	AAH91910	AAH91910 Porphorym	
295	11.6	55.2	38	11	ADL75218	Human PTG	C 368	11.2	53.3	43	2	AAH91910	AAH91910 Porphorym	
296	11.6	55.2	38	11	ADL52262	Human NOG	C 369	11.2	53.3	43	2	AAH91910	AAH91910 Porphorym	
297	11.6	55.2	38	11	ADL52304	Human NOG	C 370	11.2	53.3	43	2	AAH91910	AAH91910 Porphorym	
298	11.6	55.2	38	11	ADL75228	Human PTG	C 371	11.2	53.3	43	2	AAH91910	AAH91910 Porphorym	
299	11.6	55.2	38	11	ADL75251	Human PTG	C 372	11.2	53.3	43	2	AAH91910	AAH91910 Porphorym	
300	11.6	55.2	38	11	ADL52304	Human NOG	C 373	11.2	53.3	43	2	AAH91910	AAH91910 Porphorym	
301	11.6	55.2	38	11	ADL52304	Human NOG	C 374	11.2	53.3	43	2	AAH91910	AAH91910 Porphorym	
302	11.6	55.2	38	12	ADM61570	HepatitIs	C 375	11.2	53.3	43	2	AAH91910	AAH91910 Porphorym	
303	11.6	55.2	38	12	ADM61430	HepatitIs	C 376	11.2	53.3	43	2	AAH91910	AAH91910 Porphorym	
304	11.6	55.2	38	12	ADM61435	HepatitIs	C 377	11.2	53.3	43	2	AAH91910	AAH91910 Porphorym	
305	11.6	55.2	38	12	ADM61430	HepatitIs	C 378	11.2	53.3	43	2	AAH91910	AAH91910 Porphorym	
306	11.6	55.2	38	12	ADM61430	HepatitIs	C 379	11.2	53.3	43	2	AAH91910	AAH91910 Porphorym	
307	11.6	55.2	38	12	ADM61430	HepatitIs	C 380	11.2	53.3	43	2	AAH91910	AAH91910 Porphorym	
308	11.6	55.2	38	12	ADM61430	HepatitIs	C 381	11.2	53.3	43	2	AAH91910	AAH91910 Porphorym	
309	11.6	55.2	38	12	ADM61430	HepatitIs	C 382	11.2	53.3	43	2	AAH91910	AAH91910 Porphorym	
310	11.6	55.2	38	12	ADM61430	HepatitIs	C 383	11.2	53.3	43	2	AAH91910	AAH91910 Porphorym	
311	11.6	55.2	38	12	ADM61430	HepatitIs	C 384	11.2	53.3	43	2	AAH91910	AAH91910 Porphorym	
312	11.4	54.3	15	6	ABX01122	HepatitIs	C 385	11.2	53.3	43	2	AAH91910	AAH91910 Porphorym	
313	11.4	54.3	15	6	ABX01122	HepatitIs	C 386	11.2	53.3	43	2	AAH91910	AAH91910 Porphorym	

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channel-1 (clca-1)  
JOURNAL Patent: WO 0211674-A 3626 14-FEB-2002;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;  
Thompson, James (US)  
FEATURES  
source Location/Qualifiers  
1..37  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Enzymatic Nucleic Acid"  
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Best Local Similarity 82.4%; Pred. No. 1.7e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 4 TCATTAGACCGTAGCGG 20  
DB 34 TCATTAGACCTCCTCG 18  
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artificial sequences.  
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1 Thompson, J., Mcswigen, J., McKenzie, T., Ayers, D., Szymkowski, D.E.  
and Grube, A.  
TITLE Method and reagent for the inhibition of calcium activated chloride  
channel-1 (clca-1)  
JOURNAL Patent: WO 0211674-A 3631 14-FEB-2002;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;  
Thompson, James (US)  
FEATURES  
source Location/Qualifiers  
1..37  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Enzymatic Nucleic Acid"  
ORIGIN  
Query Match 58.1%; Score 12.2; DB 6; Length 37;  
Best Local Similarity 82.4%; Pred. No. 1.7e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 4 TCATTAGACCGTAGCGG 20  
DB 34 TCATTAGACCTCCTCG 18  
RESULT 40  
AX581826/c 37 bp RNA linear PAT 10-JAN-2003  
LOCUS AX581826  
DEFINITION Sequence 3664 from Patent WO0211674.  
ACCESSION AX581826  
VERSION AX581826.1 GI:27653636  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE  
1 Thompson, J., Mcswigen, J., McKenzie, T., Ayers, D., Szymkowski, D.E.  
and Grube, A.  
TITLE Method and reagent for the inhibition of calcium activated chloride

channel-1 (clca-1)  
JOURNAL Patent: WO 0211674-A 3664 14-FEB-2002;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;  
Thompson, James (US)  
FEATURES  
source Location/Qualifiers  
1..37  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Enzymatic Nucleic Acid"  
ORIGIN  
Query Match 58.1%; Score 12.2; DB 6; Length 37;  
Best Local Similarity 82.4%; Pred. No. 1.7e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 4 TCATTAGACCGTAGCGG 20  
DB 34 TCATTAGACCTCCTCG 18

Search completed: November 23, 2004, 18:47:25  
Job time : 379.157 secs

Db 21 CATTGACCTTAGCGA 5

RESULT 34  
AX392054/c  
LOCUS AX392054  
DEFINITION Sequence 13 from Patent WO0215920.  
ACCESSION AX392054  
VERSION AX392054.1 GI:19700558  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1  
AUTHORS Ward,S.B., Bavik,C.B., Cork,M.B. and Tazi-Ahmini,R.B.  
TITLE Treatment of hyperproliferative diseases  
JOURNAL Patent: WO 0215920-A 13 28-FEB-2002;  
THE UNIVERSITY OF SHEFFIELD (GB)  
FEATURES  
source 1..22  
/organism="synthetic construct"  
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ORIGIN

Query Match 58.1%; Score 12.2; DB 6; Length 22;  
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Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GTCATTAGACCGTAGCG 19  
18 GTCATTAGACCGTAGCG 2

Db 18 GTCATTAGACCGTAGCG 2

RESULT 35  
AX755148  
LOCUS AX755148  
DEFINITION Sequence 29 from Patent WO03025003.  
ACCESSION AX755148  
VERSION AX755148.1 GI:32167628  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1  
AUTHORS Beaton,A., Ertl,P.F., Gough,G.W., Lear,A., Tite,J.P. and van Wely,C.A.  
TITLE Vaccines  
JOURNAL Patent: WO 03025003-A 29 27-MAR-2003;  
GLAXO GROUP LIMITED (GB)  
FEATURES  
source 1..32  
/organism="synthetic construct"  
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/note="PCR primer"

ORIGIN

Query Match 58.1%; Score 12.2; DB 6; Length 32;  
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Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CATTAGACCGTAGCGCA 21  
1 CATTAGACCGCGCGCGA 17

Db 1 CATTAGACCGCGCGCGA 17

RESULT 36  
AX755156  
LOCUS AX755156  
DEFINITION Sequence 37 from Patent WO03025003.

ACCESSION AX755156  
VERSION AX755156.1 GI:32167636  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1  
AUTHORS Beaton,A., Ertl,P.F., Gough,G.W., Lear,A., Tite,J.P. and van Wely,C.A.  
TITLE Vaccines  
JOURNAL Patent: WO 03025003-A 37 27-MAR-2003;  
GLAXO GROUP LIMITED (GB)  
FEATURES  
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/note="PCR primer"

ORIGIN

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Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CATTAGACCGTAGCGCA 21  
1 CATTAGACCGCGCGCGA 17

Db 1 CATTAGACCGCGCGCGA 17

RESULT 37  
AX351239/c  
LOCUS AX351239  
DEFINITION Sequence 74 from Patent WO0194950.  
ACCESSION AX351239  
VERSION AX351239.1 GI:18616587  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1  
AUTHORS Nock,S. and Kassner,P.D.  
TITLE Screening of phage displayed peptides without clearing of the cell culture  
JOURNAL Patent: WO 0194950-A 74 13-DEC-2001;  
Zyomyx, Inc. (US)  
FEATURES  
source 1..37  
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ORIGIN

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Best Local Similarity 73.7%; Pred. No. 1.7e+05;  
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGTCACTAGACCGTAGCG 20  
30 GGTCACTAGCAATGTCGCG 12

Db 30 GGTCACTAGCAATGTCGCG 12

RESULT 38  
AX581788/c  
LOCUS AX581788  
DEFINITION Sequence 3626 from Patent WO0211674.  
ACCESSION AX581788  
VERSION AX581788.1 GI:27653598  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1



AR046887/c  
LOCUS AR046887 38 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 1680 from patent US 5817796.  
ACCESSION AR046887  
VERSION AR046887.1 GI:5968352  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 38)  
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.  
TITLE C-myb ribozymes having 2'-5'-linked adenylyate residues  
JOURNAL Patent: US 5817796-A 1680 06-OCT-1996;  
FEATURES Location/Qualifiers  
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ORIGIN  
Query Match 59.0%; Score 12.4; DB 6; Length 38;  
Best Local Similarity 92.9%; Pred. No. 1.3e+05;  
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QY 4 TCATTAGACCGTAC 17  
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15 TCATCAGACCGTAC 2

RESULT 30  
153939/c 38 bp DNA linear PAT 07-OCT-1997  
LOCUS 153939  
DEFINITION Sequence 1680 from patent US 5646042.  
ACCESSION 153939  
VERSION 153939.1 GI:2475142  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 38)  
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.  
TITLE C-myb targeted ribozymes  
JOURNAL Patent: US 5646042-A 1680 08-JUL-1997;  
FEATURES Location/Qualifiers  
source 1..38  
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ORIGIN  
Query Match 59.0%; Score 12.4; DB 6; Length 38;  
Best Local Similarity 92.9%; Pred. No. 1.3e+05;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCATTAGACCGTAC 17  
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15 TCATCAGACCGTAC 2

RESULT 31  
AX220204/c 38 bp RNA linear PAT 07-SEP-2001  
LOCUS AX220204  
DEFINITION Sequence 5646 from Patent W00159103.  
ACCESSION AX220204  
VERSION AX220204.1 GI:15547928  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM artificial sequences.

REFERENCE 1  
AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and  
JOURNAL nogo gene expression  
Patent: WO 0159103-A 5646 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;

McSwiggen, James (US) ; Chowrira, Bharat M. (US)  
FEATURES Location/Qualifiers  
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/db\_xref="taxon:32630"  
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ORIGIN  
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Best Local Similarity 92.9%; Pred. No. 1.3e+05;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGTCATTAGACCGT 15  
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37 GGTCATTAGACCTT 24

RESULT 32  
AR314417/c 20 bp DNA linear PAT 12-JUN-2003  
LOCUS AR314417  
DEFINITION Sequence 4954 from patent US 6559294.  
ACCESSION AR314417  
VERSION AR314417.1 GI:31707843  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Griffiths,R., Hoisebeth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,  
TITLE Sankaran,B. and Fletcher,J.D.  
JOURNAL Chlamydia pneumoniae polynucleotides and uses thereof  
Patent: US 6559294-A 4954 06-MAY-2003;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 58.1%; Score 12.2; DB 6; Length 20;  
Best Local Similarity 82.4%; Pred. No. 1.8e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TCATTAGACCGTACCG 20  
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18 TCATTATAGCGTCCGCG 2

RESULT 33  
AR364921/c 21 bp DNA linear PAT 03-SEP-2003  
LOCUS AR364921  
DEFINITION Sequence 8 from patent US 5451502.  
ACCESSION AR364921  
VERSION AR364921.1 GI:34428117  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS George,A.L., Jr.  
TITLE Restriction amplification assay  
JOURNAL Patent: US 5451502-A 8 19-SEP-1995;  
FEATURES Location/Qualifiers  
source 1..21  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 58.1%; Score 12.2; DB 6; Length 21;  
Best Local Similarity 82.4%; Pred. No. 1.8e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CATTAGACCGTACGCGA 21



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96	12	57.1	36	6	ABX02155	Abx02155 HCV hamme	169	11.6	55.2	25	9	AC188245	Ac188245 Human m1c
97	12	57.1	36	6	ABX02284	Abx02284 HCV hamme	170	11.6	55.2	25	9	AC97085	Ac97085 Cytochrom
98	12	57.1	37	6	ABK59280	Abk59280 Human CLC	171	11.6	55.2	26	4	AAc97084	AAc97084 Cytochrom
99	12	57.1	37	6	ACN19032	Acn19032 WNV Zinzv	172	11.6	55.2	32	12	AD059622	Ad059622 HCV RNA P
100	12	57.1	37	6	ACN30898	Acn30898 WNV minus	173	11.6	55.2	32	12	AD059629	Ad059629 HCV RNA P
101	12	57.1	37	6	ACN18884	Acn18884 WNV Zinzv	174	11.6	55.2	32	12	AD059633	Ad059633 HCV RNA P
102	12	57.1	37	6	ACN18893	Acn18893 WNV Zinzv	175	11.6	55.2	32	12	AD059628	Ad059628 HCV RNA P
103	12	57.1	37	6	ACN19198	Acn19198 WNV Zinzv	176	11.6	55.2	32	12	AD059635	Ad059635 HCV RNA P
104	12	57.1	37	6	ACN30720	Acn30720 WNV minus	177	11.6	55.2	32	12	AD059632	Ad059632 HCV RNA P
105	12	57.1	37	6	ACN19979	Acn19979 WNV Zinzv	178	11.6	55.2	32	12	AD059624	Ad059624 HCV RNA P
106	12	57.1	37	6	ACN31491	Acn31491 WNV minus	179	11.6	55.2	32	12	AD059630	Ad059630 HCV RNA P
107	12	57.1	37	6	ACN31195	Acn31195 WNV minus	180	11.6	55.2	32	12	AD059634	Ad059634 HCV RNA P
108	12	57.1	37	6	ACN31240	Acn31240 WNV minus	181	11.6	55.2	32	12	AD059636	Ad059636 HCV RNA P
109	12	57.1	37	6	ACN08151	Acn08151 Necrosis	182	11.6	55.2	32	12	AD059623	Ad059623 HCV RNA P
110	12	57.1	37	11	ADL52659	Adl52659 Human NOG	183	11.6	55.2	32	12	AD059627	Ad059627 HCV RNA P
111	12	57.1	37	11	ADL54425	Adl54425 Human IKK	184	11.6	55.2	32	12	AD059631	Ad059631 HCV RNA P
112	12	57.1	37	11	ADL73501	Adl73501 Human PKR	185	11.6	55.2	32	12	AD059626	Ad059626 HCV RNA P
113	12	57.1	37	11	ADL73524	Adl73524 Human PKR	186	11.6	55.2	34	8	ACA10065	ACA10065 Necrofib
114	12	57.1	38	6	ABK58095	Abk58095 Human CLC	187	11.6	55.2	35	2	AAV61557	AAV61557 Adaptor N
115	12	57.1	38	6	ACN27173	Acn27173 WNV minus	188	11.6	55.2	35	12	AD159444	AD159444 Inozyme B
116	12	57.1	38	6	ACN16487	Acn16487 WNV Hamme	189	11.6	55.2	37	5	AAH41019	AAH41019 PCR prime
117	12	57.1	38	6	ACN27061	Acn27061 WNV minus	190	11.6	55.2	37	6	ABK59250	Abk59250 Human CLC
118	12	57.1	38	6	ACN27710	Acn27710 WNV minus	191	11.6	55.2	37	6	ABK59311	Abk59311 Human CLC
119	12	57.1	38	6	ACN16108	Acn16108 WNV Hamme	192	11.6	55.2	37	6	ABK59311	Abk59311 Human CLC
120	12	57.1	38	6	ACN16340	Acn16340 WNV Hamme	193	11.6	55.2	37	6	ACN31481	Acn31481 WNV minus
121	12	57.1	38	6	ACN16550	Acn16550 WNV Hamme	194	11.6	55.2	37	6	ACN30995	Acn30995 WNV minus
122	12	57.1	38	6	ACN16547	Acn16547 WNV Hamme	195	11.6	55.2	37	6	ACN31582	Acn31582 WNV minus
123	12	57.1	38	8	ACD51020	AcD51020 HBV hamme	196	11.6	55.2	37	6	ACN30780	Acn30780 WNV minus
124	12	57.1	38	11	ADL53578	Adl53578 Human IKK	197	11.6	55.2	37	6	ACN31436	Acn31436 WNV minus
125	12	57.1	38	11	ADL56069	Adl56069 Human PKR	198	11.6	55.2	37	6	ACN37009	Acn37009 WNV enzym
126	12	57.1	38	11	ADL56761	Adl56761 Human PKR	199	11.6	55.2	37	6	ACN31816	Acn31816 WNV minus
127	12	57.1	38	12	ADM60741	Adm60741 Hepatitis	200	11.6	55.2	37	6	ACN31773	Acn31773 WNV minus
128	12	57.1	45	2	AAK83991	Aak83991 Mouse pro	201	11.6	55.2	37	11	ADL54295	ADL54295 Human IKK
129	12	57.1	50	8	ABZ68287	Abz68287 Nucleotid	202	11.6	55.2	38	4	ABK04734	Abk04734 Human NOG
130	12	57.1	50	10	ADD31953	Add31953 BBP-B1X a	203	11.6	55.2	38	4	ABK04713	Abk04713 Human NOG
131	12	57.1	15	3	AAZ64070	Aaz64070 Substrate	204	11.6	55.2	38	4	ABK04626	Abk04626 Human NOG
132	12	57.1	17	12	AD183905	Adi83905 HCV DNAsy	205	11.6	55.2	38	4	ABK05292	Abk05292 Human NOG
133	12	57.1	17	12	AD183905	Adi83905 HCV DNAsy	206	11.6	55.2	38	4	ABK04552	Abk04552 Human NOG
134	12	57.1	25	9	ACI98341	Acti98341 Human m1c	207	11.6	55.2	38	4	ABK04620	Abk04620 Human NOG
135	12	57.1	25	9	ACI98341	Acti98341 Human m1c	208	11.6	55.2	38	4	ABK04722	Abk04722 Human NOG
136	12	57.1	25	9	ACI98341	Acti98341 Human m1c	209	11.6	55.2	38	4	ABK04634	Abk04634 Human NOG
137	12	57.1	25	9	ACI28871	Acti28871 Human m1c	210	11.6	55.2	38	4	ABK04873	Abk04873 Human NOG
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139	12	57.1	25	9	ACI28871	Acti28871 Human m1c	212	11.6	55.2	38	4	ABK04873	Abk04873 Human NOG
140	12	57.1	25	9	ACI28871	Acti28871 Human m1c	213	11.6	55.2	38	4	ABK04873	Abk04873 Human NOG
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148	12	57.1	25	9	ACI28871	Acti28871 Human m1c	221	11.6	55.2	38	4	ABK04873	Abk04873 Human NOG
149	12	57.1	25	9	ACI28871	Acti28871 Human m1c	222	11.6	55.2	38	4	ABK04873	Abk04873 Human NOG
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159	12	57.1	25	9	ACI28871	Acti28871 Human m1c	232	11.6	55.2	38	4	ABK04873	Abk04873 Human NOG
160	12	57.1	25	9	ACI28871	Acti28871 Human m1c	233	11.6	55.2	38	4	ABK04873	Abk04873 Human NOG
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165	12	57.1	25	9	ACI28871	Acti28871 Human m1c	238	11.6	55.2	38	4	ABK04873	Abk04873 Human NOG
166	12	57.1	25	9	ACI28871	Acti28871 Human m1c	239	11.6	55.2	38	4	ABK04873	Abk04873 Human NOG
167	12	57.1	25	9	ACI28871	Acti28871 Human m1c	240	11.6	55.2	38	4	ABK04873	Abk04873 Human NOG

QY 1 CGGTCATTAGACCGTACGC 19  
DB 21 CTGTCATTGACCGACAC 3

RESULT 19  
AAC97127/c  
ID AAC97127 standard; DNA; 26 BP.  
XX  
AC AAC97127;  
XX  
DT 26-FEB-2001 (first entry)  
XX  
DE Cytochrome b PCR primer; SEQ ID 102.  
XX  
KM Mutation detection; fungi; cytochrome b; strobilurin analogue resistance;  
KW single nucleotide polymorphism; PCR primer; fungal resistance; crop;  
KW fruit; vegetable; ss.  
XX  
OS Venturia inaequalis.  
XX  
PN WO20006773-A2.  
XX  
PD 09-NOV-2000.  
XX  
PF 26-APR-2000; 2000WO-GB001620.  
XX  
PR 30-APR-1999; 99GB-00010100.  
PR 13-MAR-2000; 2000GB-00006004.  
PR 31-MAR-2000; 2000GB-00007901.  
XX  
PA (ZENE ) ZENECA LTD.  
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PI Windass JD, Heaney SP, Renwick A, Whitcombe DM, Little S,  
PI Gibson NJ, Theaker J, Stanger CP;  
XX  
DR WPI; 2001-007234/01.  
XX  
PT Detecting a cytochrome b mutation which leads to resistance to  
PT strobilurin analogs or compounds in the same resistance group in fungal  
PT nucleic acid using a single nucleotide polymorphism detection technique.  
XX  
PS Disclosure: Page 35; 173pp; English.  
XX  
CC The present invention relates to a method for detecting mutations in  
CC fungal cytochrome b coding sequences which give rise to resistance to  
CC strobilurin analogues. The method uses a single nucleotide polymorphism  
CC (SNP) detection technique. The present sequence is a PCR primer used in  
CC the method of the present invention. The method is suitable for  
CC monitoring fungal resistance to a strobilurin analogue or a compound in  
CC the same cross resistance group in crops such as cereals, fruit and  
CC vegetables such as canola, sunflower, tobacco, sugarbeet, cotton, soya,  
CC wheat, barley, rice, sorghum, tomatoes, mangoes, peaches, apples,  
CC pears, strawberries, bananas, melons, potatoes and carrot  
XX  
SQ Sequence 26 BP; 7 A; 4 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 60.0%; Score 12.6; DB 4; Length 26;  
Best Local Similarity 78.9%; Pred. No. 4.1e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGTGATTAGACCGTACGC 20  
DB 20 GGTGATTAGACCGTACGC 2

RESULT 20  
AAZ50914/c  
ID AAZ50914 standard; DNA; 31 BP.  
XX  
AC AAZ50914;  
XX

DT 31-MAY-2000 (first entry)  
XX  
DE PCR primer RO204 to amplify Piac promoter.  
XX  
KM Plasmid pRAB-84-69; recombinant; beta-casein; PCR primer; Piac promoter;  
KW casein kinase II alpha subunit; casein kinase II beta subunit;  
KW kanamycin resistance marker; iminopeptidase; genetic stability;  
KW pharmaceutical; nutritional composition; vaccine formulation; ss.  
XX  
OS Unidentified.  
XX  
PN WO200008174-A1.  
XX  
PD 17-FEB-2000.  
XX  
PF 06-AUG-1999; 99WO-US017873.  
XX  
PR 07-AUG-1998; 98US-00131028.  
XX  
PA (ABBO ) ABBOTT LAB.  
XX  
PI Mukerji P, Lemmel SA, Leonard AB, Chaudhary S;  
XX  
DR WPI; 2000-205721/18.  
XX  
PT Recombinant construct useful for producing human milk protein, edible  
PT plant protein, antibody, antigen or hormone, comprises nucleotide  
PT sequences expressing beta-casein protein.  
XX  
PS Example 1; Page 11; 73pp; English.  
XX  
CC The patent discloses a method of producing human milk protein, edible  
CC plant protein, antibody or an antigen in a host cell. It involves  
CC transforming host cells with a vector comprising the gene of interest  
CC linked to a promoter and nucleotide sequences encoding subunits of a  
CC kinase, resistance marker and a peptidase. This method is useful for  
CC improving the genetic stability of a plasmid-containing cell during  
CC fermentation. Proteins produced may be used in pharmaceutical or  
CC nutritional compositions and in vaccine formulations. The present  
CC sequence is that of PCR primer RO204, used to amplify Piac promoter with  
CC multiple cloning site and rmb1b72 terminator from plasmid pK223-3. The  
CC PCR product is used for construction of plasmid pRAB-84-69. pRAB-84-69  
CC construct comprises genes encoding human beta-casein, casein kinase II  
CC alpha and beta subunits, bacterial kanamycin resistance marker and  
CC iminopeptidase  
XX  
SQ Sequence 31 BP; 7 A; 6 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 60.0%; Score 12.6; DB 3; Length 31;  
Best Local Similarity 78.9%; Pred. No. 4.2e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGGTCATTAGACCGTACGC 19  
DB 30 CGGTCATTAGACCGTACGC 12

RESULT 21  
AAT04264/c  
ID AAT04264 standard; DNA; 33 BP.  
XX  
AC AAT04264;  
XX  
DT 16-APR-1996 (first entry)  
XX  
DE Primer #259 for IA beta chain gene.  
XX  
KM Polymerase chain reaction; PCR; primer; amplify;  
KW major histocompatibility complex; MHC; T-cell receptor; TCR;  
KW autoimmune disease; immunodeficiency disease; immune response;  
KW immunoproliferation disease; graft-host rejection; therapy; ss.  
XX  
OS Synthetic.

XX MO9523814-A1.  
 XX 08-SEP-1995.  
 XX 03-MAR-1995; 95WO-US002689.  
 XX 04-MAR-1994; 94US-00207481.  
 XX (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.  
 XX Kappler JM, Marrack P;  
 XX WPI; 1995-320543/41.  
 XX  
 XX Peptide-MHC complex comprising antigenic peptide, linker and MHC segment  
 XX PT - useful as reagents for the treatment of diseases including auto-immune  
 XX PT diseases, immuno-stimulatory diseases or graft-host rejection.

XX Example 1; Page 54; 94pp; English.

XX The sequences represented by AAT04263 and AAT04264 are amplification  
 XX primers for a fragment of the IA beta chain gene (fragment 333-259). This  
 XX fragment was used in the construction of a hybrid IA alpha beta dimer  
 XX containing the OVA peptide, and a linker. The encoded protein (pIAD-OVA)  
 XX was found to be more stable than the IA alpha beta dimer. The stability  
 XX (e.g. see AAR82527, AAR82528 and AAR82531), compared to an increase seen  
 XX on the addition of a MHC groove specific binding peptide  
 XX may be used to regulate an immune response. The complexes are capable of  
 XX being recognised by a TCR alone or in combination with additional MHC  
 XX proteins. These complexes are useful for therapeutic purposes and  
 XX experimental purposes. They can also be used as reagents for the  
 XX treatment of diseases including autoimmune diseases, immunodeficiency  
 XX diseases, immunoproliferation diseases, and graft-host rejection

XX Sequence 33 BP; 9 A; 8 C; 12 G; 4 T; 0 U; 0 Other;  
 XX  
 XX Query Match 60.0%; Score 12.6; DB 2; Length 33;  
 XX Best Local Similarity 78.9%; Pred. No. 4.2e+03;  
 XX Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGGTCAATTAGACCGTACGC 19  
 |||||  
 DB 20 CGTTCATTGTTCTGACGC 2

RESULT 22

ID ACA10066 standard; RNA; 36 BP.

XX ACA10066;

DT 03-JUN-2003 (first entry)

XX Necrosis factor kappa B (NFkB) sub-unit modulating zinzyme #16.

XX Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinzyme;  
 XX G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; lung cancer;  
 XX prostate cancer; colorectal cancer; brain cancer; oesophageal cancer;  
 XX stomach cancer; bladder cancer; pancreatic cancer; cervical cancer;  
 XX head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma;  
 XX multidrug resistant cancer; REL-A-specific inhibitor; chemotherapy;  
 XX paclitaxel; docetaxel; cisplatin; methotrexate; cyclophosphamide;  
 XX doxorubicin; fluorouracil; carboplatin; edatrexate; gemcitabine;  
 XX radiation therapy; inflammatory disease; asthma; diabetes;  
 XX rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;  
 XX gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;  
 XX transplant/graft rejection; reperfusion injury; glomerulonephritis;  
 XX allergic airway inflammation; inflammatory bowel disease; infection; ss.  
 XX Synthetic.

PN US200217568-A1.

XX 28-NOV-2002.

XX 23-MAY-2001; 2001US-00864785.

XX 07-DEC-1992; 92US-00987132.

XX 18-MAY-1994; 94US-00245466.

XX 15-AUG-1994; 94US-00291932.

XX 23-DEC-1996; 96US-00777916.

XX (STIN/) STINGCOMB D T.

XX (MCSW/) MCSWINGEN J.

XX (DRAP/) DRAPER K G.

XX Stinchcomb DT, Mcswigen J, Draper KG;  
 XX WPI; 2003-340953/32.

XX Claim 2; SEQ ID NO 3885; 72pp; English.

XX The invention describes an enzymatic nucleic acid molecule (I) which down  
 XX regulates expression of a sequence encoding a subunit of nuclear factor  
 XX kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme  
 XX configuration. The enzymatic nucleic acid molecule is adapted to treat  
 XX cancer and is useful for down-regulating REL-A activity in a cell, for  
 XX treating a patient having a condition associated with the level of REL-A.  
 XX (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in  
 XX the presence of a divalent cation, especially Mg<sup>2+</sup>. The enzymatic and  
 XX antisense nucleic acid molecules are useful for treating breast, lung,  
 XX prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,  
 XX cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or  
 XX multidrug resistant cancer. The method involves use of other drug  
 XX therapies such as monoclonal antibodies, REL-A-specific inhibitors or  
 XX chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,  
 XX cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate,  
 XX gemcitabine or radiation therapy. The enzymatic and antisense nucleic  
 XX acid molecules are also useful for treating inflammatory disease such as  
 XX rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,  
 XX obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft  
 XX rejection, gene therapy applications, ischaemia/reperfusion injury  
 XX (central nervous system (CNS) and myocardial), glomerulonephritis,  
 XX sepsis, allergic airway inflammation, inflammatory bowel disease or  
 XX infection. This sequence represents an enzymatic nucleic acid used to  
 XX modulate the function of a necrosis factor kappa B sub-unit

XX Sequence 36 BP; 10 A; 8 C; 13 G; 0 T; 4 U; 1 Other;  
 XX  
 XX Query Match 60.0%; Score 12.6; DB 8; Length 36;  
 XX Best Local Similarity 78.9%; Pred. No. 4.3e+03;  
 XX Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGTCAATTAGACCGTACGC 20  
 |||||  
 DB 35 GGCATTAGACCTCACTCG 17

RESULT 23

ID ACD66384 standard; RNA; 36 BP.

XX ACD66384;

DT 23-SEP-2003 (first entry)

XX Anti-HCV nucleic acid molecule #232.

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
 XX RNA stability; RNA expression; RNA synthesis; antisense;

KM enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;  
 KW Amberyse; G-cleaver ribozyme; decoy molecule; aptamer;  
 KM HBV reverse transcriptase; Enhancer I region; anti-HCV;  
 KM viral replication; degenerative; disease state; HBV infection;  
 KW HCV infection; cirrhosis; liver failure; hepatocellular carcinoma;  
 KM hepatotropic; cytostatic; virucide; antiinflammatory; ss.  
 OS Hepatitis C virus.  
 XX  
 XX WO200281494-A1.  
 XX  
 PD 17-OCT-2002.  
 XX  
 XX 26-MAR-2002; 2002WO-US009187.  
 XX  
 XX 26-MAR-2001; 2001US-00817879.  
 PR 08-JUN-2001; 2001US-00877478.  
 PR 08-JUN-2001; 2001US-0296876P.  
 PR 24-OCT-2001; 2001US-0335059P.  
 PR 05-DEC-2001; 2001US-0337055P.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MACE/) MACEJAK D.  
 PA (MCSW/) MCSWIGEN J.  
 PA (MORR/) MORRISSEY D.  
 PA (PAYC/) PAYCO P.  
 PA (LEBP/) LEE P.  
 PA (DRAP/) DRAPER K.  
 PA (ROBE/) ROBERTS E.  
 XX  
 PI Blatt L., Macejak D., Mcswigen J., Morrissey D., Payco P., Lee P;  
 PI Draper K., Roberts E;  
 XX  
 DR WPI; 2003-229207/22.  
 XX  
 PT Novel compound useful for treating cirrhosis, liver failure,  
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
 PT infection.  
 XX  
 PS Claim 1; Page 322; 387pp; English.  
 CC The present invention relates to nucleic acid molecules which modulate  
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
 CC inozymes, zinzymes, amberyse, and G-cleaver ribozymes. Also disclosed  
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
 CC DNA. The nucleic acids may be used to modulate the expression of HBV  
 CC genes and HBV viral replication. Also disclosed is a method for screening  
 CC compounds and/or potential therapies directed against HBV, and compounds  
 CC that modulate the expression and/or replication of HCV. The compounds and  
 CC methods of the invention are useful for the treatment of degenerative and  
 CC disease states related to HBV and HCV infection, replication and gene  
 CC expression such as cirrhosis, liver failure, and hepatocellular  
 CC carcinoma. The present sequence represents one of the anti-HCV nucleic  
 CC acid molecules disclosed in the present invention  
 XX  
 SQ Sequence 36 BP; 10 A; 6 C; 14 G; 0 T; 5 U; 1 Other;

Query Match 60.0%; Score 12.6; DB 8; Length 36;  
 Best Local Similarity 65.0%; Pred. No. 4.3e+03;  
 Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 2 GGTCATTAGACCGTACGCGA 21  
 DB 15 GGCCGUAAGCCCGAANGCGA 34

RESULT 24  
 ACN19551/c

ID ACN19551 standard; RNA; 37 BP.  
 XX  
 AC ACN19551;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE WNV Zinzyme SEQ ID NO 19567.  
 XX  
 KM WNV, West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
 KM virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KM encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KM liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;  
 KM Amberyse; Zinzyme; ss.  
 XX  
 OS West Nile Virus.  
 XX  
 XX WO200268637-A2.  
 XX  
 PD 06-SEP-2002.  
 XX  
 XX 19-OCT-2001; 2001WO-US048350.  
 PR 20-OCT-2000; 2000US-0242411P.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGEN J A.  
 XX  
 PI Blatt L., Mcswigen JA;  
 XX  
 DR WPI; 2002-706994/76.  
 XX  
 PT New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (WNV), useful for treating a condition related to WNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
 XX  
 PS Claim 24; SEQ ID NO 19567; 495pp; English.  
 CC The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for  
 CC treating a condition related to WNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberyse and Zinzyme. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention  
 XX  
 SQ Sequence 37 BP; 11 A; 8 C; 13 G; 0 T; 5 U; 0 Other;

Query Match 60.0%; Score 12.6; DB 6; Length 37;  
 Best Local Similarity 78.9%; Pred. No. 4.3e+03;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 GGTCATTAGACCGTACGCG 20  
 DB 36 GGTCACCTAGACTACTCG 18

RESULT 25  
 ACN31602/c  
 ID ACN31602 standard; RNA; 37 BP.  
 XX  
 AC ACN31602;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE WNV minus strand Zinzyme SEQ ID NO 31618.

```

XX KM MNV; West Nile Virus; antiinflammatory; cytosolic; hepatotropic;
XX KM viraemia; neuroprotective; antibacterial; replication; pancreatitis;
XX KM encephalitis; myocarditis; meningitis; infection; hepatitis;
XX KM liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
XX KM Amberzyme; Zinzyme; ss.
OS West Nile Virus.
XX WO200268637-A2.
XX 06-SEP-2002.
XX 19-OCT-2001; 2001MO-US048350.
XX 20-OCT-2000; 2000US-0242411P.
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGEN J A.
XX Blatt L, Mcswigen JA;
XX WPI; 2002-706994/76.
XX New nucleic acid molecule that modulates replication of West Nile Virus
XX (MNV), useful for treating a condition related to MNV infection e.g.
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX Claim 24; SEQ ID NO 31618; 495bp; English.
XX The invention relates to nucleic acid molecules that modulate replication
XX of the West Nile Virus (MNV). The nucleic acid molecules are useful for
XX treating a condition related to MNV infection e.g. pancreatitis,
XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
XX molecule is selected from the group of ribozymes consisting of
XX Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
XX nucleic acid molecules further comprise at least five ribose residues, at
XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at
XX least three of the 5' terminal nucleotides and a 3' end modification of a
XX 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
XX in the specification. The present sequence is that of a nucleic acid
XX molecule of the invention
SQ Sequence 37 BP; 9 A; 9 C; 13 G; 0 T; 6 U; 0 Other;
Query Match 60.0%; Score 12.6; DB 6; Length 37;
Best Local Similarity 78.9%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 2 GGTCAATTAGACCGTAGCG 20
DB 36 GGTCACTAGACCTCACTCG 18
RESULT 26
ACN19001/c
ID ACN19001 standard; RNA; 37 BP.
XX ACN19001;
XX 22-APR-2004 (first entry)
XX MNV Zinzyme SEQ ID NO 19017.
XX MNV; West Nile Virus; antiinflammatory; cytosolic; hepatotropic;
XX viraemia; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocarditis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
XX Amberzyme; Zinzyme; ss.

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OS West Nile Virus.
XX WO200268637-A2.
XX 06-SEP-2002.
XX 19-OCT-2001; 2001MO-US048350.
XX 20-OCT-2000; 2000US-0242411P.
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGEN J A.
XX Blatt L, Mcswigen JA;
XX WPI; 2002-706994/76.
XX New nucleic acid molecule that modulates replication of West Nile Virus
XX (MNV), useful for treating a condition related to MNV infection e.g.
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX Claim 24; SEQ ID NO 19017; 495bp; English.
XX The invention relates to nucleic acid molecules that modulate replication
XX of the West Nile Virus (MNV). The nucleic acid molecules are useful for
XX treating a condition related to MNV infection e.g. pancreatitis,
XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
XX molecule is selected from the group of ribozymes consisting of
XX Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
XX nucleic acid molecules further comprise at least five ribose residues, at
XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at
XX least three of the 5' terminal nucleotides and a 3' end modification of a
XX 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
XX in the specification. The present sequence is that of a nucleic acid
XX molecule of the invention
SQ Sequence 37 BP; 10 A; 6 C; 15 G; 0 T; 6 U; 0 Other;
Query Match 60.0%; Score 12.6; DB 6; Length 37;
Best Local Similarity 78.9%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 2 GGTCAATTAGACCGTAGCG 20
DB 36 GGTCACTAGACCTCACTCG 18
RESULT 27
ACA07993/c
ID ACA07993 standard; RNA; 37 BP.
XX ACA07993;
XX 03-JUN-2003 (first entry)
XX Necrosis factor kappa B (NFkB) sub-unit modulating zinzyme #97.
XX Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinzyme;
XX G-cleaver; amberzyme; cancer; RBL-A activity; breast cancer; lung cancer;
XX prostate cancer; colorectal cancer; brain cancer; oesophageal cancer;
XX stomach cancer; bladder cancer; pancreatic cancer; cervical cancer;
XX head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma;
XX multidrug resistant cancer; RBL-A-specific inhibitor; chemotherapeutic;
XX paclitaxel; docetaxel; cisplatin; edatrexate; cyclophosphamide;
XX doxorubicin; fluorouracil carboplatin; edatrexate; gemcitabine;
XX radiation therapy; inflammatory disease; asthma; diabetes;
XX rheumatoid arthritis; resensitis; Crohn's disease; obesity; ischaemia;
XX gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
XX transplant/graft rejection; reperfusion injury; glomerulonephritis;
XX allergic airway inflammation; inflammatory bowel disease; infection; ss.

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XX OS Synthetic.  
 XX PN US2002177568-A1.  
 XX PD 28-NOV-2002.  
 XX PF 23-MAY-2001; 2001US-00864785.  
 XX PR 07-DEC-1992; 92US-00967132.  
 XX PR 18-MAY-1994; 94US-00245466.  
 XX PR 15-AUG-1994; 94US-00291932.  
 XX PR 23-DEC-1996; 96US-00777916.  
 XX PA (STIN/) STINGHOMB D T.  
 XX PA (MCSW/) MCSWIGEN J.  
 XX PA (DRAV/) DRAPER K G.  
 XX PI Stinchcomb DT, Mcswigen J, Draper KG;  
 XX WPI: 2003-340953/32.  
 XX PT Novel enzymatic nucleic acid molecules which down regulates expression of  
 PT a sequence encoding a subunit of nuclear factor kappa B useful for  
 PT treating cancer, inflammatory disorders and autoimmune diseases.  
 XX PS Claim 2; Page 39; 72pp; English.  
 CC The invention describes an enzymatic nucleic acid molecule (1) which down  
 CC regulates expression of a sequence encoding a subunit of nuclear factor  
 CC kappa B (NFkB), where (1) is an inozyme, zinczyme, G-cleaver or amberzyme  
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat  
 CC cancer and is useful for down-regulating REL-A activity in a cell, for  
 CC treating a patient having a condition associated with the level of REL-A.  
 CC (1) is useful for cleaving RNA comprising a sequence of REL-A gene, in  
 CC the presence of a divalent cation, especially Mg<sup>2+</sup>. The enzymatic and  
 CC antisense nucleic acid molecules are useful for treating breast, lung,  
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,  
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or  
 CC multidrug resistant cancer. The method involves use of other drug  
 CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or  
 CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate, or  
 CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,  
 CC cyclophosphoramide, doxorubin, fluorouracil carboplatin, edatrexate,  
 CC cyclophosphoramide, doxorubin, fluorouracil carboplatin, edatrexate,  
 CC acid molecules are also useful for treating inflammatory disease such as  
 CC rheumatoid arthritis, rectorosis, asthma, Crohn's disease, diabetes,  
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft  
 CC rejection, gene therapy applications, ischaemia/reperfusion injury  
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,  
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or  
 CC infection. This sequence represents an enzymatic nucleic acid used to  
 CC modulate the function of a necrosis factor kappa B sub-unit  
 XX SO Sequence 37 BP; 11 A; 9 C; 13 G; 0 T; 4 U; 0 Other;  
 Query Match 60.0%; Score 12.6; DB 8; Length 37;  
 Best Local Similarity 78.9%; Pred. No. 4.3e+03;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 2 GGCTATTAGACCGTACGCG 20  
 DB 36 GGCCATTAGACCTCACTCG 18  
 RESULT 28  
 ABRK04673  
 ID ABRK04673 standard; RNA; 38 BP.  
 AC ABRK04673;  
 XX  
 XX 12-MAR-2002 (first entry)  
 DT  
 XX Human NOGO inozyme substrate sequence #150.

XX Human; ss; antisense therapy; cytosolic; antiinflammatory; haemostatic;  
 KW cerebroprotective; neurotrophic; neuroprotective; antiparkinsonian;  
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
 KW DNazyme; inozyme; G-cleaver; amberzyme; zinczyme; lymphoma; leukaemia;  
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
 KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;  
 KW inflammatory arthropathy; central nervous system injury;  
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
 KW Parkinson's disease; ataxia; Huntington's disease; substrate sequence;  
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.  
 XX OS Homo sapiens.  
 OS Synthetic.  
 XX WO200159103-A2.  
 XX PN 16-AUG-2001.  
 XX PD 09-FEB-2001; 2001WO-US004273.  
 XX PF 11-FEB-2000; 2000US-0181797P.  
 XX PR 28-FEB-2000; 2000US-0185516P.  
 XX PR 06-MAR-2000; 2000US-0187128P.  
 XX PA (RIBO-) RIBOZYME PHARM INC.  
 XX PA (BLAT/) BLATT L.  
 XX PA (MCSW/) MCSWIGEN J.  
 XX PA (CHOW/) CHOWRIRA B M.  
 XX PI Blatt L, Mcswigen J, Chowrira BM;  
 XX WPI: 2001-607195/69.  
 DR Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
 XX constructs, which down regulate expression of a CD20 gene or neurite  
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
 PT central nervous system injury.  
 XX PS Claim 89; Page 80; 200pp; English.  
 CC The invention relates to a nucleic acid molecule which down regulates  
 CC expression of a CD20 gene and a nucleic acid molecule which down  
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The  
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
 CC DNazyme) an inozyme (an endolytic nucleic acid cleaving a an RNA motif) or  
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or  
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinczyme (cleaving RNA  
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
 CC of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
 CC the cell and treat a patient having a condition associated with the level  
 CC of CD20. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to  
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-  
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
 CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-  
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the  
 CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the  
 CC cell and treat a patient having a condition associated with the level of  
 CC NOGO. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to  
 CC treat central nervous system (CNS) injury and cerebrovascular accident  
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
 CC disease, muscular dystrophy, and/or other neurodegenerative disease  
 CC states which respond to the modulation of NOGO expression. The present

CC sequence is a substrate sequence for a nucleic acid of the invention  
 CC based on the human NOGO sequence  
 CC  
 CC  
 CC Sequence 38 BP; 9 A; 8 C; 14 G; 0 T; 6 U; 1 Other;  
 SO  
 Query Match 60.0%; Score 12.6; DB 4; Length 38;  
 Best Local Similarity 65.0%; Pred. No. 4.3e+03;  
 Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
 OY 2 GGTGATTAGACCGTAGCGCA 21  
 DB 16 GGCCGUGAGCCGAGNCCGA 35  
 RESULT 29  
 ABK04649  
 ID ABK04649 standard; RNA; 38 BP.  
 AC ABK04649;  
 XX  
 XX  
 XX  
 XX 12-MAR-2002 (first entry)  
 DT  
 DE Human NOGO Inozyme substrate sequence #126.  
 XX  
 XX Human; ss; antisense therapy; cyostatic; antiinflammatory; haemostatic;  
 KM cerebrioprotective; neuroprotective; antiparkinsonian;  
 KM muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
 KM DNAAzyme; Inozyme; G-cleaver; amberzyme; zincyme; lymphoma; leukaemia;  
 KM B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
 KM human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
 KM MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;  
 KM inflammatory arthropathy; central nervous system injury;  
 KM cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
 KM chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
 KM Parkinson's disease; ataxia; Huntington's disease; substrate sequence;  
 KM Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.  
 KM  
 KM  
 OS Homo sapiens.  
 OS Synthetic.  
 EN WO200159103-A2.  
 XX  
 XX 16-AUG-2001.  
 PD  
 XX  
 XX 09-FEB-2001; 2001WO-US004273.  
 PF  
 XX 11-FEB-2000; 2000US-0181797P.  
 PR 28-FEB-2000; 2000US-0185516P.  
 PR 06-MAR-2000; 2000US-0187128P.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLATT) BLATT L.  
 PA (MCSM/) MCSMIRRA J.  
 PA (CHOW/) CHOWMIRA B M.  
 XX  
 XX Blatt L, Mcswiggen J, Chowmira BM;  
 FI  
 DR WPI; 2001-607195/69.  
 XX  
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
 PT constructs, which down regulate expression of a CD20 gene or neurite  
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
 PT central nervous system injury.  
 PT  
 XX  
 XX Claim 89; Page 80; 200pp; English.  
 XX  
 XX The invention relates to a nucleic acid molecule which down regulates  
 CC expression of a CD20 gene and a nucleic acid molecule which down  
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The  
 CC nucleic acids may be enzymatic nucleic acids (e.g., a ribozyme or a  
 CC DNAAzyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule  
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or  
 CC an amberzyme (cleaving RNA with an NGN triplet), a zincyme (cleaving RNA

CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
 CC of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
 CC the cell and treat a patient having a condition associated with the level  
 CC of CD20. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to  
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-  
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
 CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-  
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the  
 CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the  
 CC cell and treat a patient having a condition associated with the level of  
 CC NOGO. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to  
 CC treat central nervous system (CNS) injury and cerebrovascular accident  
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
 CC disease, muscular dystrophy, and/or other neurodegenerative disease  
 CC states which respond to the modulation of NOGO expression. The present  
 CC sequence is a substrate sequence for a nucleic acid of the invention  
 CC based on the human NOGO sequence  
 CC  
 CC  
 CC Sequence 38 BP; 6 A; 12 C; 14 G; 0 T; 5 U; 1 Other;  
 SO  
 Query Match 60.0%; Score 12.6; DB 4; Length 38;  
 Best Local Similarity 65.0%; Pred. No. 4.3e+03;  
 Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
 OY 2 GGTGATTAGACCGTAGCGCA 21  
 DB 16 GGCCGUGAGCCGAGNCCGA 35  
 RESULT 30  
 ABQ72447/C  
 ID ABQ72447 standard; DNA; 38 BP.  
 XX  
 XX ABQ72447;  
 AC  
 XX 30-AUG-2002 (first entry)  
 DT  
 XX  
 XX PCR primer MKV24 for ScFv and Fab library generation.  
 DE  
 XX  
 XX PCR; primer; replicable genetic package; phage display; scFv; Fab;  
 KM heavy chain variable region; light chain variable region; HPe002; HPe025;  
 KM HPe054; ss.  
 KM  
 XX  
 OS Synthetic.  
 OS  
 PN WO200194950-A2.  
 XX  
 PD 13-DEC-2001.  
 XX  
 XX 05-JUN-2001; 2001WO-US018421.  
 PF  
 XX 05-JUN-2000; 2000US-0209503P.  
 PR 04-JUN-2001; 2001US-00874547.  
 PR  
 XX (ZYOM-) ZYOMTX INC.  
 PA  
 XX  
 XX Nock S, Kassner PD;  
 PI  
 DR WPI; 2002-519063/55.  
 XX  
 XX Screening phase displayed peptides, for obtaining a replicable genetic  
 PT package (RGP) that displays a fusion protein that binds to a target  
 PT molecule, comprises contacting the molecule with an uncleared cell  
 PT culture comprising the RGPs.  
 PT  
 XX

PS Example 1; Page 20; 39pp; English.  
XX  
CC The present invention relates to a method for screening replicable  
CC genetic packages (RGPs) to obtain RGP that display on their surface a  
CC fusion protein that specifically binds to a target molecule. The method  
CC comprises contacting a target molecule with an uncloned cell culture  
CC having: (1) RGPs, each displaying a fusion protein having a surface-  
CC displayed RGP polypeptide and a potential binding polypeptide; and (11)  
CC cells in which RGP were amplified. Phage displaying antibody fragments  
CC scFvs or Fab's were generated by PCR amplification of cDNA corresponding  
CC to the heavy and light chain variable regions from the H6002, H6025,  
CC and H6054 hybridomas. The regions were amplified using the PCR primers  
CC ABQ2365-ABQ7248  
XX  
SQ Sequence 38 BP; 8 A; 13 C; 7 G; 10 T; 0 U; 0 Other;  
Query Match 60.0%; Score 12.6; DB 6; Length 38;  
Best Local Similarity 78.9%; Pred. No. 4.3e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 2 GGTCAATTGACCGTACGCG 20  
Db 30 GGTCAATTGACATGTCGCG 12  
RESULT 31  
ABK20307  
ID ABK20307 standard; RNA; 38 BP.  
XX  
AC ABK20307;  
XX  
DT 09-APR-2002 (first entry)  
XX  
DE Human ERG inozyme, Seq ID No 2954.  
XX  
KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;  
KW ophthalmological; antiarthritic; antipsoriatic; vitruide; osteopathic;  
KW vulnery; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;  
KW tumour angiogenesis; diabetic degeneration; macular degeneration;  
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;  
KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;  
KW Sturge Weber syndrome; Kipfel-Trenauay-Weber syndrome; leukaemia; ss;  
KW Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNAzyme; inozyme;  
KW amberzyme.  
XX  
OS Homo sapiens.  
XX  
FN WO200188124-A2.  
XX  
PD 22-NOV-2001.  
XX  
PF 16-MAY-2001; 2001WO-US015866.  
XX  
PR 16-MAY-2000; 2000US-00572021.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX (GLAX ) GLAXO GROUP LTD.  
XX  
PI Jarvis T, Von Carlowitz I, Mcswigen JA, McLaughlin F, Randi AM,  
XX WPI; 2002-082995/11.  
XX  
PT Novel polynucleotide which down regulates expression of Ets-related gene,  
XX useful for treating cancer, diabetic retinopathy, macular degeneration,  
XX arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.  
XX  
PS Claim 5; Page 74; 149pp; English.  
XX  
CC The invention relates to a nucleic acid molecule (I) which down regulates  
CC expression of an Ets-related gene (ERG). (I) is useful for treating  
CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,  
CC tumour angiogenesis, diabetic retinopathy, macular degeneration,  
CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca

CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge  
CC Weber syndrome, Kipfel-Trenauay-Weber syndrome, Osler-Weber-rendu  
CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for  
CC treating a patient having a condition associated with the level of ERG,  
CC by contacting cells of the patient with (I) under conditions suitable for  
CC the treatment. The method comprises the use of one or more therapies  
CC under conditions suitable for the treatment. Leukaemia or tumour  
CC angiogenesis is treated by administering (I) to the patient in  
CC conjunction with one or more of other therapies such as radiation or  
CC chemotherapy treatment. (I) is useful for reducing ERG activity in a  
CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of  
CC ERG gene, by contacting (I) with RNA, in the presence of a divalent  
CC cation such as Mg2+. (I) is useful for diagnosis of conditions and  
CC diseases related to the expression of ERG, and as diagnostic tool to  
CC examine genetic drift and mutations within diseased cells or to detect  
CC the presence of ERG RNA in a cell. (I) is useful for specifically  
CC targeting genes that share homology with ERG gene or ERG fusion genes.  
CC ABK17354-ABK22719 represent nucleic acids, including antisense and  
CC enzymatic nucleic acid molecules which regulate expression of ERG, and  
CC related PCR primers of the invention  
XX  
SQ Sequence 38 BP; 7 A; 10 C; 14 G; 0 T; 6 U; 1 Other;  
Query Match 60.0%; Score 12.6; DB 6; Length 38;  
Best Local Similarity 65.0%; Pred. No. 4.3e+03;  
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
OY 2 GGTCAATTGACCGTACGCGA 21  
Db 16 GGCGGUVAGCGCGAANGCGA 35  
RESULT 32  
ABK20420  
ID ABK20420 standard; RNA; 38 BP.  
XX  
AC ABK20420;  
XX  
DT 09-APR-2002 (first entry)  
XX  
DE Human ERG inozyme, Seq ID No 3067.  
XX  
KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;  
KW ophthalmological; antiarthritic; antipsoriatic; vitruide; osteopathic;  
KW vulnery; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;  
KW tumour angiogenesis; diabetic degeneration; macular degeneration;  
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;  
KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;  
KW Sturge Weber syndrome; Kipfel-Trenauay-Weber syndrome; leukaemia; ss;  
KW Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNAzyme; inozyme;  
KW amberzyme.  
XX  
OS Homo sapiens.  
XX  
FN WO200188124-A2.  
XX  
PD 22-NOV-2001.  
XX  
PF 16-MAY-2001; 2001WO-US015866.  
XX  
PR 16-MAY-2000; 2000US-00572021.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX (GLAX ) GLAXO GROUP LTD.  
XX  
PI Jarvis T, Von Carlowitz I, Mcswigen JA, McLaughlin F, Randi AM,  
XX WPI; 2002-082995/11.  
XX  
PT Novel polynucleotide which down regulates expression of Ets-related gene,  
XX useful for treating cancer, diabetic retinopathy, macular degeneration,  
XX arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.  
XX

PS Claim 5; Page 76; 149pp; English.

CC The invention relates to a nucleic acid molecule (I) which down regulates

CC expression of an Ets-related gene (ERG). (I) is useful for treating

CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,

CC tumour angiogenesis, diabetic retinopathy, macular degeneration,

CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca

CC vulgaris, angiodioma of tuberosus sclerosis, port-wine stains, Sturge

CC Weber syndrome, Kippel-Trenamay-Weber syndrome, Osler-Weber-rendu

CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for

CC treating a patient having a condition associated with the level of ERG,

CC by contacting cells of the patient with (I) under conditions suitable for

CC the treatment. The method comprises the use of one or more therapies

CC under conditions suitable for the treatment. Leukaemia or tumour

CC angiogenesis is treated by administering (I) to the patient in

CC conjunction with one or more of other therapies such as radiation or

CC chemotherapy treatment. (I) is useful for reducing ERG activity in a

CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of

CC ERG gene, by contacting (I) with RNA, in the presence of a divalent

CC cation such as Mg<sup>2+</sup>. (I) is useful for diagnosis of conditions and

CC diseases related to the expression of ERG, and as diagnostic tool to

CC examine genetic drift and mutations within diseased cells or to detect

CC the presence of ERG RNA in a cell. (I) is useful for specifically

CC targeting genes that share homology with ERG gene or ERG fusion genes.

CC ABK17354-ABK22719 represent nucleic acids, including antisense and

CC enzymatic nucleic acid molecules which regulate expression of ERG, and

CC related PCR primers of the invention

CC

XX Sequence 38 BP; 8 A; 6 C; 15 G; 0 T; 8 U; 1 Other;

XX

SO

Query Match 60.0%; Score 12.6; DB 6; Length 38;

Best Local Similarity 65.0%; Pred. No. 4.3e+03;

Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 2 GGTCTATTAGACCGTAGCGGA 21

DB 16 GGCCGUVAGCCGAGANGCGA 35

RESULT 33

ABK58655

ID ABK58655 standard; RNA; 38 BP.

XX

AC ABK58655;

XX

XX

DT 02-JUL-2002 (first entry)

XX

DE Human CLCA1 gene enzymatic nucleic acid #3026.

XX

KW Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;

XX

KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;

XX

KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;

XX

KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;

XX

KW acetylcysteine.

XX

OS Homo sapiens.

XX

XX WO200211674-A2.

XX

PD 14-FEB-2002.

XX

XX

PF 09-AUG-2001; 2001MO-US024970.

XX

XX

PR 09-AUG-2000; 2000US-0224383P.

XX

XX

PA (RIBO-) RIBOZYME PHARM INC.

XX

PA (SYNT) SYNTX USA LLC.

XX

PA (THOM) THOMPSON J.

XX

XX Thompson J, Mcswigen J, McKenzie T, Ayers D, Szymkowski DE;

PI Grube A;

XX

DR WPI; 2002-217145/27.

XX

PT Enzymatic polynucleotide that down regulates expression of chloride

PT channel calcium activated gene, useful for treating Chronic obstructive

PT pulmonary disease (COPD), chronic bronchitis and asthma.

XX

PS Claim 5; Page 71; 152pp; English.

XX

CC The invention relates to enzymatic nucleic acid molecules that down

CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes

CC by cleaving RNA derived from the genes. The nucleic acid sequences are

CC useful as pharmaceutical agents for treating conditions such as chronic

CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic

CC fibrosis, obstructive bowel syndrome and any other diseases or conditions

CC that are related to or will respond to the levels of CLCA1 in a cell or

CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,

CC hence, are useful for treatment of a patient having a condition

CC associated with the level of CLCA1, where the invention further comprises

CC the use of one or more therapies under conditions suitable for the

CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,

CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The

CC nucleic acids of the invention are also used as diagnostic tools to

CC examine genetic drift and mutations within diseased cells or to detect

CC the presence of CLCA1 RNA in a cell. This sequence represents an

CC enzymatic nucleic acid molecule of the invention

CC

XX Sequence 38 BP; 8 A; 7 C; 12 G; 0 T; 10 U; 1 Other;

XX

SO

Query Match 60.0%; Score 12.6; DB 6; Length 38;

Best Local Similarity 65.0%; Pred. No. 4.3e+03;

Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 2 GGTCTATTAGACCGTAGCGGA 21

DB 16 GGCCGUVAGCCGAGANGCGA 35

RESULT 34

ABK58826

ID ABK58826 standard; RNA; 38 BP.

XX

AC ABK58826;

XX

XX

DT 02-JUL-2002 (first entry)

XX

DE Human CLCA1 gene enzymatic nucleic acid #3197.

XX

XX

KW Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;

XX

KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;

XX

KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;

XX

KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;

XX

KW acetylcysteine.

XX

OS Homo sapiens.

XX

XX WO200211674-A2.

XX

PD 14-FEB-2002.

XX

XX

PF 09-AUG-2001; 2001MO-US024970.

XX

XX

PR 09-AUG-2000; 2000US-0224383P.

XX

XX

PA (RIBO-) RIBOZYME PHARM INC.

XX

PA (SYNT) SYNTX USA LLC.

XX

PA (THOM) THOMPSON J.

XX

XX Thompson J, Mcswigen J, McKenzie T, Ayers D, Szymkowski DE;

PI Grube A;

XX

DR WPI; 2002-217145/27.

XX

PT Enzymatic polynucleotide that down regulates expression of chloride

PT channel calcium activated gene, useful for treating Chronic obstructive

PT pulmonary disease (COPD), chronic bronchitis and asthma.  
XX  
PS Claim 5; Page 76; 152pp; English.  
XX  
CC The invention relates to enzymatic nucleic acid molecules that down  
CC regulate expression of chloride channel calcium activated 1 (ClCA1) genes  
CC by cleaving RNA derived from the genes. The nucleic acid sequences are  
CC useful as pharmaceutical agents for treating conditions such as chronic  
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic  
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions  
CC that are related to or will respond to the levels of ClCA1 in a cell or  
CC tissue. The sequences are useful for reducing ClCA1 activity in a cell,  
CC hence, are useful for treatment of a patient having a condition  
CC associated with the level of ClCA1, where the invention further comprises  
CC the use of one or more therapies under conditions suitable for the  
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,  
CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The  
CC nucleic acids of the invention are also used as diagnostic tools to  
CC examine genetic drift and mutations within diseased cells or to detect  
CC the presence of ClCA1 RNA in a cell. This sequence represents an  
CC enzymatic nucleic acid molecule of the invention  
XX  
SQ Sequence 38 BP; 9 A; 9 C; 12 G; 0 T; 7 U; 1 Other;  
Query Match 60.0%; Score 12.6; DB 6; Length 38;  
Best Local Similarity 65.0%; Pred. No. 4.3e+03;  
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 2 GGTCAATTGACCGTAGCGCA 21  
Db 16 GGCCGUVAGCCGAGNCGCA 35  
ACN17900  
ID ACN17900 standard; RNA; 38 BP.  
XX  
AC ACN17900;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE MNV Inozyme SEQ ID NO 17916.  
XX  
XX MNV, West Nile Virus; antiinflammatory; cytosolic; hepatotropic;  
KM virucide; neuroprotective; antibacterial; replication; pancreatitis;  
KM encephalitis; myocarditis; meningitis; infection; hepatitis;  
KM liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;  
KM Amberzyme; Zinzyme; ss.  
XX  
OS West Nile Virus.  
XX  
PN WO200268637-A2.  
XX  
PD 06-SEP-2002.  
XX  
PE 19-OCT-2001; 2001WO-US048350.  
XX  
PR 20-OCT-2000; 2000US-0242411P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MCSW/) MCSWIGEN J A.  
XX  
PI Blatt L, Mcswigen JA;  
XX  
DR WPI; 2002-706994/76.  
XX  
PT New nucleic acid molecule that modulates replication of West Nile Virus  
PT (MNV), useful for treating a condition related to MNV infection e.g.  
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
XX  
PS Claim 24; SEQ ID NO 17916; 495pp; English.  
XX

CC The invention relates to nucleic acid molecules that modulate replication  
CC of the West Nile Virus (MNV). The nucleic acid molecules are useful for  
CC treating a condition related to MNV infection e.g. pancreatitis,  
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
CC molecule is selected from the group of ribozymes consisting of  
CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The  
CC nucleic acid molecules further comprise at least five ribose residues, at  
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
CC least three of the 5' terminal nucleotides and a 3' end modification of a  
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
CC in the specification. The present sequence is that of a nucleic acid  
CC molecule of the invention  
XX  
SQ Sequence 38 BP; 7 A; 9 C; 12 G; 0 T; 9 U; 1 Other;  
Query Match 60.0%; Score 12.6; DB 6; Length 38;  
Best Local Similarity 65.0%; Pred. No. 4.3e+03;  
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 2 GGTCAATTGACCGTAGCGCA 21  
Db 16 GGCCGUVAGCCGAGNCGCA 35  
ACN17240  
ID ACN17240 standard; RNA; 38 BP.  
XX  
AC ACN17240;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE MNV Inozyme SEQ ID NO 17243.  
XX  
XX MNV, West Nile Virus; antiinflammatory; cytosolic; hepatotropic;  
KM virucide; neuroprotective; antibacterial; replication; pancreatitis;  
KM encephalitis; myocarditis; meningitis; infection; hepatitis;  
KM liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;  
KM Amberzyme; Zinzyme; ss.  
XX  
OS West Nile Virus.  
XX  
PN WO200268637-A2.  
XX  
PD 06-SEP-2002.  
XX  
PE 19-OCT-2001; 2001WO-US048350.  
XX  
PR 20-OCT-2000; 2000US-0242411P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MCSW/) MCSWIGEN J A.  
XX  
PI Blatt L, Mcswigen JA;  
XX  
DR WPI; 2002-706994/76.  
XX  
PT New nucleic acid molecule that modulates replication of West Nile Virus  
PT (MNV), useful for treating a condition related to MNV infection e.g.  
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.  
XX  
PS Claim 24; SEQ ID NO 17243; 495pp; English.  
XX  
XX The invention relates to nucleic acid molecules that modulate replication  
CC of the West Nile Virus (MNV). The nucleic acid molecules are useful for  
CC treating a condition related to MNV infection e.g. pancreatitis,  
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
CC molecule is selected from the group of ribozymes consisting of  
CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The

CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention

XX  
 SQ Sequence 38 BP; 6 A; 6 C; 15 G; 0 T; 10 U; 1 Other;

Query Match 60.0%; Score 12.6; DB 6; Length 38;  
 Best Local Similarity 65.0%; Pred. No. 4.3e+03;  
 Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 GGTCATTAGACCGTAGCCGA 21  
 16 GGCCGUUAGGCCGANAAGCGA 35

DB

RESULT 37  
 ACN16711  
 ID ACN16711 standard; RNA; 38 BP.  
 XX  
 AC ACN16711;  
 XX  
 XX 22-APR-2004 (first entry)  
 DT  
 XX  
 DE MNV Inozyme SEQ ID NO 16714.  
 XX  
 XX MNV; West Nile Virus; antiinflammatory; cytosstatic; hepatotropic;  
 KM virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KM encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KM liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;  
 KM Amberzyme; Zinzyme; ss.

XX  
 OS West Nile Virus.  
 XX  
 PN WO200268637-A2.  
 XX  
 PD 06-SEP-2002.  
 XX  
 PF 19-OCT-2001; 2001WO-US048350.  
 XX  
 PR 20-OCT-2000; 2000US-0242411P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGEN J A.  
 XX  
 PI Blatt L, Mcswigen JA;  
 XX  
 DR WPI; 2002-706994/76.  
 XX  
 PT New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (MNV), useful for treating a condition related to MNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX  
 PS Claim 24; SEQ ID NO 16714; 495pp; English.

XX  
 CC The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (MNV). The nucleic acid molecules are useful for  
 CC treating a condition related to MNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention

XX  
 SQ Sequence 38 BP; 9 A; 11 C; 11 G; 0 T; 6 U; 1 Other;

Query Match 60.0%; Score 12.6; DB 6; Length 38;  
 Best Local Similarity 65.0%; Pred. No. 4.3e+03;  
 Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 GGTCATTAGACCGTAGCCGA 21  
 16 GGCCGUUAGGCCGANAAGCGA 35

DB

RESULT 38  
 ACN30373  
 ID ACN30373 standard; RNA; 38 BP.  
 XX  
 AC ACN30373;  
 XX  
 XX 22-APR-2004 (first entry)  
 DT  
 XX  
 DE MNV minus strand Inozyme SEQ ID NO 30389.  
 XX  
 XX MNV; West Nile Virus; antiinflammatory; cytosstatic; hepatotropic;  
 KM virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 KM encephalitis; myocarditis; meningitis; infection; hepatitis;  
 KM liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;  
 KM Amberzyme; Zinzyme; ss.

XX  
 OS West Nile Virus.  
 XX  
 PN WO200268637-A2.  
 XX  
 PD 06-SEP-2002.  
 XX  
 PF 19-OCT-2001; 2001WO-US048350.  
 XX  
 PR 20-OCT-2000; 2000US-0242411P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGEN J A.  
 XX  
 PI Blatt L, Mcswigen JA;  
 XX  
 DR WPI; 2002-706994/76.  
 XX  
 PT New nucleic acid molecule that modulates replication of West Nile Virus  
 PT (MNV), useful for treating a condition related to MNV infection e.g.  
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX  
 PS Claim 24; SEQ ID NO 30389; 495pp; English.

XX  
 CC The invention relates to nucleic acid molecules that modulate replication  
 CC of the West Nile Virus (MNV). The nucleic acid molecules are useful for  
 CC treating a condition related to MNV infection e.g. pancreatitis,  
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,  
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid  
 CC molecule is selected from the group of ribozymes consisting of  
 CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The  
 CC nucleic acid molecules further comprise at least five ribose residues, at  
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at  
 CC least three of the 5' terminal nucleotides and a 3' end modification of a  
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080  
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given  
 CC in the specification. The present sequence is that of a nucleic acid  
 CC molecule of the invention

XX  
 SQ Sequence 38 BP; 8 A; 9 C; 13 G; 0 T; 7 U; 1 Other;

Query Match 60.0%; Score 12.6; DB 6; Length 38;  
 Best Local Similarity 65.0%; Pred. No. 4.3e+03;  
 Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 GGTCAATGACCGTAGCGGA 21  
 |||::|||  
 DB 16 GGCCGUNAGCCGGAANGCGA 35

## RESULT 39

ID ACN29690 standard; RNA; 38 BP.  
 ACN29690

ACN29690;

22-APR-2004 (first entry)

WNV minus strand Inozyme SEQ ID NO 29706.

WNV, West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
 virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 encephalitis; myocarditis; meningitis; infection; hepatitis;  
 liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;  
 Amberzyme; Zinzyme; ss.

West Nile Virus.

WO200268637-A2.

06-SEP-2002.

19-OCT-2001; 2001WO-US048350.

20-OCT-2000; 2000US-0242411P.

(RIBO-) RIBOZYME PHARM INC.

(BLAT/) BLATT L.

(MCSW/) MCSWIGEN J A.

Blatt L, Mcswigen JA;

WPI, 2002-706994/76.

New nucleic acid molecule that modulates replication of West Nile Virus (WNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

Claim 24; SEQ ID NO 29706; 495bp; English.

The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (WNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The nucleic acid molecules further comprise at least five ribose residues, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at least three of the 5' terminal nucleotides and a 3' end modification of a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nucleic acid molecule of the invention

Sequence 38 BP; 7 A; 11 C; 13 G; 0 T; 6 U; 1 Other;

Query Match 60.0%; Score 12.6; DB 6; Length 38;

Best Local Similarity 65.0%; Pred. No. 4.3e+03;

Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

2 GGTCAATGACCGTAGCGGA 21  
 |||::|||  
 DB 16 GGCCGUNAGCCGGAANGCGA 35

## RESULT 40

ACN27931

ID ACN27931 standard; RNA; 38 BP.

ACN27931;

22-APR-2004 (first entry)

WNV minus strand Inozyme SEQ ID NO 27947.

WNV, West Nile Virus; antiinflammatory; cytostatic; hepatotropic;  
 virucide; neuroprotective; antibacterial; replication; pancreatitis;  
 encephalitis; myocarditis; meningitis; infection; hepatitis;  
 liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;  
 Amberzyme; Zinzyme; ss.

West Nile Virus.

WO200268637-A2.

06-SEP-2002.

19-OCT-2001; 2001WO-US048350.

20-OCT-2000; 2000US-0242411P.

(RIBO-) RIBOZYME PHARM INC.

(BLAT/) BLATT L.

(MCSW/) MCSWIGEN J A.

Blatt L, Mcswigen JA;

WPI, 2002-706994/76.

New nucleic acid molecule that modulates replication of West Nile Virus (WNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

Claim 24; SEQ ID NO 27947; 495bp; English.

The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (WNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The nucleic acid molecules further comprise at least five ribose residues, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at least three of the 5' terminal nucleotides and a 3' end modification of a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nucleic acid molecule of the invention

Sequence 38 BP; 11 A; 8 C; 12 G; 0 T; 6 U; 1 Other;

Query Match 60.0%; Score 12.6; DB 6; Length 38;

Best Local Similarity 65.0%; Pred. No. 4.3e+03;

Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

2 GGTCAATGACCGTAGCGGA 21  
 |||::|||  
 DB 16 GGCCGUNAGCCGGAANGCGA 35

Search completed: November 23, 2004, 17:30:10  
 Job time : 113.708 secs

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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:59:48 ; Search time 24.3034 Seconds  
(without alignments)  
614.177 Million cell updates/sec

Title: US-10-087-631B-17

Perfect score: 21  
Sequence: 1 cgcgcataagacgcgtacgcga 21

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 905748

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database :

Issued Patents NA: \*  
1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/6C.COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/6D.COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	13.2	62.9	35 3	US-09-056-052-12 Sequence 12, Appl
2	13.2	62.9	39 3	US-09-056-052-13 Sequence 13, Appl
3	12.6	60.0	31 3	US-09-131-028A-17 Sequence 17, Appl
4	12.6	60.0	33 1	US-08-207-481-29 Sequence 29, Appl
5	12.6	60.0	33 5	PCT-US95-02689-31 Sequence 31, Appl
6	12.6	60.0	38 4	US-09-371-772B-11935 Sequence 11935, A
7	12.6	60.0	38 4	US-09-371-772B-13181 Sequence 13181, A
8	12.6	60.0	38 4	US-09-371-772B-13811 Sequence 13811, A
9	12.6	60.0	38 4	US-09-874-547-83 Sequence 83, Appl
10	12.4	59.0	38 1	US-08-373-124A-1680 Sequence 1680, Ap
11	12.4	59.0	38 1	US-08-433-628-1680 Sequence 1680, Ap
12	12.2	58.1	20 4	US-09-198-452A-4954 Sequence 4954, Ap
13	12.2	58.1	21 6	5451502-8 Patent No. 5451502
14	12.2	58.1	41 4	US-09-313-221A-19 Sequence 19, Appl
15	12.2	57.1	25 2	US-08-860-882A-75 Sequence 75, Appl
16	12.2	57.1	25 4	US-09-011-769A-61 Sequence 61, Appl
17	12.2	57.1	29 4	US-09-814-351-25 Sequence 25, Appl
18	12.2	57.1	32 4	US-09-814-351-25 Sequence 25, Appl
19	12.2	57.1	32 4	US-09-439-410A-34 Sequence 34, Appl
20	12.2	57.1	38 4	US-09-371-772B-7357 Sequence 7357, Ap
21	12.2	57.1	38 4	US-09-371-772B-7797 Sequence 7797, Ap
22	12.2	57.1	38 4	US-09-371-772B-8104 Sequence 8104, Ap
23	12.2	57.1	38 4	US-09-371-772B-8341 Sequence 8341, Ap
24	12.2	57.1	38 4	US-09-371-772B-9392 Sequence 9392, Ap
25	12.2	57.1	38 4	US-09-371-772B-9781 Sequence 9781, Ap
26	12.2	57.1	38 4	US-09-371-772B-9974 Sequence 9974, Ap
27	12.2	57.1	38 4	US-09-371-772B-10321 Sequence 10321, A

28	12	57.1	38 4	US-09-371-772B-10352 Sequence 10352, A
29	12	57.1	38 4	US-09-371-772B-10512 Sequence 10512, A
30	11.6	55.2	20 3	US-09-172-045-20 Sequence 20, Appl
31	11.6	55.2	20 4	US-09-342-325C-20 Sequence 20, Appl
32	11.6	55.2	37 3	US-09-056-052-10 Sequence 10, Appl
33	11.6	55.2	37 4	US-10-009-332-10 Sequence 10, Appl
34	11.6	55.2	38 4	US-09-371-772B-11413 Sequence 11413, A
35	11.6	55.2	38 4	US-09-371-772B-12074 Sequence 12074, A
36	11.6	55.2	38 4	US-09-371-772B-12155 Sequence 12155, A
37	11.6	55.2	38 4	US-09-371-772B-12380 Sequence 12380, A
38	11.6	55.2	38 4	US-09-371-772B-12386 Sequence 12386, A
39	11.6	55.2	38 4	US-09-371-772B-12396 Sequence 12396, A
40	11.6	55.2	38 4	US-09-371-772B-13189 Sequence 13189, A
41	11.6	55.2	39 3	US-09-056-052-11 Sequence 11, Appl
42	11.6	55.2	39 3	US-09-056-052-11 Sequence 11, Appl
43	11.6	55.2	39 3	US-09-694-531-26 Sequence 26, Appl
44	11.6	55.2	39 4	US-10-072-152-26 Sequence 26, Appl
45	11.4	54.3	27 4	US-09-877-243A-11 Sequence 11, Appl
46	11.4	54.3	27 4	US-09-877-243A-12 Sequence 12, Appl
47	11.4	54.3	28 3	US-09-518-386B-31 Sequence 31, Appl
48	11.4	54.3	37 2	US-08-527-060-20 Sequence 30, Appl
49	11.4	54.3	43 1	US-08-616-133-5 Sequence 5, Appl1
50	11.4	54.3	43 1	US-08-802-985-5 Sequence 5, Appl1
51	11.4	54.3	44 1	US-08-452-083-17 Sequence 17, Appl
52	11.4	54.3	44 1	US-08-452-083-18 Sequence 18, Appl
53	11.2	53.3	28 2	US-08-781-620B-14 Sequence 14, Appl
54	11.2	53.3	31 3	US-08-860-904-23 Sequence 23, Appl
55	11.2	53.3	31 3	US-08-679-645-388 Sequence 388, App
56	11.2	53.3	34 4	US-09-205-114-3 Sequence 3, Appl1
57	11.2	53.3	34 4	US-10-038-520-3 Sequence 65, Appl
58	11.2	53.3	38 4	US-09-874-547-65 Sequence 55, Appl
59	11.2	53.3	42 2	US-08-343-443B-55 Patent No. 5240845
60	11.2	53.3	48 6	5240845-9 Patent No. 5240845
61	11.2	53.3	48 6	5240845-10 Patent No. 5240845
62	11.2	53.3	17 3	US-08-584-040-8046 Sequence 8046, Ap
63	11.2	53.3	17 3	US-08-584-040-8047 Sequence 8047, Ap
64	11.2	53.3	17 4	US-09-371-772B-13829 Sequence 3829, Ap
65	11.2	53.3	17 4	US-09-371-772B-13830 Sequence 3830, Ap
66	11.2	53.3	20 4	US-09-422-978-6875 Sequence 6875, Ap
67	11.2	53.3	20 4	US-09-198-452A-5503 Sequence 5503, Ap
68	11.2	53.3	22 4	US-10-270-313-4 Sequence 4, Appl1
69	11.2	53.3	22 4	US-08-324-003A-7 Sequence 6, Appl1
70	11.2	53.3	24 2	US-08-324-003A-7 Sequence 7, Appl1
71	11.2	53.3	24 2	US-08-937-993-44 Sequence 44, Appl1
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73	11.2	53.3	24 4	US-09-755-836-7 Sequence 7, Appl1
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75	11.2	53.3	36 2	US-08-709-874A-29 Sequence 29, Appl
76	11.2	53.3	36 2	US-08-897-340-8 Sequence 8, Appl1
77	11.2	53.3	36 3	US-09-252-339-8 Sequence 8, Appl1
78	11.2	53.3	36 3	US-09-104-382-29 Sequence 29, Appl
79	11.2	53.3	36 4	US-09-833-555-29 Sequence 29, Appl
80	11.2	53.3	37 4	US-09-629-732-12 Sequence 12, Appl
81	11.2	53.3	38 4	US-09-371-772B-1156 Sequence 7156, Ap
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86	11.2	53.3	38 4	US-09-371-772B-9462 Sequence 9462, Ap
87	11.2	53.3	38 4	US-09-371-772B-9690 Sequence 9690, Ap
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90	11.2	53.3	38 4	US-09-371-772B-9766 Sequence 9766, Ap
91	11.2	53.3	38 4	US-09-371-772B-9773 Sequence 9773, Ap
92	11.2	53.3	38 4	US-09-371-772B-10460 Sequence 10460, A
93	11.2	53.3	38 4	US-09-371-772B-10654 Sequence 10654, A
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95	11.2	53.3	38 4	US-09-371-772B-10776 Sequence 10776, A
96	11.2	53.3	38 4	US-09-371-772B-10822 Sequence 10822, A
97	11.2	53.3	38 4	US-09-371-772B-10862 Sequence 10862, A
98	11.2	53.3	38 4	US-09-371-772B-11264 Sequence 11264, A
99	11.2	53.3	38 4	US-09-371-772B-11244 Sequence 11244, A
100	11.2	53.3	38 4	US-09-371-772B-11261 Sequence 11261, A

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Sequence 10, Appl
Sequence 11413, A
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Sequence 12380, A
Sequence 12396, A
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Sequence 13450, A
Sequence 11, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 31, Appl
Sequence 30, Appl
Sequence 5, Appl1
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Sequence 17, Appl
Sequence 18, Appl
Sequence 14, Appl
Sequence 23, Appl
Sequence 388, App
Sequence 3, Appl1
Sequence 65, Appl
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Patent No. 5240845
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Sequence 3829, Ap
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Sequence 15, Appl
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Sequence 29, Appl
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Sequence 12, Appl
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Sequence 7161, Ap
Sequence 7794, Ap
Sequence 9089, Ap
Sequence 9378, Ap
Sequence 9462, Ap
Sequence 9690, Ap
Sequence 9720, Ap
Sequence 9731, Ap
Sequence 9766, Ap
Sequence 9773, Ap
Sequence 10460, A
Sequence 10654, A
Sequence 10718, A
Sequence 10776, A
Sequence 10822, A
Sequence 10862, A
Sequence 11264, A
Sequence 11244, A
Sequence 11261, A

101	11	52.4	38	4	US-09-371-772B-11301	Sequence 11301, A	C 174	11	52.4	38	4	US-09-874-547-79	Sequence 79, Appl
101	11	52.4	38	4	US-09-371-772B-11309	Sequence 11309, A	C 175	11	52.4	38	4	US-09-874-547-84	Sequence 84, Appl
103	11	52.4	38	4	US-09-371-772B-11358	Sequence 11358, A	176	11	52.4	40	3	US-09-133-914-5	Sequence 5, Appl
104	11	52.4	38	4	US-09-371-772B-11365	Sequence 11365, A	177	11	52.4	40	3	US-09-469-197-5	Sequence 5, Appl
105	11	52.4	38	4	US-09-371-772B-11401	Sequence 11401, A	178	11	52.4	40	4	US-09-949-109-5	Sequence 28, Appl
106	11	52.4	38	4	US-09-371-772B-11624	Sequence 11624, A	179	11	52.4	42	1	US-08-433-126A-238	Sequence 28, Appl
107	11	52.4	38	4	US-09-371-772B-11674	Sequence 11674, A	180	11	52.4	42	2	US-08-433-124A-238	Sequence 17, Appl
108	11	52.4	38	4	US-09-371-772B-11796	Sequence 11796, A	181	11	52.4	42	2	US-08-846-338-17	Sequence 28, Appl
109	11	52.4	38	4	US-09-371-772B-11790	Sequence 11790, A	182	11	52.4	42	2	US-08-976-413A-238	Sequence 28, Appl
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113	11	52.4	38	4	US-09-371-772B-11880	Sequence 11880, A	186	10.8	51.4	20	4	US-09-930-589-5	Sequence 5, Appl
114	11	52.4	38	4	US-09-371-772B-11897	Sequence 11897, A	187	10.8	51.4	27	3	US-08-584-040-1315	Sequence 115, Ap
115	11	52.4	38	4	US-09-371-772B-11899	Sequence 11899, A	188	10.8	51.4	27	3	US-08-584-040-6604	Sequence 6605, Ap
116	11	52.4	38	4	US-09-371-772B-11904	Sequence 11904, A	189	10.8	51.4	27	3	US-08-584-040-6805	Sequence 6805, Ap
117	11	52.4	38	4	US-09-371-772B-11924	Sequence 11924, A	190	10.8	51.4	31	3	US-09-195-666A-26	Sequence 26, Appl
118	11	52.4	38	4	US-09-371-772B-11927	Sequence 11927, A	191	10.8	51.4	31	3	US-09-635-705-26	Sequence 26, Appl
119	11	52.4	38	4	US-09-371-772B-12021	Sequence 12021, A	192	10.8	51.4	31	4	US-09-634-858A-26	Sequence 26, Appl
120	11	52.4	38	4	US-09-371-772B-12024	Sequence 12024, A	193	10.8	51.4	31	4	US-08-869-927C-26	Sequence 26, Appl
121	11	52.4	38	4	US-09-371-772B-12030	Sequence 12030, A	194	10.8	51.4	34	2	US-08-319-866-23	Sequence 23, Appl
122	11	52.4	38	4	US-09-371-772B-12063	Sequence 12063, A	195	10.8	51.4	34	4	US-08-809-917-23	Sequence 47, Ap
123	11	52.4	38	4	US-09-371-772B-12108	Sequence 12108, A	196	10.8	51.4	36	1	US-08-363-240A-407	Sequence 812, App
124	11	52.4	38	4	US-09-371-772B-12168	Sequence 12168, A	197	10.8	51.4	36	2	US-08-292-620A-812	Sequence 812, App
125	11	52.4	38	4	US-09-371-772B-12194	Sequence 12194, A	198	10.8	51.4	36	3	US-09-071-845-812	Sequence 815, App
126	11	52.4	38	4	US-09-371-772B-12201	Sequence 12201, A	199	10.8	51.4	38	1	US-08-373-124A-635	Sequence 635, App
127	11	52.4	38	4	US-09-371-772B-12281	Sequence 12281, A	200	10.8	51.4	38	1	US-08-435-628-635	Sequence 8412, Ap
128	11	52.4	38	4	US-09-371-772B-12284	Sequence 12284, A	201	10.8	51.4	38	4	US-09-371-772B-10476	Sequence 10476, A
129	11	52.4	38	4	US-09-371-772B-12288	Sequence 12288, A	202	10.8	51.4	38	4	US-09-371-772B-10653	Sequence 10653, A
130	11	52.4	38	4	US-09-371-772B-12310	Sequence 12310, A	203	10.8	51.4	39	2	US-08-467-963C-18	Sequence 18, Appl
131	11	52.4	38	4	US-09-371-772B-12328	Sequence 12328, A	204	10.8	51.4	39	2	US-08-467-963C-18	Sequence 18, Appl
132	11	52.4	38	4	US-09-371-772B-12360	Sequence 12360, A	205	10.8	51.4	39	2	US-08-852-344D-18	Sequence 18, Appl
133	11	52.4	38	4	US-09-371-772B-12375	Sequence 12375, A	206	10.8	51.4	39	3	US-08-852-344D-18	Sequence 18, Appl
134	11	52.4	38	4	US-09-371-772B-12455	Sequence 12455, A	207	10.8	51.4	39	3	US-08-344-639E-18	Sequence 18, Appl
135	11	52.4	38	4	US-09-371-772B-12461	Sequence 12461, A	208	10.8	51.4	39	3	US-08-467-969A-18	Sequence 18, Appl
136	11	52.4	38	4	US-09-371-772B-12503	Sequence 12503, A	209	10.8	51.4	39	3	US-08-467-969A-18	Sequence 18, Appl
137	11	52.4	38	4	US-09-371-772B-12557	Sequence 12557, A	210	10.8	51.4	39	3	US-08-001-554A-18	Sequence 18, Appl
138	11	52.4	38	4	US-09-371-772B-12588	Sequence 12588, A	211	10.8	51.4	45	1	US-08-483-415-22	Sequence 22, Appl
139	11	52.4	38	4	US-09-371-772B-12598	Sequence 12598, A	212	10.8	51.4	45	6	5487983-19	Patent No. 5487983
140	11	52.4	38	4	US-09-371-772B-12636	Sequence 12636, A	213	10.6	50.5	18	3	US-09-156-807-25	Sequence 25, Appl
141	11	52.4	38	4	US-09-371-772B-12636	Sequence 12636, A	214	10.6	50.5	18	4	US-09-387-341-127	Sequence 127, App
142	11	52.4	38	4	US-09-371-772B-12681	Sequence 12681, A	215	10.6	50.5	18	4	US-09-422-978-5416	Sequence 5416, Ap
143	11	52.4	38	4	US-09-371-772B-12685	Sequence 12685, A	216	10.6	50.5	21	3	US-09-344-520-3	Sequence 3, Appl
144	11	52.4	38	4	US-09-371-772B-12685	Sequence 12685, A	217	10.6	50.5	21	3	US-09-275-680-13	Sequence 13, Appl
145	11	52.4	38	4	US-09-371-772B-13192	Sequence 13192, A	218	10.6	50.5	24	3	US-08-624-655A-3	Sequence 3, Appl
146	11	52.4	38	4	US-09-371-772B-13218	Sequence 13218, A	219	10.6	50.5	30	4	US-09-293-427-8	Sequence 2, Appl
147	11	52.4	38	4	US-09-371-772B-13226	Sequence 13226, A	220	10.6	50.5	34	4	US-09-859-724-2	Sequence 6, Appl
148	11	52.4	38	4	US-09-371-772B-13246	Sequence 13246, A	221	10.6	50.5	34	4	US-09-387-376-6	Sequence 11, Appl
149	11	52.4	38	4	US-09-371-772B-13421	Sequence 13421, A	222	10.6	50.5	36	1	US-08-074-121-11	Sequence 11, Appl
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151	11	52.4	38	4	US-09-371-772B-13487	Sequence 13487, A	224	10.6	50.5	37	1	US-08-411-796-517	Sequence 517, App
152	11	52.4	38	4	US-09-371-772B-13518	Sequence 13518, A	225	10.6	50.5	37	3	US-08-471-035-517	Sequence 517, App
153	11	52.4	38	4	US-09-371-772B-13529	Sequence 13529, A	226	10.6	50.5	37	3	US-08-559-390-517	Sequence 517, App
154	11	52.4	38	4	US-09-371-772B-13591	Sequence 13591, A	227	10.6	50.5	37	5	PCT-US93-11198-517	Sequence 517, App
155	11	52.4	38	4	US-09-371-772B-13633	Sequence 13633, A	228	10.6	50.5	38	4	US-09-371-772B-11237	Sequence 11237, A
156	11	52.4	38	4	US-09-371-772B-13652	Sequence 13652, A	229	10.6	50.5	38	4	US-09-371-772B-11239	Sequence 11239, A
157	11	52.4	38	4	US-09-371-772B-13662	Sequence 13662, A	230	10.6	50.5	38	4	US-09-371-772B-11295	Sequence 11295, A
158	11	52.4	38	4	US-09-371-772B-13681	Sequence 13681, A	231	10.6	50.5	38	4	US-09-371-772B-11305	Sequence 11305, A
159	11	52.4	38	4	US-09-371-772B-13710	Sequence 13710, A	232	10.6	50.5	38	4	US-09-371-772B-11315	Sequence 11315, A
160	11	52.4	38	4	US-09-371-772B-13740	Sequence 13740, A	233	10.6	50.5	38	4	US-09-371-772B-11418	Sequence 11418, A
161	11	52.4	38	4	US-09-371-772B-13758	Sequence 13758, A	234	10.6	50.5	38	4	US-09-371-772B-11448	Sequence 11448, A
162	11	52.4	38	4	US-09-371-772B-13760	Sequence 13760, A	235	10.6	50.5	38	4	US-09-371-772B-11514	Sequence 11514, A
163	11	52.4	38	4	US-09-371-772B-13805	Sequence 13805, A	236	10.6	50.5	38	4	US-09-371-772B-11600	Sequence 11600, A
164	11	52.4	38	4	US-09-371-772B-13816	Sequence 13816, A	237	10.6	50.5	38	4	US-09-371-772B-11647	Sequence 11647, A
165	11	52.4	38	4	US-09-371-772B-13833	Sequence 13833, A	238	10.6	50.5	38	4	US-09-371-772B-11650	Sequence 11650, A
166	11	52.4	38	4	US-09-371-772B-13887	Sequence 13887, A	239	10.6	50.5	38	4	US-09-371-772B-11689	Sequence 11689, A
167	11	52.4	38	4	US-09-371-772B-13922	Sequence 13922, A	240	10.6	50.5	38	4	US-09-371-772B-11700	Sequence 11700, A
168	11	52.4	38	4	US-09-371-772B-13931	Sequence 13931, A	241	10.6	50.5	38	4	US-09-371-772B-11713	Sequence 11713, A
169	11	52.4	38	4	US-09-371-772B-13974	Sequence 13974, A	242	10.6	50.5	38	4	US-09-371-772B-11773	Sequence 11773, A
170	11	52.4	38	4	US-09-371-772B-13985	Sequence 13985, A	243	10.6	50.5	38	4	US-09-371-772B-11796	Sequence 11796, A
171	11	52.4	38	4	US-09-371-772B-14014	Sequence 14014, A	244	10.6	50.5	38	4	US-09-371-772B-11798	Sequence 11798, A
172	11	52.4	38	4	US-09-874-547-75	Sequence 75, Appl	245	10.6	50.5	38	4	US-09-371-772B-11818	Sequence 11818, A
173	11	52.4	38	4			246	10.6	50.5	38	4		

247	10.6	50.5	38	4	US-09-371-772B-11824	Sequence 11824, A	320	10.6	50.5	45	3	US-08-939-323-13	Sequence 13, Appl
248	10.6	50.5	38	4	US-09-371-772B-11847	Sequence 11847, A	321	10.6	50.5	47	4	US-09-422-978-195	Sequence 495, App
249	10.6	50.5	38	4	US-09-371-772B-11849	Sequence 11849, A	322	10.6	50.5	47	4	US-09-422-978-195	Sequence 2156, App
250	10.6	50.5	38	4	US-09-371-772B-11851	Sequence 11851, A	323	10.4	49.5	18	3	US-08-642-807A-11	Sequence 11, Appl
251	10.6	50.5	38	4	US-09-371-772B-11871	Sequence 11871, A	324	10.4	49.5	20	4	US-09-527-030G-150	Sequence 150, App
252	10.6	50.5	38	4	US-09-371-772B-11957	Sequence 11957, A	325	10.4	49.5	21	4	US-09-501-612A-27	Sequence 27, Appl
253	10.6	50.5	38	4	US-09-371-772B-11973	Sequence 11973, A	326	10.4	49.5	22	4	US-09-527-030G-151	Sequence 151, App
254	10.6	50.5	38	4	US-09-371-772B-11983	Sequence 11983, A	327	10.4	49.5	24	1	US-08-470-179-197	Sequence 197, App
255	10.6	50.5	38	4	US-09-371-772B-12000	Sequence 12000, A	328	10.4	49.5	24	3	US-07-876-288-12	Sequence 12, Appl
256	10.6	50.5	38	4	US-09-371-772B-12007	Sequence 12007, A	329	10.4	49.5	25	4	US-09-538-709-348	Sequence 348, App
257	10.6	50.5	38	4	US-09-371-772B-12038	Sequence 12038, A	330	10.4	49.5	27	1	US-08-513-764-6	Sequence 6, Appl
258	10.6	50.5	38	4	US-09-371-772B-12049	Sequence 12049, A	331	10.4	49.5	29	3	US-09-118-841B-20	Sequence 20, Appl
259	10.6	50.5	38	4	US-09-371-772B-12053	Sequence 12053, A	332	10.4	49.5	29	3	US-09-414-439-20	Sequence 20, Appl
260	10.6	50.5	38	4	US-09-371-772B-12096	Sequence 12096, A	333	10.4	49.5	32	4	US-09-373-720-3	Sequence 3, Appl
261	10.6	50.5	38	4	US-09-371-772B-12117	Sequence 12117, A	334	10.4	49.5	33	3	US-09-303-064-42	Sequence 42, Appl
262	10.6	50.5	38	4	US-09-371-772B-12178	Sequence 12178, A	335	10.4	49.5	33	3	US-09-086-503-42	Sequence 42, Appl
263	10.6	50.5	38	4	US-09-371-772B-12180	Sequence 12180, A	336	10.4	49.5	33	4	US-09-301-593-16	Sequence 76, Appl
264	10.6	50.5	38	4	US-09-371-772B-12184	Sequence 12184, A	337	10.4	49.5	34	1	US-08-044-621D-16	Sequence 16, Appl
265	10.6	50.5	38	4	US-09-371-772B-12192	Sequence 12192, A	338	10.4	49.5	34	1	US-08-044-621D-16	Sequence 22, Appl
266	10.6	50.5	38	4	US-09-371-772B-12210	Sequence 12210, A	339	10.4	49.5	34	1	US-08-803-973-8	Sequence 8, Appl
267	10.6	50.5	38	4	US-09-371-772B-12224	Sequence 12224, A	340	10.4	49.5	34	1	US-08-803-972-8	Sequence 8, Appl
268	10.6	50.5	38	4	US-09-371-772B-12238	Sequence 12238, A	341	10.4	49.5	35	4	US-09-165-868-9	Sequence 9, Appl
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270	10.6	50.5	38	4	US-09-371-772B-12270	Sequence 12270, A	343	10.4	49.5	36	2	US-08-292-620A-806	Sequence 806, App
271	10.6	50.5	38	4	US-09-371-772B-12286	Sequence 12286, A	344	10.4	49.5	36	2	US-08-292-620A-815	Sequence 815, App
272	10.6	50.5	38	4	US-09-371-772B-12364	Sequence 12364, A	345	10.4	49.5	36	2	US-08-292-620A-1147	Sequence 1147, App
273	10.6	50.5	38	4	US-09-371-772B-12368	Sequence 12368, A	346	10.4	49.5	36	2	US-08-292-620A-1195	Sequence 1195, App
274	10.6	50.5	38	4	US-09-371-772B-12387	Sequence 12387, A	347	10.4	49.5	36	2	US-08-292-620A-1225	Sequence 1225, App
275	10.6	50.5	38	4	US-09-371-772B-12404	Sequence 12404, A	348	10.4	49.5	36	2	US-08-292-620A-1289	Sequence 1289, App
276	10.6	50.5	38	4	US-09-371-772B-12424	Sequence 12424, A	349	10.4	49.5	36	2	US-08-292-620A-1289	Sequence 1289, App
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279	10.6	50.5	38	4	US-09-371-772B-12471	Sequence 12471, A	352	10.4	49.5	36	3	US-09-071-845-815	Sequence 815, App
280	10.6	50.5	38	4	US-09-371-772B-12584	Sequence 12584, A	353	10.4	49.5	36	3	US-09-071-845-1147	Sequence 1147, App
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282	10.6	50.5	38	4	US-09-371-772B-12693	Sequence 12693, A	355	10.4	49.5	36	3	US-09-071-845-1195	Sequence 1195, App
283	10.6	50.5	38	4	US-09-371-772B-13197	Sequence 13197, A	356	10.4	49.5	36	3	US-09-071-845-1225	Sequence 1225, App
284	10.6	50.5	38	4	US-09-371-772B-13238	Sequence 13238, A	357	10.4	49.5	36	3	US-09-071-845-1289	Sequence 1289, App
285	10.6	50.5	38	4	US-09-371-772B-13364	Sequence 13364, A	358	10.4	49.5	36	3	US-09-071-845-1346	Sequence 1346, App
286	10.6	50.5	38	4	US-09-371-772B-13405	Sequence 13405, A	359	10.4	49.5	36	3	US-08-948-381-19	Sequence 19, Appl
287	10.6	50.5	38	4	US-09-371-772B-13435	Sequence 13435, A	360	10.4	49.5	38	4	US-09-371-772B-12201	Sequence 7201, App
288	10.6	50.5	38	4	US-09-371-772B-13452	Sequence 13452, A	361	10.4	49.5	38	4	US-09-371-772B-12293	Sequence 7293, App
289	10.6	50.5	38	4	US-09-371-772B-13455	Sequence 13455, A	362	10.4	49.5	38	4	US-09-371-772B-1344	Sequence 7344, App
290	10.6	50.5	38	4	US-09-371-772B-13501	Sequence 13501, A	363	10.4	49.5	38	4	US-09-371-772B-1348	Sequence 7348, App
291	10.6	50.5	38	4	US-09-371-772B-13522	Sequence 13522, A	364	10.4	49.5	38	4	US-09-371-772B-1361	Sequence 7361, App
292	10.6	50.5	38	4	US-09-371-772B-13525	Sequence 13525, A	365	10.4	49.5	38	4	US-09-371-772B-1364	Sequence 7364, App
293	10.6	50.5	38	4	US-09-371-772B-13539	Sequence 13539, A	366	10.4	49.5	38	4	US-09-371-772B-1394	Sequence 7394, App
294	10.6	50.5	38	4	US-09-371-772B-13558	Sequence 13558, A	367	10.4	49.5	38	4	US-09-371-772B-1401	Sequence 7401, App
295	10.6	50.5	38	4	US-09-371-772B-13611	Sequence 13611, A	368	10.4	49.5	38	4	US-09-371-772B-1424	Sequence 7424, App
296	10.6	50.5	38	4	US-09-371-772B-13617	Sequence 13617, A	369	10.4	49.5	38	4	US-09-371-772B-1428	Sequence 7428, App
297	10.6	50.5	38	4	US-09-371-772B-13626	Sequence 13626, A	370	10.4	49.5	38	4	US-09-371-772B-1441	Sequence 7441, App
298	10.6	50.5	38	4	US-09-371-772B-13645	Sequence 13645, A	371	10.4	49.5	38	4	US-09-371-772B-1482	Sequence 7482, App
299	10.6	50.5	38	4	US-09-371-772B-13662	Sequence 13662, A	372	10.4	49.5	38	4	US-09-371-772B-1485	Sequence 7485, App
300	10.6	50.5	38	4	US-09-371-772B-13664	Sequence 13664, A	373	10.4	49.5	38	4	US-09-371-772B-1485	Sequence 7485, App
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306	10.6	50.5	38	4	US-09-371-772B-13764	Sequence 13764, A	379	10.4	49.5	38	4	US-09-371-772B-1590	Sequence 7590, App
307	10.6	50.5	38	4	US-09-371-772B-13764	Sequence 13764, A	380	10.4	49.5	38	4	US-09-371-772B-1619	Sequence 7619, App
308	10.6	50.5	38	4	US-09-371-772B-13838	Sequence 13838, A	381	10.4	49.5	38	4	US-09-371-772B-1652	Sequence 7652, App
309	10.6	50.5	38	4	US-09-371-772B-13853	Sequence 13853, A	382	10.4	49.5	38	4	US-09-371-772B-1656	Sequence 7656, App
310	10.6	50.5	38	4	US-09-371-772B-13882	Sequence 13882, A	383	10.4	49.5	38	4	US-09-371-772B-1738	Sequence 7738, App
311	10.6	50.5	38	4	US-09-371-772B-13907	Sequence 13907, A	384	10.4	49.5	38	4	US-09-371-772B-1783	Sequence 7783, App
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313	10.6	50.5	38	4	US-09-371-772B-13970	Sequence 13970, A	386	10.4	49.5	38	4	US-09-371-772B-1973	Sequence 7973, App
314	10.6	50.5	38	4	US-09-371-772B-13976	Sequence 13976, A	387	10.4	49.5	38	4	US-09-371-772B-8031	Sequence 8031, App
315	10.6	50.5	38	4	US-09-371-772B-14021	Sequence 14021, A	388	10.4	49.5	38	4	US-09-371-772B-8084	Sequence 8084, App
316	10.6	50.5	38	4	US-09-874-547-67	Sequence 67, Appl	389	10.4	49.5	38	4	US-09-371-772B-8105	Sequence 8105, App
317	10.6	50.5	39	4	US-09-060-299-189	Sequence 189, App	390	10.4	49.5	38	4	US-09-371-772B-8166	Sequence 8166, App
318	10.6	50.5	39	4	US-09-402-932A-189	Sequence 189, App	391	10.4	49.5	38	4	US-09-371-772B-8168	Sequence 8168, App
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3	US-08-943-731-238	Sequence 20, Appl
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ALIGNMENTS

RESULT 1  
US-09-056-052-12  
; Sequence 12, Application US/09056052  
; Patent No. 6090556  
; GENERAL INFORMATION:  
; APPLICANT: Kato, Kikuya  
; TITLE OF INVENTION: Adaptor-Tagged Competitive PCR  
; FILE REFERENCE: 07899/026001  
; CURRENT APPLICATION NUMBER: US/09/056,052  
; CURRENT FILING DATE: 1998-04-06  
; EARLIER APPLICATION NUMBER: JP88495/1997  
; EARLIER FILING DATE: 1997-04-07  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
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US-09-056-052-12

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Db 10 GTCGTTAGAACGACGCG 27

RESULT 2  
US-09-056-052-13/c  
; Sequence 13, Application US/09056052  
; Patent No. 6090556  
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; APPLICANT: Kato, Kikuya  
; TITLE OF INVENTION: Adaptor-Tagged Competitive PCR  
; FILE REFERENCE: 07898/026001  
; CURRENT APPLICATION NUMBER: US/09/056,052  
; CURRENT FILING DATE: 1998-04-06  
; EARLIER APPLICATION NUMBER: JP88495/1997  
; EARLIER FILING DATE: 1997-04-07  
; NUMBER OF SEQ ID NOS: 13

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US-09-056-052-13

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Best Local Similarity 83.3%; Pred. No. 3e+02; 3; Indels 0; Gaps 0;  
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RESULT 3  
US-09-131-028A-17/c  
; Sequence 17, Application US/09131028A  
; Patent No. 6287866  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pradip  
; APPLICANT: Lemmer, Steven A.  
; APPLICANT: Leonard, Amanda Eun-Yeong  
; APPLICANT: Chaudhary, Sunita  
; TITLE OF INVENTION: BETA-CASEIN EXPRESSING CONSTRUCTS  
; FILE REFERENCE: 6004.US.P1  
; CURRENT APPLICATION NUMBER: US/09/131,028A  
; CURRENT FILING DATE: 1998-08-07  
; PRIOR APPLICATION NUMBER: US 08/064,440  
; PRIOR FILING DATE: 1993-05-21  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 31  
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US-09-131-028A-17

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RESULT 4  
US-08-207-481-29/c  
; Sequence 29, Application US/08207481  
; Patent No. 5820866  
; GENERAL INFORMATION:  
; APPLICANT: Kappler, John W.  
; APPLICANT: Marrack, Philippa  
; TITLE OF INVENTION: PRODUCT AND PROCESS FOR T CELL  
; TITLE OF INVENTION: REGULATION  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SHERIDAN ROSS & MCINTOSH  
; STREET: 1700 LINCOLN STREET, SUITE 3500  
; CITY: DENVER  
; STATE: COLORADO  
; COUNTRY: USA



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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/207,481
; FILING DATE: 04-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2879-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303/863-9700
; TELEFAX: 303/863-0223
; INFORMATION FOR SEQ ID NO: 29:
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-207-481-29

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RESULT 5
PCT-US95-02689-31/c
; Sequence 31, Application PC/TUS9502689
; GENERAL INFORMATION:
; APPLICANT: National Jewish Center for Immunology and
; APPLICANT: Respiratory Medicine
; APPLICANT: Kappler, John W.
; APPLICANT: Marrack, Philippa
; TITLE OF INVENTION: PRODUCT AND PROCESS FOR T CELL REGULATION
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SHERIDAN ROSS & MCINTOSH
; STREET: 1700 LINCOLN STREET, SUITE 3500
; CITY: DENVER
; STATE: COLORADO
; COUNTRY: USA
; ZIP: 80202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02689
; FILING DATE: 03-MAR-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2879-8-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303/863-9700
; TELEFAX: 303/863-0223
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
```

```
;
;
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; PCT-US95-02689-31

Query Match          60.0%; Score 12.6; DB 5; Length 33;
Best Local Similarity 78.9%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGGTCAATTAGACCGTACGC 19
Db 20 CGTTCATTGTTCTGTCAGC 2

RESULT 6
US-09-371-772B-11935
; Sequence 11935, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11935
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
; US-09-371-772B-11935

Query Match          60.0%; Score 12.6; DB 4; Length 38;
Best Local Similarity 65.0%; Pred. No. 6.5e+02;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGTCAATTAGACCGTACGCA 21
Db 16 GGCGGUUAGCGCGAANGCGA 35

RESULT 7
US-09-371-772B-13181
; Sequence 13181, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
```

```

; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13181
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-371-772B-13181

Query Match          60.0%; Score 12.6; DB 4; Length 38;
Best Local Similarity 65.0%; Pred. No. 6.5e+02;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 GGTCATTAGACCGTACGCGA 21
   |||::||| |||
Db 16 GGCCGUUAGGCCGAANGCGA 35

RESULT 8
US-09-371-772B-13811
; Sequence 13811, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13811
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-371-772B-13811

Query Match          60.0%; Score 12.6; DB 4; Length 38;
Best Local Similarity 65.0%; Pred. No. 6.5e+02;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 GGTCATTAGACCGTACGCGA 21
   |||::||| |||
Db 16 GGCCGUUAGGCCGAANGCGA 35

RESULT 9
US-09-874-547-83/C
; Sequence 83, Application US/09874547
; Patent No. 6686154
; GENERAL INFORMATION:
; APPLICANT: No. 6686154K, Steffen
; APPLICANT: Kassner, Paul D.
; APPLICANT: Zyomvix, Inc.
; TITLE OF INVENTION: Screening of Phage Displayed Peptides
; TITLE OF INVENTION: Without Clearing of the Cell Culture
; INFORMATION FOR SEQ ID NO: 1680:

```

```

; FILE REFERENCE: 020144-001110US
; CURRENT APPLICATION NUMBER: US/09/874,547
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/209,503
; PRIOR FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 83
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primers for ScFv and Fab library generation (Table
; OTHER INFORMATION: I) - MVK24
US-09-874-547-83

Query Match          60.0%; Score 12.6; DB 4; Length 38;
Best Local Similarity 78.9%; Pred. No. 6.5e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGTCATTAGACCGTACGCG 20
   ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 30 GGTCATTACATGTCGCG 12

RESULT 10
US-08-373-124A-1680/c
; Sequence 1680, Application US/08373124A
; Patent No. 5646042
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,124A
; FILING DATE: January 13, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1680:

```

## ; SEQUENCE CHARACTERISTICS:

; LENGTH: 38 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-373-124A-1680

Query Match 59.0%; Score 12.4; DB 1; Length 38;  
Best Local Similarity 92.9%; Pred. No. 8.4e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCATTAGACCGTAC 17  
|||||  
Db 15 TCATCAGACCGTAC 2

## RESULT 11

US-08-435-628-1680/c  
; Sequence 1680, Application US/08435628  
; Patent No. 5817796

## ; GENERAL INFORMATION:

; APPLICANT: Stinchcomb, Dan T.  
; APPLICANT: Draper, Kenneth  
; APPLICANT: McSwiggen, James  
; APPLICANT: Jarvis, Thale  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND  
; TITLE OF INVENTION: CANCER USING RIBOZYMES  
; NUMBER OF SEQUENCES: 2627

## ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071

## ; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1

## ; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/435.628  
; FILING DATE: 05-MAY-1995

## ; CLASSIFICATION: 514

## ; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/373,124  
; FILING DATE: January 13, 1995  
; APPLICATION NUMBER: 08/245,466  
; FILING DATE: May 18, 1994  
; APPLICATION NUMBER: 08/192,943  
; FILING DATE: February 7, 1994  
; APPLICATION NUMBER: 07/987,132  
; FILING DATE: December 7, 1992  
; APPLICATION NUMBER: 07/936,422  
; FILING DATE: August 26, 1992

## ; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 209/035  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510

## ; INFORMATION FOR SEQ ID NO: 1680:

## ; SEQUENCE CHARACTERISTICS:

; LENGTH: 38 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

US-08-435-628-1680

Query Match 59.0%; Score 12.4; DB 1; Length 38;  
Best Local Similarity 92.9%; Pred. No. 8.4e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCATTAGACCGTAC 17  
|||||  
Db 15 TCATCAGACCGTAC 2

## RESULT 12

US-09-198-452A-4954/c  
; Sequence 4954, Application US/09198452A  
; Patent No. 6559294

## ; GENERAL INFORMATION:

; APPLICANT: Griffois, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments  
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention  
; TITLE OF INVENTION: and treatment of infection  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/09/198.452A  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 4954  
; LENGTH: 20  
; TYPE: DNA

## ; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-4954

Query Match 58.1%; Score 12.2; DB 4; Length 20;  
Best Local Similarity 82.4%; Pred. No. 1e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TCATTAGACCGTACGCG 20  
|||||  
Db 18 TCATTATAGCGTCCGCG 2

## RESULT 13

5451502-8/c

## ; Patent No. 5451502

; APPLICANT: GEORGE JR., ALBERT L.

## ; TITLE OF INVENTION: RESTRICTION AMPLIFICATION ASSAY

## ; NUMBER OF SEQUENCES: 18

## ; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/114,997

; FILING DATE: 31-AUG-1993

## ; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 998,644

; FILING DATE: 16-DEC-1992

; APPLICATION NUMBER: 790,174

; FILING DATE: 12-NOV-1991

; APPLICATION NUMBER: 519,146

; FILING DATE: 04-MAY-1990

; SEQ ID NO:8:

; LENGTH: 21

5451502-8

## Query Match

Best Local Similarity 82.4%; Score 12.2; DB 6; Length 21;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CATTAGACCGTACGCGA 21  
|||||  
Db 21 CATTGACCTTATCGGA 5

## RESULT 14

US-09-313-221A-19

; Sequence 19, Application US/09313221A

; Patent No. 6468743

## ; GENERAL INFORMATION:

; APPLICANT: Thomas L. Romick (Inventor)

APPLICANT: Mark S. Fraser (Inventor)  
 TITLE OF INVENTION: PCR TECHNIQUES FOR DETECTING MICROBIAL  
 TITLE OF INVENTION: AND VIRAL CONTAMINANTS IN FOODSTUFFS  
 FILE REFERENCE: HUNT-042784  
 CURRENT APPLICATION NUMBER: US/09/313,221A  
 PRIOR FILING DATE: 1999-05-17  
 PRIOR APPLICATION NUMBER: US 60/086,025  
 PRIOR FILING DATE: 1998-05-18  
 NUMBER OF SEQ ID NOS: 145  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 19  
 LENGTH: 41  
 TYPE: DNA  
 ORGANISM: Escherichia coli  
 US-09-313-221A-19

Query Match 58.1%; Score 12.2; DB 4; Length 41;  
 Best Local Similarity 82.4%; Pred. No. 1.1e+03;  
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CATTAGACCGTAGCGGA 21  
 ||||| ||||| |||||  
 Db 8 CATTATACCGTAGCGGA 24

RESULT 15  
 US-08-860-882A-75  
 ; Sequence 75, Application US/08860882A  
 ; Patent No. 5985281  
 ; GENERAL INFORMATION:  
 ; APPLICANT: TAYLORSON, CHRISTOPHER JOHN  
 ; APPLICANT: EGGELTE, HENDRIKUS JOHANNES  
 ; APPLICANT: TARRAGONA-FIOL, ANTONIO  
 ; APPLICANT: RABIN, BRIAN ROBERT  
 ; APPLICANT: BOYLE, FRANCIS THOMAS  
 ; APPLICANT: HENNAM, JOHN FREDERICK  
 ; APPLICANT: BLAKELY, DAVID CHARLES  
 ; APPLICANT: MARSHAM, PETER ROBERT  
 ; APPLICANT: HEATON, DAVID WILLIAM  
 ; APPLICANT: DAVIES, DAVID HUW  
 ; TITLE OF INVENTION: CHEMICAL COMPOUNDS  
 ; NUMBER OF SEQUENCES: 77  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: PILLSBURY, MADISON & SUTRO  
 ; STREET: 1100 NEW YORK AVENUE, N.W.  
 ; CITY: WASHINGTON  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/860,882A  
 ; FILING DATE: JUNE 23, 1997  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: DONALD J. BIRD  
 ; REGISTRATION NUMBER: 25,323  
 ; REFERENCE/DOCKET NUMBER: 9901/238653  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202) 861-3027  
 ; TELEFAX: (202) 822-0944  
 ; TELEX: 6174627 CUSH  
 ; INFORMATION FOR SEQ ID NO: 75:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 25 bases  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-860-882A-75

Query Match 57.1%; Score 12; DB 2; Length 25;  
 Best Local Similarity 75.0%; Pred. No. 1.4e+03;  
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 2 GGTCAATTAGACCGTAGCGGA 21  
 ||||| ||||| |||||  
 Db 1 GGTCAATAAGCCCGTAGCGGA 20  
 ||||| ||||| |||||  
 RESULT 16  
 US-09-011-769A-61  
 ; Sequence 61, Application US/09011769A  
 ; Patent No. 6436691  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SLATER, Anthony M.  
 ; BLAKEY, David C.  
 ; DAVIES, David H.  
 ; HENNAM, John F.  
 ; HENNEQUIN, Laurent F.A.  
 ; MARSHAM, Peter R.  
 ; DOWELL, Robert I.  
 ; TITLE OF INVENTION: Chemical Compounds  
 ; NUMBER OF SEQUENCES: 87  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Pillsbury Madison & Sutro, LLP  
 ; STREET: 1100 New York Ave., N.W.  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: U.S.A.  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 1.44 Mb disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: MS Word  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/011,769A  
 ; FILING DATE: 13-Feb-1998  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/GB96/01975  
 ; FILING DATE: 13-AUG-1996  
 ; APPLICATION NUMBER: GB 9612295.7  
 ; FILING DATE: 12-JUN-1996  
 ; APPLICATION NUMBER: GB 9611019.2  
 ; FILING DATE: 25-MAY-1996  
 ; APPLICATION NUMBER: GB 9516810.0  
 ; FILING DATE: 16-AUG-1995  
 ; INFORMATION FOR SEQ ID NO: 61:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 25 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: other nucleic acid  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 61:  
 US-09-011-769A-61

Query Match 57.1%; Score 12; DB 4; Length 25;  
 Best Local Similarity 75.0%; Pred. No. 1.4e+03;  
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 GGTCAATTAGACCGTAGCGGA 21  
 ||||| ||||| |||||  
 Db 1 GGTCAATAAGCCCGTAGCGGA 20  
 ||||| ||||| |||||

RESULT 17  
 US-09-814-351-25  
 ; Sequence 25, Application US/09814351  
 ; Patent No. 6692736  
 ; GENERAL INFORMATION:

APPLICANT: Yu, De-Chao  
APPLICANT: Li, Yuanhao  
APPLICANT: Henderson, Daniel R.  
TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS  
TITLE OF INVENTION: COMPRISING AN INTERNAL RIBOSOME ENTRY SITE  
FILE REFERENCE: 348022001700  
CURRENT APPLICATION NUMBER: US/09/814,351  
CURRENT FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/192,156  
PRIOR FILING DATE: 2000-03-24  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 25  
LENGTH: 29  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Human UPII (PCR primer 127.2.1)  
US-09-814-351-25

Query Match 57.1%; Score 12; DB 4; Length 29;  
Best Local Similarity 75.0%; Pred. No. 1.4e+03;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGGTCATTAGACCGTACCGC 20  
Db 6 CGGTCATTATAGGGCAGCG 25

## RESULT 18

US-09-709-103-34  
Sequence 34, Application US/09709103  
Patent No. 6733991  
GENERAL INFORMATION:  
APPLICANT: Cismowski, Mary  
APPLICANT: Duzic, Emir  
TITLE OF INVENTION: AGS Proteins and Nucleic Acid Molecules and Uses Therefor  
FILE REFERENCE: 60388-A-PCT-US  
CURRENT APPLICATION NUMBER: US/09/709,103  
CURRENT FILING DATE: 2000-11-08  
NUMBER OF SEQ ID NOS: 73  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 34  
LENGTH: 32  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Probe/Primer  
US-09-709-103-34

Query Match 57.1%; Score 12; DB 4; Length 32;  
Best Local Similarity 75.0%; Pred. No. 1.4e+03;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGTCAATTAGACCGTACCGCA 21  
Db 2 GGTCAATGAACCTGGCCGCA 21

## RESULT 19

US-09-439-410A-34  
Sequence 34, Application US/09439410A  
Patent No. 6746852  
GENERAL INFORMATION:  
APPLICANT: Cismowski, Mary  
APPLICANT: Duzic, Emir  
TITLE OF INVENTION: AGS PROTEIN AND NUCLEIC ACID MOLECULES AND USES THEREOF  
FILE REFERENCE: 1919/60388-B  
CURRENT APPLICATION NUMBER: US/09/439,410A  
CURRENT FILING DATE: 1999-11-11  
NUMBER OF SEQ ID NOS: 118  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 34

LENGTH: 32  
TYPE: DNA  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Probe/Primer  
US-09-439-410A-34

Query Match 57.1%; Score 12; DB 4; Length 32;  
Best Local Similarity 75.0%; Pred. No. 1.4e+03;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGTCAATTAGACCGTACCGCA 21  
Db 2 GGTCAATGAACCTGGCCGCA 21

## RESULT 20

US-09-371-772B-7357  
Sequence 7357, Application US/09371772B  
Patent No. 6566127  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: McSwiggen, Jim  
APPLICANT: Stinchcomb, Dan  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel  
FILE REFERENCE: MEHB00,876-J (237/198)  
CURRENT APPLICATION NUMBER: US/09/371,772B  
CURRENT FILING DATE: 1999-08-10  
PRIOR APPLICATION NUMBER: US 60/005,974  
PRIOR FILING DATE: 1995-10-26  
PRIOR APPLICATION NUMBER: US 08/584,040  
PRIOR FILING DATE: 1996-01-08  
NUMBER OF SEQ ID NOS: 14225  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 7357  
LENGTH: 38  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-371-772B-7357

Query Match 57.1%; Score 12; DB 4; Length 38;  
Best Local Similarity 65.0%; Pred. No. 1.4e+03;  
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGTCAATTAGACCGTACCGCA 21  
Db 16 GGCCGUAGGCCGGAACGCA 35

## RESULT 21

US-09-371-772B-7797  
Sequence 7797, Application US/09371772B  
Patent No. 6566127  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: McSwiggen, Jim  
APPLICANT: Stinchcomb, Dan  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel  
FILE REFERENCE: MEHB00,876-J (237/198)  
CURRENT APPLICATION NUMBER: US/09/371,772B  
CURRENT FILING DATE: 1999-08-10  
PRIOR APPLICATION NUMBER: US 60/005,974  
PRIOR FILING DATE: 1995-10-26  
PRIOR APPLICATION NUMBER: US 08/584,040  
PRIOR FILING DATE: 1996-01-08

```

; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7797
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-7797

Query Match          57.1%; Score 12; DB 4; Length 38;
Best Local Similarity 65.0%; Pred. No. 1.4e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 GGTCAATTAGACCGTAGCGGA 21
   ||::||| ||| |||
Db 16 GGCCGUUAGGCCGGAAGCGA 35

RESULT 22
US-09-371-772B-8104
; Sequence 8104, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR FILING DATE: 1995-10-26
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8104
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-8104

Query Match          57.1%; Score 12; DB 4; Length 38;
Best Local Similarity 65.0%; Pred. No. 1.4e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 GGTCAATTAGACCGTAGCGGA 21
   ||::||| ||| |||
Db 16 GGCCGUUAGGCCGGAAGCGA 35

RESULT 23
US-09-371-772B-8341
; Sequence 8341, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR FILING DATE: 1995-10-26
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8341
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-8341

Query Match          57.1%; Score 12; DB 4; Length 38;
Best Local Similarity 65.0%; Pred. No. 1.4e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 GGTCAATTAGACCGTAGCGGA 21
   ||::||| ||| |||
Db 16 GGCCGUUAGGCCGGAAGCGA 35

RESULT 24
US-09-371-772B-9392
; Sequence 9392, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR FILING DATE: 1995-10-26
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9392
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-9392

Query Match          57.1%; Score 12; DB 4; Length 38;
Best Local Similarity 65.0%; Pred. No. 1.4e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 GGTCAATTAGACCGTAGCGGA 21
   ||::||| ||| |||
Db 16 GGCCGUUAGGCCGGAAGCGA 35

RESULT 25
US-09-371-772B-9781
; Sequence 9781, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR FILING DATE: 1995-10-26
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9781
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-9781

Query Match          57.1%; Score 12; DB 4; Length 38;
Best Local Similarity 65.0%; Pred. No. 1.4e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 GGTCAATTAGACCGTAGCGGA 21
   ||::||| ||| |||
Db 16 GGCCGUUAGGCCGGAAGCGA 35
```

; CURRENT APPLICATION NUMBER: US/09/371,772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9781  
; LENGTH: 38  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-371-772B-9781

Query Match 57.1%; Score 12; DB 4; Length 38;  
Best Local Similarity 65.0%; Pred. No. 1.4e+03;  
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGTCATTAGACCGTACGCGA 21  
|||::|||  
Db 16 GGCCGUUAGGCCGAAAGCGA 35

RESULT 26  
US-09-371-772B-9974  
; Sequence 9974, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MEHB00,876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9974  
; LENGTH: 38  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-371-772B-9974

Query Match 57.1%; Score 12; DB 4; Length 38;  
Best Local Similarity 65.0%; Pred. No. 1.4e+03;  
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGTCATTAGACCGTACGCGA 21  
|||::|||  
Db 16 GGCCGUUAGGCCGAAAGCGA 35

RESULT 27  
US-09-371-772B-10321  
; Sequence 10321, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MEHB00,876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 10321  
; LENGTH: 38  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-371-772B-10321

Query Match 57.1%; Score 12; DB 4; Length 38;  
Best Local Similarity 65.0%; Pred. No. 1.4e+03;  
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGTCATTAGACCGTACGCGA 21  
|||::|||  
Db 16 GGCCGUUAGGCCGAAAGCGA 35

RESULT 28  
US-09-371-772B-10352  
; Sequence 10352, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MEHB00,876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 10352  
; LENGTH: 38  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-371-772B-10352

Query Match 57.1%; Score 12; DB 4; Length 38;  
Best Local Similarity 65.0%; Pred. No. 1.4e+03;  
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGTCATTAGACCGTACGCGA 21  
|||::|||  
Db 16 GGCCGUUAGGCCGAAAGCGA 35

RESULT 29  
US-09-371-772B-10512  
; Sequence 10512, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam

; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MH00.876-J (237/198)  
; CURRENT APPLICATION NUMBER: US/09/371,772B  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 10512  
; LENGTH: 38  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-09-371-772B-10512

Query Match 57.1%; Score 12; DB 4; Length 38;  
Best Local Similarity 65.0%; Pred. No. 1.4e+03;  
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 GGTCAATTAGACCGTACGCGA 21  
|||:|||||  
Db 16 GCGCGUUGGCGGAAGCGA 35

RESULT 30  
US-09-172-045-20/c  
; Sequence 20, Application US/09172045  
; Patent No. 6277594  
; GENERAL INFORMATION:  
; APPLICANT: Mikoshiba, Katsuhiko  
; APPLICANT: Aruga, Jun  
; APPLICANT: Nagai, Takeharu  
; APPLICANT: Nakata, Katsunori  
; TITLE OF INVENTION: Neurogenesis Inducing Gene  
; FILE REFERENCE: Hiraki-03497  
; CURRENT APPLICATION NUMBER: US/09/172,045  
; CURRENT FILING DATE: 1998-10-08  
; EARLIER APPLICATION NUMBER: JP98/86979  
; EARLIER FILING DATE: 1998-03-31  
; EARLIER APPLICATION NUMBER: JP98/121456  
; EARLIER FILING DATE: 1998-04-30  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA  
US-09-172-045-20

Query Match 55.2%; Score 11.6; DB 3; Length 20;  
Best Local Similarity 77.8%; Pred. No. 2.3e+03;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GTCATTAGACCGTACGCG 20  
|||||  
Db 20 GTCATTACCGGAAGGAG 3

RESULT 31  
US-09-342-325C-20/c  
; Sequence 20, Application US/09342325C  
; Patent No. 6500637  
; GENERAL INFORMATION:  
; APPLICANT: Mikoshiba, Katsuhiko

; APPLICANT: Aruga, Jun  
; APPLICANT: Nagai, Takeharu  
; APPLICANT: Katsunori, Nakata  
; TITLE OF INVENTION: Neurogenesis Inducing Gene  
; FILE REFERENCE: HIRAKI-03814  
; CURRENT APPLICATION NUMBER: US/09/342,325C  
; CURRENT FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: JP98/86979  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: JP98/121456  
; PRIOR FILING DATE: 1998-04-30  
; PRIOR APPLICATION NUMBER: 09/172,045  
; PRIOR FILING DATE: 1998-09-28  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-342-325C-20

Query Match 55.2%; Score 11.6; DB 4; Length 20;  
Best Local Similarity 77.8%; Pred. No. 2.3e+03;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GTCATTAGACCGTACGCG 20  
|||||  
Db 20 GTCATTACCGGAAGGAG 3

RESULT 32  
US-09-056-052-10  
; Sequence 10, Application US/09056052  
; Patent No. 6090556  
; GENERAL INFORMATION:  
; APPLICANT: Kato, Kikuya  
; TITLE OF INVENTION: Adaptor-Tagged Competitive PCR  
; FILE REFERENCE: 07898/026001  
; CURRENT APPLICATION NUMBER: US/09/056,052  
; CURRENT FILING DATE: 1998-04-06  
; EARLIER APPLICATION NUMBER: JP88495/1997  
; EARLIER FILING DATE: 1997-04-07  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 35  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA  
US-09-056-052-10

Query Match 55.2%; Score 11.6; DB 3; Length 35;  
Best Local Similarity 77.8%; Pred. No. 2.4e+03;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GTCATTAGACCGTACGCG 20  
|||||  
Db 10 GTCGTTAGACGCACTCG 27

RESULT 33  
US-10-009-332-10/c  
; Sequence 10, Application US/10009332  
; Patent No. 6716613  
; GENERAL INFORMATION:  
; APPLICANT: Yamouchi Pharmaceutical Co., Ltd.  
; APPLICANT: Kazusa DNA Research Institute  
; TITLE OF INVENTION: NOVEL METALLOPROTEASE HAVING AGGREGANASE ACTIVITY  
; FILE REFERENCE: Q67541  
; CURRENT APPLICATION NUMBER: US/10/009,332



RESULT 35  
US-09-371-772B-12074  
; Sequence 12074, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: MCSwigen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime

Qy 2 GGTCATTAGACCGTACGCG 20  
||| : ||| |||  
pb 16 GGCCGTTUAGGCCGAANGCG 34

RESULT 37

US-09-371-772B-12380  
; Sequence 12380, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to the Growth of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MHB00.876-J (237/198)  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 12380  
; LENGTH: 38  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
; NAME/KEY: misc.feature  
; LOCATION: (31)..(31)  
; OTHER INFORMATION: n stands for inosine  
US-09-371-772B-12380  
Query Match 55.2%; Score 11.6; DB 4; Length 38;  
Best Local Similarity 63.2%; Pred. No. 2.4e+03;  
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 2 GGTCATTAGACCGTACGCG 20  
DB 16 GGCCGUUAGCGCGANGCG 34  
RESULT 38  
US-09-371-772B-12396  
; Sequence 12396, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to the Growth of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MHB00.876-J (237/198)  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 12396  
; LENGTH: 38  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
; NAME/KEY: misc.feature  
; LOCATION: (31)..(31)  
; OTHER INFORMATION: n stands for inosine  
US-09-371-772B-12396  
Query Match 55.2%; Score 11.6; DB 4; Length 38;  
Best Local Similarity 63.2%; Pred. No. 2.4e+03;  
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 2 GGTCATTAGACCGTACGCG 20  
DB 16 GGCCGUUAGCGCGANGCG 34  
RESULT 39  
US-09-371-772B-13189  
; Sequence 13189, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to the Growth of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MHB00.876-J (237/198)  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 13189  
; LENGTH: 38  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
; NAME/KEY: misc.feature  
; LOCATION: (31)..(31)  
; OTHER INFORMATION: n stands for inosine  
US-09-371-772B-13189  
Query Match 55.2%; Score 11.6; DB 4; Length 38;  
Best Local Similarity 63.2%; Pred. No. 2.4e+03;  
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 2 GGTCATTAGACCGTACGCG 20  
DB 16 GGCCGUUAGCGCGANGCG 34  
RESULT 40  
US-09-371-772B-13450  
; Sequence 13450, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to the Growth of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MHB00.876-J (237/198)  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 13450  
; LENGTH: 38  
; TYPE: RNA

Best Local Similarity 63.2%; Pred. No. 2.4e+03;  
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 2 GGTCATTAGACCGTACGCG 20  
DB 16 GGCCGUUAGCGCGANGCG 34  
RESULT 39  
US-09-371-772B-13189  
; Sequence 13189, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to the Growth of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MHB00.876-J (237/198)  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 13189  
; LENGTH: 38  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
; NAME/KEY: misc.feature  
; LOCATION: (31)..(31)  
; OTHER INFORMATION: n stands for inosine  
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Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
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; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to the Growth of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MHB00.876-J (237/198)  
; CURRENT FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; PRIOR FILING DATE: 1996-01-08  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 13450  
; LENGTH: 38  
; TYPE: RNA

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
; NAME/KEY: misc feature  
; LOCATION: (31)..(31)  
; OTHER INFORMATION: n stands for inosine  
US-09-371-772B-13450

Query Match 55.2%; Score 11.6; DB 4; Length 38;  
Best Local Similarity 63.2%; Pred. NO. 2.4e+03;  
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

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Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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25	15	US-10-098-263B-25744	Sequence 25744, A
25	15	US-10-098-263B-56048	Sequence 56048, A
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155	11.8	56.2	38	17	US-10-244-367-20	Sequence 20, Appl	228	11.6	55.2	38	10	US-09-930-423-2091	Sequence 2091, Ap
156	11.6	55.2	20	15	US-10-098-263B-787	Sequence 787, App	229	11.6	55.2	38	10	US-09-930-423-2102	Sequence 2102, Ap
157	11.6	55.2	25	15	US-10-098-263B-788	Sequence 788, App	230	11.6	55.2	38	10	US-09-930-423-2106	Sequence 2106, Ap
158	11.6	55.2	25	15			231	11.6	55.2	38	10		

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233	11.6	55.2	38	10	US-09-930-423-2199	Sequence 2199, Ap	306	11.6	55.2	38	17	US-10-712-672-3326	Sequence 3326, Ap
234	11.6	55.2	38	10	US-09-930-423-2248	Sequence 2248, Ap	307	11.6	55.2	38	17	US-10-712-672-3370	Sequence 3370, Ap
235	11.6	55.2	38	10	US-09-930-423-2574	Sequence 2574, Ap	308	11.6	55.2	38	17	US-10-712-672-3401	Sequence 3401, Ap
236	11.6	55.2	38	10	US-09-930-423-2595	Sequence 2595, Ap	309	11.6	55.2	38	17	US-10-712-672-3412	Sequence 3412, Ap
237	11.6	55.2	38	10	US-09-827-395A-1245	Sequence 1245, Ap	310	11.6	55.2	38	17	US-10-712-672-3434	Sequence 3434, Ap
238	11.6	55.2	38	10	US-09-827-395A-1307	Sequence 1307, Ap	311	11.6	55.2	38	17	US-10-712-672-3494	Sequence 3494, Ap
239	11.6	55.2	38	10	US-09-827-395A-1337	Sequence 1337, Ap	312	11.6	55.2	38	17	US-10-712-672-3559	Sequence 3559, Ap
240	11.6	55.2	38	10	US-09-827-395A-1379	Sequence 1379, Ap	313	11.6	55.2	38	17	US-10-712-672-3666	Sequence 3666, Ap
241	11.6	55.2	38	10	US-09-827-395A-1404	Sequence 1404, Ap	314	11.6	55.2	38	17	US-10-712-672-3701	Sequence 3701, Ap
242	11.6	55.2	38	10	US-09-827-395A-1411	Sequence 1411, Ap	315	11.6	55.2	38	17	US-10-712-672-3708	Sequence 3708, Ap
243	11.6	55.2	38	10	US-09-827-395A-1465	Sequence 1465, Ap	316	11.6	55.2	38	17	US-10-712-672-3729	Sequence 3729, Ap
244	11.6	55.2	38	10	US-09-792-818-1284	Sequence 1284, Ap	317	11.6	55.2	38	17	US-10-712-672-3761	Sequence 3761, Ap
245	11.6	55.2	38	10	US-09-792-818-1359	Sequence 1359, Ap	318	11.6	55.2	38	17	US-10-712-672-4076	Sequence 4076, Ap
246	11.6	55.2	38	10	US-09-745-237A-2065	Sequence 2065, Ap	319	11.6	55.2	38	17	US-10-669-841-8341	Sequence 8341, Ap
247	11.6	55.2	38	10	US-09-745-237A-2091	Sequence 2091, Ap	320	11.6	55.2	38	17	US-10-669-841-8455	Sequence 8455, Ap
248	11.6	55.2	38	10	US-09-745-237A-2097	Sequence 2097, Ap	321	11.6	55.2	38	17	US-10-669-841-8460	Sequence 8460, Ap
249	11.6	55.2	38	10	US-09-745-237A-2102	Sequence 2102, Ap	322	11.6	55.2	38	17	US-10-669-841-8495	Sequence 8495, Ap
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251	11.6	55.2	38	10	US-09-745-237A-2119	Sequence 2119, Ap	324	11.6	55.2	38	17	US-10-669-841-8575	Sequence 8575, Ap
252	11.6	55.2	38	10	US-09-745-237A-2199	Sequence 2199, Ap	325	11.6	55.2	38	17	US-10-669-841-8782	Sequence 8782, Ap
253	11.6	55.2	38	10	US-09-745-237A-2248	Sequence 2248, Ap	326	11.6	55.2	39	13	US-10-072-152-26	Sequence 26, Appl
254	11.6	55.2	38	10	US-09-745-237A-2574	Sequence 2574, Ap	327	11.6	55.2	39	15	US-10-277-471A-11	Sequence 11, Appl
255	11.6	55.2	38	10	US-09-745-237A-2595	Sequence 2595, Ap	328	11.6	55.2	39	15	US-10-339-674-633	Sequence 633, App
256	11.6	55.2	38	15	US-10-156-306-2222	Sequence 2222, Ap	329	11.6	55.2	39	15	US-10-339-674-2615	Sequence 2615, Ap
257	11.6	55.2	38	15	US-10-156-306-5439	Sequence 5439, Ap	330	11.6	55.2	39	16	US-10-655-433-26	Sequence 26, Appl
258	11.6	55.2	38	15	US-10-156-306-5442	Sequence 5442, Ap	331	11.4	54.3	15	9	US-09-504-231A-904	Sequence 904, App
259	11.6	55.2	38	15	US-10-156-306-5538	Sequence 5538, Ap	332	11.4	54.3	15	9	US-09-274-553D-904	Sequence 904, App
260	11.6	55.2	38	15	US-10-156-306-5615	Sequence 5615, Ap	333	11.4	54.3	19	9	US-09-969-373-4574	Sequence 4574, App
261	11.6	55.2	38	15	US-10-156-306-5717	Sequence 5717, Ap	334	11.4	54.3	22	15	US-10-296-995-93	Sequence 93, Appl
262	11.6	55.2	38	15	US-10-157-580A-88	Sequence 88, Appl	335	11.4	54.3	23	15	US-10-214-932-14	Sequence 14, Appl
263	11.6	55.2	38	15	US-10-230-006-863	Sequence 863, App	336	11.4	54.3	23	16	US-10-474-290-6	Sequence 6, Appl
264	11.6	55.2	38	15	US-10-230-006-873	Sequence 873, App	337	11.4	54.3	24	10	US-09-940-185-2381	Sequence 2381, Ap
265	11.6	55.2	38	15	US-10-230-006-887	Sequence 887, App	338	11.4	54.3	25	14	US-10-215-112-3435	Sequence 3435, Ap
266	11.6	55.2	38	15	US-10-230-006-896	Sequence 896, App	339	11.4	54.3	25	14	US-10-215-112-5874	Sequence 5874, Ap
267	11.6	55.2	38	15	US-10-230-006-930	Sequence 930, App	340	11.4	54.3	25	14	US-10-215-112-10677	Sequence 10677, A
268	11.6	55.2	38	15	US-10-230-006-970	Sequence 970, App	341	11.4	54.3	25	15	US-10-098-2638-34732	Sequence 34732, A
269	11.6	55.2	38	15	US-10-230-006-1002	Sequence 1002, Ap	342	11.4	54.3	25	15	US-10-098-2638-56624	Sequence 56624, A
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271	11.6	55.2	38	15	US-10-230-006-1058	Sequence 1058, Ap	344	11.4	54.3	25	15	US-10-098-2638-71594	Sequence 71594, A
272	11.6	55.2	38	15	US-10-230-006-1108	Sequence 1108, Ap	345	11.4	54.3	25	15	US-10-098-2638-89565	Sequence 89565, A
273	11.6	55.2	38	15	US-10-430-882-1245	Sequence 1245, Ap	346	11.4	54.3	25	15	US-10-098-2638-89566	Sequence 89566, A
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275	11.6	55.2	38	15	US-10-430-882-1337	Sequence 1337, Ap	348	11.4	54.3	25	15	US-10-098-2638-104438	Sequence 104438, A
276	11.6	55.2	38	15	US-10-430-882-1379	Sequence 1379, Ap	349	11.4	54.3	25	15	US-10-098-2638-110567	Sequence 110567, A
277	11.6	55.2	38	15	US-10-430-882-1404	Sequence 1404, Ap	350	11.4	54.3	25	15	US-10-098-2638-121446	Sequence 121446, A
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279	11.6	55.2	38	15	US-10-430-882-1465	Sequence 1465, Ap	352	11.4	54.3	27	10	US-09-877-705A-11	Sequence 11, Appl
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281	11.6	55.2	38	16	US-10-342-902-3564	Sequence 3564, Ap	354	11.4	54.3	27	10	US-09-947-274-11	Sequence 11, Appl
282	11.6	55.2	38	16	US-10-342-902-3569	Sequence 3569, Ap	355	11.4	54.3	27	10	US-09-947-274-12	Sequence 12, Appl
283	11.6	55.2	38	16	US-10-342-902-3604	Sequence 3604, Ap	356	11.4	54.3	27	10	US-09-877-738A-11	Sequence 11, Appl
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285	11.6	55.2	38	16	US-10-342-902-3836	Sequence 3836, Ap	358	11.4	54.3	27	12	US-09-877-403A-11	Sequence 11, Appl
286	11.6	55.2	38	16	US-10-342-902-3891	Sequence 3891, Ap	359	11.4	54.3	27	12	US-09-877-403A-12	Sequence 12, Appl
287	11.6	55.2	38	16	US-10-138-674-13690	Sequence 13690, A	360	11.4	54.3	27	15	US-10-057-810-11	Sequence 11, Appl
288	11.6	55.2	38	16	US-10-138-674-14351	Sequence 14351, A	361	11.4	54.3	27	15	US-10-057-810-12	Sequence 12, Appl
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291	11.6	55.2	38	16	US-10-138-674-14673	Sequence 14673, A	364	11.4	54.3	27	17	US-10-779-595-11	Sequence 11, Appl
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295	11.6	55.2	38	17	US-10-287-949A-14351	Sequence 14351, A	368	11.2	53.3	18	18	US-10-740-926-436	Sequence 436, App
296	11.6	55.2	38	17	US-10-287-949A-14432	Sequence 14432, A	369	11.2	53.3	20	17	US-10-319-914-77	Sequence 77, Appl
297	11.6	55.2	38	17	US-10-287-949A-14657	Sequence 14657, A	370	11.2	53.3	20	17	US-10-319-914-155	Sequence 155, App
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302	11.6	55.2	38	17	US-10-712-672-3228	Sequence 3228, Ap	375	11.2	53.3	25	14	US-10-215-112-10028	Sequence 10028, A
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304	11.6	55.2	38	17	US-10-712-672-3242	Sequence 3242, Ap	377	11.2	53.3	25	15	US-10-098-2638-2080	Sequence 2080, Ap

c 378	11.2	53.3	25	15	US-10-098-263B-9678	Sequence 9678, Ap	c 451	11	52.4	24	9	US-09-993-687-459	Sequence 459, App
c 379	11.2	53.3	25	15	US-10-098-263B-11931	Sequence 11931, A	c 452	11	52.4	24	10	US-09-989-734-459	Sequence 459, App
c 380	11.2	53.3	25	15	US-10-098-263B-26773	Sequence 26773, A	c 453	11	52.4	24	10	US-09-997-653-459	Sequence 459, App
c 381	11.2	53.3	25	15	US-10-098-263B-30572	Sequence 30572, A	c 454	11	52.4	24	10	US-09-989-724-459	Sequence 459, App
c 382	11.2	53.3	25	15	US-10-098-263B-34409	Sequence 34409, A	c 455	11	52.4	24	10	US-09-989-728-459	Sequence 459, App
c 383	11.2	53.3	25	15	US-10-098-263B-34906	Sequence 34906, A	c 456	11	52.4	24	10	US-09-990-441-459	Sequence 459, App
c 384	11.2	53.3	25	15	US-10-098-263B-36180	Sequence 36180, A	c 457	11	52.4	24	10	US-09-993-667-459	Sequence 459, App
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c 386	11.2	53.3	25	15	US-10-098-263B-44094	Sequence 44094, A	c 459	11	52.4	24	10	US-09-997-666-459	Sequence 459, App
c 387	11.2	53.3	25	15	US-10-098-263B-59261	Sequence 59261, A	c 460	11	52.4	24	10	US-09-990-438-459	Sequence 459, App
c 388	11.2	53.3	25	15	US-10-098-263B-71007	Sequence 71007, A	c 461	11	52.4	24	10	US-09-990-562-459	Sequence 459, App
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c 390	11.2	53.3	25	15	US-10-098-263B-72284	Sequence 72284, A	c 463	11	52.4	24	10	US-09-989-726-459	Sequence 459, App
c 391	11.2	53.3	25	15	US-10-098-263B-75762	Sequence 75762, A	c 464	11	52.4	24	10	US-09-998-156-459	Sequence 459, App
c 392	11.2	53.3	25	15	US-10-098-263B-121458	Sequence 121458, A	c 465	11	52.4	24	10	US-09-990-437-459	Sequence 459, App
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c 396	11.2	53.3	29	18	US-10-471-868-23	Sequence 23, Appl	c 469	11	52.4	24	10	US-09-991-172-459	Sequence 459, App
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c 400	11.2	53.3	37	9	US-09-864-785-1839	Sequence 1839, Ap	c 473	11	52.4	24	10	US-09-990-443-459	Sequence 459, App
c 401	11.2	53.3	37	9	US-09-927-046-3665	Sequence 3665, Ap	c 474	11	52.4	24	10	US-09-991-854-459	Sequence 459, App
c 402	11.2	53.3	37	10	US-09-848-754A-6432	Sequence 6432, Ap	c 475	11	52.4	24	10	US-09-997-628-459	Sequence 459, App
c 403	11.2	53.3	37	10	US-09-848-754A-6515	Sequence 6516, Ap	c 476	11	52.4	24	10	US-09-997-683-459	Sequence 459, App
c 404	11.2	53.3	37	16	US-10-138-674-20489	Sequence 20489, A	c 477	11	52.4	24	10	US-09-989-729A-459	Sequence 459, App
c 405	11.2	53.3	37	16	US-10-138-674-20600	Sequence 20600, A	c 478	11	52.4	24	10	US-09-997-349-459	Sequence 459, App
c 406	11.2	53.3	37	16	US-10-138-674-20710	Sequence 20710, A	c 479	11	52.4	24	10	US-09-997-440-459	Sequence 459, App
c 407	11.2	53.3	37	17	US-10-287-949A-20489	Sequence 20489, A	c 480	11	52.4	24	10	US-09-990-440-459	Sequence 459, App
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c 409	11.2	53.3	37	17	US-10-287-949A-20710	Sequence 20710, A	c 482	11	52.4	24	10	US-09-993-469-459	Sequence 459, App
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c 413	11.2	53.3	40	9	US-09-791-153A-121	Sequence 4, Appli	c 486	11	52.4	24	10	US-09-990-427-459	Sequence 459, App
c 414	11.2	53.3	45	10	US-09-927-046-5230	Sequence 121, App	c 487	11	52.4	24	10	US-09-989-328-459	Sequence 459, App
c 415	11.2	53.3	48	10	US-09-930-423-4525	Sequence 5230, Ap	c 488	11	52.4	24	10	US-09-993-583-459	Sequence 459, App
c 416	11.2	53.3	48	10	US-09-745-237A-4525	Sequence 4525, Ap	c 489	11	52.4	24	10	US-09-941-992-459	Sequence 459, App
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c 421	11	52.4	17	16	US-10-138-674-3829	Sequence 3829, Ap	c 494	11	52.4	24	10	US-09-998-041-459	Sequence 459, App
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853	11	52.4	38	10	US-09-827-395A-1344	Sequence 1344, Ap	926	11	52.4	38	15	US-10-156-306-5297	Sequence 5297, Ap
854	11	52.4	38	10	US-09-827-395A-1357	Sequence 1357, Ap	927	11	52.4	38	15	US-10-156-306-5311	Sequence 5311, Ap
855	11	52.4	38	10	US-09-827-395A-1421	Sequence 1421, Ap	928	11	52.4	38	15	US-10-156-306-5318	Sequence 5318, Ap
856	11	52.4	38	10	US-09-827-395A-1460	Sequence 1460, Ap	929	11	52.4	38	15	US-10-156-306-5374	Sequence 5374, Ap
857	11	52.4	38	10	US-09-827-395A-1474	Sequence 1474, Ap	930	11	52.4	38	15	US-10-156-306-5445	Sequence 5445, Ap
858	11	52.4	38	10	US-09-827-395A-1482	Sequence 1482, Ap	931	11	52.4	38	15	US-10-156-306-5449	Sequence 5449, Ap
859	11	52.4	38	10	US-09-827-395A-1510	Sequence 1510, Ap	932	11	52.4	38	15	US-10-156-306-5452	Sequence 5452, Ap
860	11	52.4	38	10	US-09-827-395A-1551	Sequence 1551, Ap	933	11	52.4	38	15	US-10-156-306-5479	Sequence 5479, Ap
861	11	52.4	38	10	US-09-827-395A-1557	Sequence 1557, Ap	934	11	52.4	38	15	US-10-156-306-5519	Sequence 5519, Ap
862	11	52.4	38	10	US-09-792-818-1108	Sequence 1108, Ap	935	11	52.4	38	15	US-10-156-306-5525	Sequence 5525, Ap
863	11	52.4	38	10	US-09-792-818-1112	Sequence 1112, Ap	936	11	52.4	38	15	US-10-156-306-5533	Sequence 5533, Ap
864	11	52.4	38	10	US-09-792-818-1133	Sequence 1133, Ap	937	11	52.4	38	15	US-10-156-306-5547	Sequence 5547, Ap
865	11	52.4	38	10	US-09-792-818-1163	Sequence 1163, Ap	938	11	52.4	38	15	US-10-156-306-5550	Sequence 5550, Ap
866	11	52.4	38	10	US-09-792-818-1184	Sequence 1184, Ap	939	11	52.4	38	15	US-10-156-306-5552	Sequence 5552, Ap
867	11	52.4	38	10	US-09-792-818-1188	Sequence 1188, Ap	940	11	52.4	38	15	US-10-156-306-5554	Sequence 5554, Ap
868	11	52.4	38	10	US-09-792-818-1217	Sequence 1217, Ap	941	11	52.4	38	15	US-10-156-306-5613	Sequence 5613, Ap
869	11	52.4	38	10	US-09-792-818-1253	Sequence 1253, Ap	942	11	52.4	38	15	US-10-156-306-5619	Sequence 5619, Ap
870	11	52.4	38	10	US-09-792-818-1263	Sequence 1263, Ap	943	11	52.4	38	15	US-10-156-306-5623	Sequence 5623, Ap
871	11	52.4	38	10	US-09-745-237A-1790	Sequence 1790, Ap	944	11	52.4	38	15	US-10-156-306-5650	Sequence 5650, Ap
872	11	52.4	38	10	US-09-745-237A-1804	Sequence 1804, Ap	945	11	52.4	38	15	US-10-156-306-5672	Sequence 5672, Ap
873	11	52.4	38	10	US-09-745-237A-1943	Sequence 1943, Ap	946	11	52.4	38	15	US-10-156-306-5700	Sequence 5700, Ap
874	11	52.4	38	10	US-09-745-237A-2070	Sequence 2070, Ap	947	11	52.4	38	15	US-10-156-306-5735	Sequence 5735, Ap
875	11	52.4	38	10	US-09-745-237A-2083	Sequence 2083, Ap	948	11	52.4	38	15	US-10-230-006-246	Sequence 246, App
876	11	52.4	38	10	US-09-745-237A-2138	Sequence 2138, Ap	949	11	52.4	38	15	US-10-230-006-249	Sequence 249, App
877	11	52.4	38	10	US-09-745-237A-2140	Sequence 2140, Ap	950	11	52.4	38	15	US-10-230-006-289	Sequence 289, App
878	11	52.4	38	10	US-09-745-237A-2148	Sequence 2148, Ap	951	11	52.4	38	15	US-10-230-006-302	Sequence 302, App
879	11	52.4	38	10	US-09-745-237A-2150	Sequence 2150, Ap	952	11	52.4	38	15	US-10-230-006-339	Sequence 339, App
880	11	52.4	38	10	US-09-745-237A-2155	Sequence 2155, Ap	953	11	52.4	38	15	US-10-230-006-366	Sequence 366, App
881	11	52.4	38	10	US-09-745-237A-2163	Sequence 2163, Ap	954	11	52.4	38	15	US-10-230-006-383	Sequence 383, App
882	11	52.4	38	10	US-09-745-237A-2185	Sequence 2185, Ap	955	11	52.4	38	15	US-10-230-006-839	Sequence 839, App
883	11	52.4	38	10	US-09-745-237A-2214	Sequence 2214, Ap	956	11	52.4	38	15	US-10-230-006-854	Sequence 854, App
884	11	52.4	38	10	US-09-745-237A-2336	Sequence 2336, Ap	957	11	52.4	38	15	US-10-230-006-867	Sequence 867, App
885	11	52.4	38	10	US-09-745-237A-2339	Sequence 2339, Ap	958	11	52.4	38	15	US-10-230-006-959	Sequence 959, App
886	11	52.4	38	10	US-09-745-237A-2366	Sequence 2366, Ap	959	11	52.4	38	15	US-10-230-006-980	Sequence 980, App
887	11	52.4	38	10	US-09-745-237A-2369	Sequence 2369, Ap	960	11	52.4	38	15	US-10-230-006-1020	Sequence 1020, Ap
888	11	52.4	38	10	US-09-745-237A-2394	Sequence 2394, Ap	961	11	52.4	38	15	US-10-230-006-1021	Sequence 1021, Ap

11 52.4 38 15 US-10-230-006-1028 Sequence 1028, Ap  
11 52.4 38 15 US-10-230-006-1035 Sequence 1035, Ap  
11 52.4 38 15 US-10-230-006-1048 Sequence 1048, Ap  
11 52.4 38 15 US-10-230-006-1055 Sequence 1055, Ap  
11 52.4 38 15 US-10-230-006-1061 Sequence 1061, Ap  
11 52.4 38 15 US-10-230-006-1132 Sequence 1132, Ap  
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11 52.4 38 15 US-10-230-006-1141 Sequence 1141, Ap  
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11 52.4 38 15 US-10-230-006-1189 Sequence 1189, Ap  
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11 52.4 38 15 US-10-430-882-1202 Sequence 1202, Ap  
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11 52.4 38 15 US-10-430-882-1210 Sequence 1210, Ap  
11 52.4 38 15 US-10-430-882-1217 Sequence 1217, Ap  
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11 52.4 38 15 US-10-430-882-1303 Sequence 1303, Ap  
11 52.4 38 15 US-10-430-882-1314 Sequence 1314, Ap  
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11 52.4 38 15 US-10-430-882-1324 Sequence 1324, Ap  
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11 52.4 38 15 US-10-430-882-1482 Sequence 1482, Ap  
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11 52.4 38 15 US-10-430-882-1511 Sequence 1511, Ap  
11 52.4 38 15 US-10-430-882-1551 Sequence 1551, Ap  
11 52.4 38 15 US-10-430-882-1557 Sequence 1557, Ap  
11 52.4 38 16 US-10-342-902-2820 Sequence 2820, Ap  
11 52.4 38 16 US-10-342-902-2852 Sequence 2852, Ap  
11 52.4 38 16 US-10-342-902-2855 Sequence 2855, Ap  
11 52.4 38 16 US-10-342-902-3191 Sequence 3191, Ap  
11 52.4 38 16 US-10-342-902-3247 Sequence 3247, Ap  
11 52.4 38 16 US-10-342-902-3288 Sequence 3288, Ap  
11 52.4 38 16 US-10-342-902-3295 Sequence 3295, Ap  
11 52.4 38 16 US-10-342-902-3300 Sequence 3300, Ap  
11 52.4 38 16 US-10-342-902-3331 Sequence 3331, Ap  
11 52.4 38 16 US-10-342-902-3399 Sequence 3399, Ap  
11 52.4 38 16 US-10-342-902-3435 Sequence 3435, Ap  
11 52.4 38 16 US-10-342-902-3481 Sequence 3481, Ap  
11 52.4 38 16 US-10-342-902-3497 Sequence 3497, Ap

ALIGNMENTS

RESULT 1  
US-10-087-631B-2/c  
; Sequence 2, Application US/10087631B  
; Publication No. US20030054372A1  
; GENERAL INFORMATION:  
; APPLICANT: JAEGER, STEPHAN  
; TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A  
; TITLE OF INVENTION: CONTROL  
; FILE REFERENCE: 1803-335-999  
; CURRENT APPLICATION NUMBER: US/10/087,631B  
; CURRENT FILING DATE: 2002-03-01  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Artificial sequence to exemplify principle  
; OTHER INFORMATION: principle  
US-10-087-631B-2

Query Match 100.0%; Score 21; DB 14; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGGTCATTAGACCGTACGCGA 21  
DB 21 CGGTCATTAGACCGTACGCGA 1

RESULT 2  
US-10-087-631B-17  
; Sequence 17, Application US/10087631B  
; Publication No. US20030054372A1  
; GENERAL INFORMATION:  
; APPLICANT: JAEGER, STEPHAN  
; TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A  
; TITLE OF INVENTION: CONTROL  
; FILE REFERENCE: 1803-335-999  
; CURRENT APPLICATION NUMBER: US/10/087,631B  
; CURRENT FILING DATE: 2002-03-01  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 17  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Sequence to exemplify principle  
; OTHER INFORMATION: principle  
US-10-087-631B-17

Query Match 100.0%; Score 21; DB 14; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGTCATTAGACCGTACGCGA 21  
DB 1 CGGTCATTAGACCGTACGCGA 21

RESULT 3  
US-10-419-022-2/c  
; Sequence 2, Application US/10419022  
; Publication No. US20030165982A1  
; GENERAL INFORMATION:  
; APPLICANT: JAEGER, STEPHAN  
; TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A  
; TITLE OF INVENTION: CONTROL  
; FILE REFERENCE: 1803-335-999  
; CURRENT APPLICATION NUMBER: US/10/419,022  
; CURRENT FILING DATE: 2003-04-17  
; PRIOR APPLICATION NUMBER: US/10/087,631B  
; PRIOR FILING DATE: 2002-03-01  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Artificial sequence to exemplify principle  
; OTHER INFORMATION: principle  
US-10-419-022-2

Query Match 100.0%; Score 21; DB 15; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGTCATTAGACCGTACGCGA 21  
DB 21 CGGTCATTAGACCGTACGCGA 1

RESULT 4  
US-10-419-022-17  
; Sequence 17, Application US/10419022  
; Publication No. US20030165982A1  
; GENERAL INFORMATION:  
; APPLICANT: JAEGER, STEPHAN  
; TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A  
; TITLE OF INVENTION: CONTROL  
US-10-419-022-17

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; FILE REFERENCE: 1803-335-999
; CURRENT APPLICATION NUMBER: US/10/419,022
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US/10/087,631B
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence to exemplify princ
US-10-419-022-17

Query Match      100.0%; Score 21; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGTCATTAGACCGTACGCGA 21
    |||||
Db 1 CGGTCATTAGACCGTACGCGA 21
    |||||

RESULT 5
US-10-098-263B-56047
; Sequence 56047, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 56047
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-56047

Query Match      67.6%; Score 14.2; DB 15; Length 25;
Best Local Similarity 84.2%; Pred. No. 8.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GTCATTAGACCGTACGCGA 21
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Db 6 GTCATTAGACCGTGTTCGA 24
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RESULT 6
US-09-374-046A-218
; Sequence 218, Application US/09374046A
; Publication No. US20030096951A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fachtel, Kim
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
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; FILE REFERENCE: GI 6075-83A
; CURRENT APPLICATION NUMBER: US/09/374,046A
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 218
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)
; OTHER INFORMATION: biotinylated phosphoramidite residue
US-09-374-046A-218

Query Match      64.8%; Score 13.6; DB 10; Length 29;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGTCAATTAGACCGTACGCGA 21
    |||||
Db 5 GGTCAATAGACAGTACTCCA 24
    |||||

RESULT 7
US-10-616-263-218
; Sequence 218, Application US/10616263
; Publication No. US20040039276A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fachtel, Kim
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000103.5
; CURRENT APPLICATION NUMBER: US/10/616,263
; CURRENT FILING DATE: 2003-07-08
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 218
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)
; OTHER INFORMATION: biotinylated phosphoramidite residue
US-10-616-263-218

Query Match      64.8%; Score 13.6; DB 16; Length 29;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGTCAATTAGACCGTACGCGA 21
    |||||
Db 5 GGTCAATAGACAGTACTCCA 24
    |||||

RESULT 8
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US-10-138-674-20182/c
; Sequence 20182, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20182
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-138-674-20182
Query Match      64.8%; Score 13.6; DB 16; Length 37;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGGTCATTAGACCGTACGCG 20
Db 37 CGGTCATTAGACCTCACTCG 18

RESULT 9
US-10-138-674-20479/c
; Sequence 20479, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20479
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-138-674-20479
Query Match      64.8%; Score 13.6; DB 16; Length 37;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGGTCATTAGACCGTACGCG 20
Db 37 CGGTCATTAGACCTCACTCG 18

RESULT 10
US-10-287-949A-20182/c
; Sequence 20182, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759

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; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20182
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-287-949A-20182
Query Match      64.8%; Score 13.6; DB 17; Length 37;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGGTCATTAGACCGTACGCG 20
Db 37 CGGTCATTAGACCTCACTCG 18

RESULT 11
US-10-287-949A-20479/c
; Sequence 20479, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20479
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-287-949A-20479
Query Match      64.8%; Score 13.6; DB 17; Length 37;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGGTCATTAGACCGTACGCG 20
Db 37 CGGTCATTAGACCTCACTCG 18

RESULT 12
US-10-098-263B-9436/c
; Sequence 9436, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759

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; PRIOR FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 131066  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 9436  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-098-263B-9436

Query Match 63.8%; Score 13.4; DB 15; Length 25;  
Best Local Similarity 93.3%; Pred. No. 2.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GTCATTAGACCGTAC 17  
| | | | | | | | | | | | | | | | | | | | | |  
Db 18 GTCATTAGACGTAC 4

RESULT 13  
US-10-098-263B-88235  
; Sequence 88235, Application US/10098263B  
; Publication No. US20030104410A1  
; GENERAL INFORMATION:  
; APPLICANT: Mittman, Michael  
; TITLE OF INVENTION: Human Microarray  
; FILE REFERENCE: 3118.1  
; CURRENT APPLICATION NUMBER: US/10/098,263B  
; PRIOR FILING DATE: 2003-01-08  
; PRIOR APPLICATION NUMBER: 60/276,759  
; PRIOR FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 131066  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 88235  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-098-263B-88235

Query Match 62.9%; Score 13.2; DB 15; Length 25;  
Best Local Similarity 83.3%; Pred. No. 2.9e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TCATTAGACCGTACGCGA 21  
| | | | | | | | | | | | | | | | | | | | | |  
Db 7 TCAATAGACCTTACGGGA 24

RESULT 14  
US-10-098-263B-88853  
; Sequence 88853, Application US/10098263B  
; Publication No. US20030104410A1  
; GENERAL INFORMATION:  
; APPLICANT: Mittman, Michael  
; TITLE OF INVENTION: Human Microarray  
; FILE REFERENCE: 3118.1  
; CURRENT APPLICATION NUMBER: US/10/098,263B  
; PRIOR FILING DATE: 2003-01-08  
; PRIOR APPLICATION NUMBER: 60/276,759  
; PRIOR FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 131066  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 88853  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-098-263B-88853

Query Match 62.9%; Score 13.2; DB 15; Length 25;  
Best Local Similarity 83.3%; Pred. No. 2.9e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TCATTAGACCGTACGCGA 21  
| | | | | | | | | | | | | | | | | | | | | |

Db 8 TCAATAGACCTTACGGGA 25  
RESULT 15  
US-10-098-263B-71593/c  
; Sequence 71593, Application US/10098263B  
; Publication No. US20030104410A1  
; GENERAL INFORMATION:  
; APPLICANT: Mittman, Michael  
; TITLE OF INVENTION: Human Microarray  
; FILE REFERENCE: 3118.1  
; CURRENT APPLICATION NUMBER: US/10/098,263B  
; PRIOR FILING DATE: 2003-01-08  
; PRIOR APPLICATION NUMBER: 60/276,759  
; PRIOR FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 131066  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 71593  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-098-263B-71593

Query Match 61.9%; Score 13; DB 15; Length 25;  
Best Local Similarity 76.2%; Pred. No. 3.8e+03;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGGTCAATTAGACCGTACGCGA 21  
| | | | | | | | | | | | | | | | | | | | | |  
Db 21 CGGTGGGTAGTCCGTACGAGA 1

RESULT 16  
US-10-098-263B-71008  
; Sequence 71008, Application US/10098263B  
; Publication No. US20030104410A1  
; GENERAL INFORMATION:  
; APPLICANT: Mittman, Michael  
; TITLE OF INVENTION: Human Microarray  
; FILE REFERENCE: 3118.1  
; CURRENT APPLICATION NUMBER: US/10/098,263B  
; CURRENT FILING DATE: 2003-01-08  
; PRIOR APPLICATION NUMBER: 60/276,759  
; PRIOR FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 131066  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 71008  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-098-263B-71008

Query Match 61.0%; Score 12.8; DB 15; Length 25;  
Best Local Similarity 87.5%; Pred. No. 4.9e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GTCATTAGACCGTACG 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 5 GTCATGTGACCGTACG 20

RESULT 17  
US-10-098-263B-25744  
; Sequence 25744, Application US/10098263B  
; Publication No. US20030104410A1  
; GENERAL INFORMATION:  
; APPLICANT: Mittman, Michael  
; TITLE OF INVENTION: Human Microarray  
; FILE REFERENCE: 3118.1  
; CURRENT APPLICATION NUMBER: US/10/098,263B  
; CURRENT FILING DATE: 2003-01-08  
; PRIOR APPLICATION NUMBER: 60/276,759  
; PRIOR FILING DATE: 2001-03-16

Wed Nov 24 08:46:00 2004

us-10-087-631b-17.max.rnpb

NUMBER OF SEQ ID NOS: 131066  
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 SEQ ID NO 25744  
 LENGTH: 25  
 TYPE: DNA  
 ORGANISM: Homo sapien  
 US-10-098-263B-25744

Query Match 60.0%; Score 12.6; DB 15; Length 25;  
 Best Local Similarity 78.9%; Pred. No. 6.3e+03;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGGTCATTAGACCGTACGC 19  
 Db 7 CGTCCCTTAGACCGACGC 25

RESULT 18  
 US-10-098-263B-56048  
 Sequence 56048, Application US/10098263B  
 Publication No. US20030104410A1  
 GENERAL INFORMATION:  
 APPLICANT: Mittman, Michael  
 TITLE OF INVENTION: Human Microarray  
 FILE REFERENCE: 3118.1  
 CURRENT APPLICATION NUMBER: US/10/098,263B  
 CURRENT FILING DATE: 2003-01-08  
 PRIOR APPLICATION NUMBER: 60/276,759  
 PRIOR FILING DATE: 2001-03-16  
 NUMBER OF SEQ ID NOS: 131066  
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 SEQ ID NO 56048  
 LENGTH: 25  
 TYPE: DNA  
 ORGANISM: Homo sapien  
 US-10-098-263B-56048

Query Match 60.0%; Score 12.6; DB 15; Length 25;  
 Best Local Similarity 78.9%; Pred. No. 6.3e+03;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GTCATTAGACCGTACGGCA 21  
 Db 6 GTCATTACACGGTTCGA 24

RESULT 19  
 US-10-098-263B-118819/c  
 Sequence 118819, Application US/10098263B  
 Publication No. US20030104410A1  
 GENERAL INFORMATION:  
 APPLICANT: Mittman, Michael  
 TITLE OF INVENTION: Human Microarray  
 FILE REFERENCE: 3118.1  
 CURRENT APPLICATION NUMBER: US/10/098,263B  
 CURRENT FILING DATE: 2003-01-08  
 PRIOR APPLICATION NUMBER: 60/276,759  
 PRIOR FILING DATE: 2001-03-16  
 NUMBER OF SEQ ID NOS: 131066  
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 SEQ ID NO 118819  
 LENGTH: 25  
 TYPE: DNA  
 ORGANISM: Homo sapien  
 US-10-098-263B-118819

Query Match 60.0%; Score 12.6; DB 15; Length 25;  
 Best Local Similarity 78.9%; Pred. No. 6.3e+03;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGGTCATTAGACCGTACGC 19  
 Db 21 CTGTCATTGACCGCACAC 3

RESULT 20  
 US-10-098-263B-118820/c  
 Sequence 118820, Application US/10098263B  
 Publication No. US20030104410A1  
 GENERAL INFORMATION:  
 APPLICANT: Mittman, Michael  
 TITLE OF INVENTION: Human Microarray  
 FILE REFERENCE: 3118.1  
 CURRENT APPLICATION NUMBER: US/10/098,263B  
 CURRENT FILING DATE: 2003-01-08  
 PRIOR APPLICATION NUMBER: 60/276,759  
 PRIOR FILING DATE: 2001-03-16  
 NUMBER OF SEQ ID NOS: 131066  
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 SEQ ID NO 118820  
 LENGTH: 25  
 TYPE: DNA  
 ORGANISM: Homo sapien  
 US-10-098-263B-118820

Query Match 60.0%; Score 12.6; DB 15; Length 25;  
 Best Local Similarity 78.9%; Pred. No. 6.3e+03;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGGTCATTAGACCGTACGC 19  
 Db 21 CTGTCATTGACCGCACAC 3

RESULT 21  
 US-09-864-785-3885/c  
 Sequence 3885, Application US/09864785  
 Patent No. US2002017568A1  
 GENERAL INFORMATION:  
 APPLICANT: Ribozyme Pharmaceuticals, Inc.  
 APPLICANT: Stinchcomb, Dan  
 APPLICANT: Draper, Ken  
 APPLICANT: McSwiggen, Jim  
 TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related  
 FILE REFERENCE: 400/022 (MBH00-812-D)  
 CURRENT APPLICATION NUMBER: US/09/864,785  
 CURRENT FILING DATE: 2001-05-23  
 NUMBER OF SEQ ID NOS: 3929  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 3885  
 LENGTH: 36  
 TYPE: RNA  
 ORGANISM: Artificial Sequence

FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
 NAME/KEY: misc feature  
 LOCATION: (1)..(4)  
 OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage  
 NAME/KEY: misc feature  
 LOCATION: (1)..(16)  
 OTHER INFORMATION: 2'-O-Methyl  
 NAME/KEY: misc feature  
 LOCATION: (18)..(23)  
 OTHER INFORMATION: 2'-O-Methyl  
 NAME/KEY: misc feature  
 LOCATION: (25)..(26)  
 OTHER INFORMATION: 2'-O-Methyl  
 NAME/KEY: misc feature  
 LOCATION: (28)..(35)  
 OTHER INFORMATION: 2'-O-Methyl  
 NAME/KEY: misc feature  
 LOCATION: (17)..(17)  
 OTHER INFORMATION: 2'-deoxy-2'-Amino  
 NAME/KEY: misc feature  
 LOCATION: (27)..(27)



;  
; OTHER INFORMATION: 2'-deoxy-2'-Amino  
; NAME/KEY: misc\_feature  
; LOCATION: (36)..(36)  
; OTHER INFORMATION: n stands for inverted deoxyabasic derivative  
US-09-864-785-3885

Query Match 60.0%; Score 12.6; DB 9; Length 36;  
Best Local Similarity 78.9%; Pred. No. 6.5e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGTCATTAGACGTACGCG 20  
Db 35 GGCCATTAGACCTCACTCG 17

RESULT 22  
US-09-864-785-1812/c  
; Sequence 1812, Application US/09864785  
; Patent No. US20020177568A1

;  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Draper, Ken  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related  
; FILE REFERENCE: Levels of NP-Kappa B  
; FILE REFERENCE: 400/022 (MBH800-812-D)  
; CURRENT APPLICATION NUMBER: US/09/864,785  
; CURRENT FILING DATE: 2001-05-23  
; NUMBER OF SEQ ID NOS: 3929  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1812  
; LENGTH: 37  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid  
US-09-864-785-1812

Query Match 60.0%; Score 12.6; DB 9; Length 37;  
Best Local Similarity 78.9%; Pred. No. 6.5e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGTCATTAGACGTACGCG 20  
Db 36 GGCCATTAGACCTCACTCG 18

RESULT 23  
US-09-740-332-9583  
; Sequence 9583, Application US/09740332  
; Publication No. US20030125270A1

;  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related  
; FILE REFERENCE: RPI 400/003  
; CURRENT APPLICATION NUMBER: US/09/740,332  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9704  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9583  
; LENGTH: 37  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (37)..(37)  
; OTHER INFORMATION: n is an inverted deoxyabasic moiety  
; NAME/KEY: misc\_feature  
; LOCATION: (30)..(30)  
; OTHER INFORMATION: n is inosine  
; NAME/KEY: misc\_feature

;  
; LOCATION: (1)..(7)  
; OTHER INFORMATION: 2'-O-methyl derivative  
; NAME/KEY: misc\_feature  
; LOCATION: (15)..(26)  
; OTHER INFORMATION: 2'-O-methyl derivative  
; NAME/KEY: misc\_feature  
; LOCATION: (31)..(36)  
; OTHER INFORMATION: 2'-O-methyl derivative  
US-09-740-332-9583

Query Match 60.0%; Score 12.6; DB 10; Length 37;  
Best Local Similarity 65.0%; Pred. No. 6.5e+03;  
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGTCATTAGACGTACGCGA 21  
Db 15 GGCCGUUAGCCGAANGCGA 34

RESULT 24

US-09-817-879-9583  
; Sequence 9583, Application US/09817879  
; Publication No. US20030171311A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related  
; FILE REFERENCE: Hepatitis C Virus Infection  
; FILE REFERENCE: MBH800-801-F  
; CURRENT APPLICATION NUMBER: US/09/817,879  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9703  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9583  
; LENGTH: 37  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (37)..(37)  
; OTHER INFORMATION: n is an inverted deoxyabasic moiety  
; NAME/KEY: misc\_feature  
; LOCATION: (30)..(30)  
; OTHER INFORMATION: n is inosine  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(7)  
; OTHER INFORMATION: 2'-O-methyl derivative  
; NAME/KEY: misc\_feature  
; LOCATION: (15)..(26)  
; OTHER INFORMATION: 2'-O-methyl derivative  
; NAME/KEY: misc\_feature  
; LOCATION: (31)..(36)  
; OTHER INFORMATION: 2'-O-methyl derivative  
US-09-817-879-9583

Query Match 60.0%; Score 12.6; DB 10; Length 37;  
Best Local Similarity 65.0%; Pred. No. 6.5e+03;  
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGTCATTAGACGTACGCGA 21  
Db 15 GGCCGUUAGCCGAANGCGA 34

RESULT 25

US-10-138-674-18225/c  
; Sequence 18225, Application US/10138674  
; Publication No. US20040077565A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime

```
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18225
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-138-674-18225

Query Match          60.0%; Score 12.6; DB 16; Length 37;
Best Local Similarity 78.9%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGTCATTAGACCGTACGCG 20
Db 36 GGTCTTTAGACCTCACTCG 18

RESULT 26
US-10-138-674-18462/c
; Sequence 18462, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18462
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-138-674-18462

Query Match          60.0%; Score 12.6; DB 16; Length 37;
Best Local Similarity 78.9%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGTCATTAGACCGTACGCG 20
Db 36 GGTCTTTAGACCTCACTCG 18

RESULT 27
US-10-138-674-20525/c
; Sequence 20525, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
```

```
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20525
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-138-674-20525
```

```
Query Match          60.0%; Score 12.6; DB 16; Length 37;
Best Local Similarity 78.9%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 2 GGTCATTAGACCGTACGCG 20
Db 36 GGTCTTTAGACCTCACTCG 18
```

```
RESULT 28
US-10-287-949A-18225/c
; Sequence 18225, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18225
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-287-949A-18225
```

```
Query Match          60.0%; Score 12.6; DB 17; Length 37;
Best Local Similarity 78.9%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 2 GGTCATTAGACCGTACGCG 20
Db 36 GGTCTTTAGACCTCACTCG 18
```

```
RESULT 29
US-10-287-949A-18462/c
; Sequence 18462, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18462
; LENGTH: 37
; TYPE: RNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-287-949A-18462

Query Match          60.0%; Score 12.6; DB 17; Length 37;
Best Local Similarity 78.9%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy  2  GGTGATTAGACCTCACTCG 20
Db   36  GGTGATTAGACCTCACTCG 18

RESULT 30
US-10-287-949A-20525/c
; Sequence 20525, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20525
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-287-949A-20525

Query Match          60.0%; Score 12.6; DB 17; Length 37;
Best Local Similarity 78.9%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy  2  GGTGATTAGACCTCACTCG 20
Db   36  GGTGATTAGACCTCACTCG 18

RESULT 31
US-10-669-841-16128
; Sequence 16128, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patricia, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPA
; FILE REFERENCE: 400/042US (MHB02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
```

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; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16128
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (37)..(37)
; OTHER INFORMATION: n stands for inverted deoxyabasic derivative
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (30)..(30)
; OTHER INFORMATION: n is inosine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(7)
; OTHER INFORMATION: 2'-O-Methyl
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15)..(26)
; OTHER INFORMATION: 2'-O-Methyl
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (31)..(36)
; OTHER INFORMATION: 2'-O-Methyl
; OTHER INFORMATION: 2'-O-Methyl
US-10-669-841-16128

Query Match          60.0%; Score 12.6; DB 17; Length 37;
Best Local Similarity 65.0%; Pred. No. 6.5e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Oy  2  GGTGATTAGACCTCACTCG 21
Db   15  GGTGATTAGACCTCACTCG 34

RESULT 32
US-09-874-547-83/c
; Sequence 83, Application US/09874547
; Patent No. US20020058269A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020058269A1k, Steffen
; APPLICANT: Kassner, Paul D.
; APPLICANT: Zyomyx, Inc.
; TITLE OF INVENTION: Screening of Phage Displayed Peptides
; FILE REFERENCE: 020144-001110US
; CURRENT APPLICATION NUMBER: US/09/874,547
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/209,503
; PRIOR FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 83
; LENGTH: 38
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primers for ScFv and Fab library generation (Table
; OTHER INFORMATION: I) - MVR24
US-09-874-547-83

Query Match          60.0%; Score 12.6; DB 9; Length 38;
Best Local Similarity 78.9%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY  2  GGTCAATTAGACCGTACGCG 20
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Db   30  GGTCAATCAATGTCGCG 12

RESULT 33
US-09-864-785-1169.
; Sequence 1169, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of NF-Kappa B
; FILE REFERENCE: 400/022 (MBH00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1169
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-864-785-1169

Query Match          60.0%; Score 12.6; DB 9; Length 38;
Best Local Similarity 65.0%; Pred. No. 6.5e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY  2  GGTCAATTAGACCGTACGCG 21
      |||||  |||||
Db   16  GGCCGUUAGGCCGAANGCGA 35

RESULT 34
US-09-780-533A-3557
; Sequence 3557, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00, 878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3557
; LENGTH: 38
; TYPE: RNA
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-780-533A-3557

Query Match          60.0%; Score 12.6; DB 10; Length 38;
Best Local Similarity 65.0%; Pred. No. 6.5e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY  2  GGTCAATTAGACCGTACGCG 21
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Db   16  GGCCGUUAGGCCGAANGCGA 35

RESULT 35
US-09-780-533A-3581
; Sequence 3581, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00, 878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3581
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-780-533A-3581

Query Match          60.0%; Score 12.6; DB 10; Length 38;
Best Local Similarity 65.0%; Pred. No. 6.5e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY  2  GGTCAATTAGACCGTACGCG 21
      |||||  |||||
Db   16  GGCCGUUAGGCCGAANGCGA 35

RESULT 36
US-09-927-046-3026
; Sequence 3026, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric
; TITLE OF INVENTION: Channel-1
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3026
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-927-046-3026

Query Match          60.0%; Score 12.6; DB 10; Length 38;
Best Local Similarity 65.0%; Pred. No. 6.5e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy      2  GGTCAATTAGACCGTAGCGCA 21
Db      16  GCGCGUAGGCCGAANGCGCA 35

RESULT 37
US-09-927-046-3197
; Sequence 3197, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloride Channel-1
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3197
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-927-046-3197

Query Match          60.0%; Score 12.6; DB 10; Length 38;
Best Local Similarity 65.0%; Pred. No. 6.5e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy      2  GGTCAATTAGACCGTAGCGCA 21
Db      16  GCGCGUAGGCCGAANGCGCA 35

RESULT 38
US-09-927-478-3468
; Sequence 3468, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBHB00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3468
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-877-478-3468

Query Match          60.0%; Score 12.6; DB 10; Length 38;
Best Local Similarity 65.0%; Pred. No. 6.5e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy      2  GGTCAATTAGACCGTAGCGCA 21
Db      16  GCGCGUAGGCCGAANGCGCA 35

RESULT 39
US-09-877-478-3764
; Sequence 3764, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBHB00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3764
; LENGTH: 38
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Wed Nov 24 08:46:00 2004

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; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-877-478-3764

Query Match          60.0%; Score 12.6; DB 10; Length 38;
Best Local Similarity 65.0%; Pred. No. 6.5e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      2 GGTCAATTAGACCGTACGCGA 21
Db      16 GGCCGUUAGCGCGAANGCGA 35
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RESULT 40
US-09-848-754A-5094
; Sequence 5094, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MEHB00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5094
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid
; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-848-754A-5094

Query Match          60.0%; Score 12.6; DB 10; Length 38;
Best Local Similarity 65.0%; Pred. No. 6.5e+03;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      2 GGTCAATTAGACCGTACGCGA 21
Db      16 GGCCGUUAGCGCGAANGCGA 35
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Search completed: November 24, 2004, 03:43:10  
Job time : 99.5719 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:59:28 ; Search time 1006.82 Seconds  
(without alignments)  
760.051 Million cell updates/sec

Title: US-10-087-631B-17

Perfect score: 21  
Sequence: 1 cggcttagaccgtacgcga 21

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 158194

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : EST.\*

- 1: gb\_est1.\*
- 2: gb\_est2.\*
- 3: gb\_hic.\*
- 4: gb\_est3.\*
- 5: gb\_est4.\*
- 6: gb\_est5.\*
- 7: gb\_est6.\*
- 8: gb\_gss1.\*
- 9: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 2	12.2	58.1	50	1	AW004201
c 3	12	57.1	33	6	CF338319
c 4	11.6	55.2	36	5	BQ592384
c 5	11.6	55.2	43	8	BH903257
c 6	11.4	54.3	29	9	CL660557
c 7	11.4	54.3	39	9	CL293866
c 8	11.4	54.3	50	1	AU106620
c 9	11.4	54.3	50	1	AU106626
c 10	11.2	53.3	31	8	BH615074
c 11	11.2	53.3	43	9	CL303319
c 12	11.2	53.3	45	9	BX287629
c 13	11.2	53.3	45	9	BX650703
c 14	11.2	53.3	46	8	AZ583945
c 15	11.2	53.3	49	9	CG774856
c 16	11	52.4	42	9	AL754718
c 17	11	52.4	47	9	AL939959
c 18	11	52.4	48	8	BH895527
c 19	10.8	51.4	32	4	B1223057
c 20	10.8	51.4	36	8	BH810122
c 21	10.8	51.4	36	8	BH810143
c 22	10.8	51.4	36	9	CH360542
c 23	10.8	51.4	44	9	CL524591
c 24	10.8	51.4	45	9	AG192385

C 98 9.8 46.7 37 1 AA765049  
C 99 9.8 46.7 38 1 AJ803928  
C 100 9.8 46.7 39 8 BZ289706 SALK 0231  
C 101 9.8 46.7 39 8 CC053623 SALK 0458  
C 102 9.8 46.7 40 5 BX564806 BX564806  
C 103 9.8 46.7 40 8 BZ287846 SALK 0212  
C 104 9.8 46.7 40 9 AL759372 Arabidops  
C 105 9.8 46.7 41 8 BH863752 SALK 0944  
C 106 9.8 46.7 41 8 BH863753 SALK 0944  
C 107 9.8 46.7 41 8 BH864990 SALK 0972  
C 108 9.8 46.7 42 6 CD530457 06G12 Ara  
C 109 9.8 46.7 43 1 AI196640 uis3d01.y  
C 110 9.8 46.7 44 9 TA130E32Q  
C 111 9.8 46.7 44 9 CL528344 ASV25C07.  
C 112 9.8 46.7 45 8 BZ384047 SALK 1349  
C 113 9.8 46.7 45 9 CL002876 02S0169-0  
C 114 9.8 46.7 46 1 AA736376 zg77a12.s  
C 115 9.8 46.7 46 8 BZ770587 SALK 1435  
C 116 9.8 46.7 46 8 CC027411 3591\_1\_5  
C 117 9.8 46.7 47 9 AL758197 Arabidops  
C 118 9.8 46.7 48 1 AI313698 EST010 Mo  
C 119 9.8 46.7 49 1 AI359268 qy27c06.x  
C 120 9.8 46.7 49 1 AA124225 mp98d08.r  
C 121 9.8 46.7 49 1 AV833344 AV833344  
C 122 9.8 46.7 49 6 CC0961 HUMGS00331  
C 123 9.8 46.7 49 9 CR402941 Arabidops  
C 124 9.8 46.7 49 9 CR402942 Arabidops  
C 125 9.8 46.7 50 1 AU104155 Arabidops  
C 126 9.8 46.7 50 1 AU105980 Arabidops  
C 127 9.8 46.7 50 1 AU106625 Arabidops  
C 128 9.8 46.7 50 9 BX945487 Arabidops  
C 129 9.8 46.7 50 9 BM397712 5009-0-35  
C 130 9.6 45.7 24 8 CC458426 SALK 1187  
C 131 9.6 45.7 27 9 TA143H1LP  
C 132 9.6 45.7 30 8 BH849994 SALK 0706  
C 133 9.6 45.7 31 1 AU258240 AU258240  
C 134 9.6 45.7 31 7 D18722 MUSGS01784  
C 135 9.6 45.7 31 8 BH810158 SALK 0414  
C 136 9.6 45.7 34 9 TA124F07P  
C 137 9.6 45.7 35 2 BE275280 Arabidops  
C 138 9.6 45.7 38 8 BH613959 SALK 0352  
C 139 9.6 45.7 40 4 BJ060137 Arabidops  
C 140 9.6 45.7 40 8 BH911408 SALK 0684  
C 141 9.6 45.7 40 9 TA71C08Q Arabidops  
C 142 9.6 45.7 41 7 CN755514 ID0AA16A  
C 143 9.6 45.7 41 8 BH908133 SALK 0458  
C 144 9.6 45.7 41 9 CNS07FPE Arabidops  
C 145 9.6 45.7 42 9 AL763403 Arabidops  
C 146 9.6 45.7 43 9 AG217405 Drosophil  
C 147 9.6 45.7 44 8 BH172536 SALK 0058  
C 148 9.6 45.7 44 8 BH214294 SALK 0105  
C 149 9.6 45.7 44 8 BH252344 SALK 0131  
C 150 9.6 45.7 44 8 BH612495 SALK 0328  
C 151 9.6 45.7 44 8 BH635702 SALK 0140  
C 152 9.6 45.7 44 8 DR102GGS Arabidops  
C 153 9.6 45.7 44 8 BH752299 SALK 0140  
C 154 9.6 45.7 45 8 CC023725 3591\_1\_36  
C 155 9.6 45.7 45 7 CN758478 ID0AA22B  
C 156 9.6 45.7 46 8 BH610910 SALK 0182  
C 157 9.6 45.7 46 9 AB081994 Arabidops  
C 158 9.6 45.7 47 9 CL523386 Drosophil  
C 159 9.6 45.7 48 4 BG253356 602362952  
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C 162 9.6 45.7 48 9 TA194C12Q Arabidops  
C 163 9.6 45.7 50 1 AU102458 Arabidops  
C 164 9.6 45.7 50 1 AU103408 Arabidops  
C 165 9.6 45.7 50 1 AU106624 Arabidops  
C 166 9.6 45.7 50 1 AV969171 Arabidops  
C 167 9.6 45.7 50 4 BG222716 nah37e07.  
C 168 9.4 44.8 27 8 AZ794090 2M0047009  
C 169 9.4 44.8 27 8 BZ378105 SALK 1071  
C 170 9.4 44.8 29 1 AU007063 Arabidops

C 171 9.4 44.8 29 9 CL685499 Arabidops  
C 172 9.4 44.8 31 1 AU266472 Arabidops  
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C 176 9.4 44.8 34 1 AI185295 qz36b09.s  
C 177 9.4 44.8 34 1 AU007062 Arabidops  
C 178 9.4 44.8 34 8 BH911674 SALK 0714  
C 179 9.4 44.8 35 8 AZ591995 1M0402F06  
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C 181 9.4 44.8 35 9 CG709475 1110913C1  
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C 183 9.4 44.8 36 9 TA38H05P Arabidops  
C 184 9.4 44.8 37 9 DR68G5T Arabidops  
C 185 9.4 44.8 37 9 TA3SD05P Arabidops  
C 186 9.4 44.8 37 9 CC797773 SALK 1453  
C 187 9.4 44.8 38 5 BX559481 Arabidops  
C 188 9.4 44.8 38 9 CNS07FAG Arabidops  
C 189 9.4 44.8 39 9 BX650160 Arabidops  
C 190 9.4 44.8 39 9 TA38H06P Arabidops  
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C 192 9.4 44.8 40 8 BH900955 KGO7812-3  
C 193 9.4 44.8 40 9 CR361442 Arabidops  
C 194 9.4 44.8 41 5 BU637476 mgcw003xJ  
C 195 9.4 44.8 42 8 AZ806216 2M0068D09  
C 196 9.4 44.8 42 9 TA157C05P Arabidops  
C 197 9.4 44.8 42 9 CL265604 02S0166-0  
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C 200 9.4 44.8 44 4 B1829988 603080234  
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C 202 9.4 44.8 44 8 CC455081 SALK 0476  
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C 204 9.4 44.8 44 9 CC797754 SALK 1453  
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C 206 9.4 44.8 45 8 BH908303 SALK 0471  
C 207 9.4 44.8 46 6 BH902367 Arabidops  
C 208 9.4 44.8 47 6 CB305190 3'EST-Nf1  
C 209 9.4 44.8 47 9 CG466461 01S0600-0  
C 210 9.4 44.8 48 2 BE738353 601572748  
C 211 9.4 44.8 48 4 BJ083470 BJ083470  
C 212 9.4 44.8 48 5 BU582005 195 Oryct  
C 213 9.4 44.8 48 8 AQ026317 Arabidops  
C 214 9.4 44.8 48 8 BH865457 SALK 0985  
C 215 9.4 44.8 48 8 BH866365 SALK 1012  
C 216 9.4 44.8 48 9 BX204287 Arabidops  
C 217 9.4 44.8 48 9 CR399068 Arabidops  
C 218 9.4 44.8 48 9 CG808438 Arabidops  
C 219 9.4 44.8 49 4 BJ040441 Arabidops  
C 220 9.4 44.8 49 9 TA101C02Q Arabidops  
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C 222 9.4 44.8 49 9 AU103207 Arabidops  
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C 227 9.4 44.8 50 1 AU106578 Arabidops  
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C 229 9.4 44.8 50 1 AU107230 Arabidops  
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C 231 9.4 44.8 50 2 AW630853 Arabidops  
C 232 9.4 44.8 50 4 BF708333 Arabidops  
C 233 9.4 44.8 50 7 CF641166 D36\_E05 F  
C 234 9.4 44.8 50 9 AJ588199 Arabidops  
C 235 9.4 44.8 50 9 TA154F10Q Arabidops  
C 236 9.4 44.8 50 9 AZ372259 1M0124J02  
C 237 9.2 43.8 22 8 AZ496170 1M0332N13  
C 238 9.2 43.8 22 8 AZ840154 2M0136N05  
C 239 9.2 43.8 23 8 A2840154 Arabidops  
C 240 9.2 43.8 25 1 AU1000280 Arabidops  
C 241 9.2 43.8 26 9 AJ595210 Arabidops  
C 242 9.2 43.8 27 1 AU254174 Arabidops  
C 243 9.2 43.8 27 7 D18735 MUSGS01797

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AL453570 T. brucei  
AL975855 Danio rer  
AL453874 T. brucei  
CC797773 SALK 1453  
BX559481 Arabidops  
AL608218 Anopheles  
BX650160 Arabidops  
AL497739 T. brucei  
CC796635 SALK 1362  
BH900955 KGO7812-3  
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B1829988 603080234  
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CO789074 NT005D\_H0  
CO26317 1(3)J4A6  
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BH866365 SALK 1012  
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BF708333 tt46c02.y  
CF641166 D36\_E05 F  
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AU1000280 cv10e04.s  
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AU254174 Arabidops  
D18735 MUSGS01797



244	9.2	43.8	27	8	AZ427088	AZ427088	1M0208B24	C 317	9.2	43.8	50	1	AU105480	AU105480
245	9.2	43.8	27	8	AZ8110485	AZ8110485	1M007GH05	C 318	9.2	43.8	50	1	AU108048	AU108048
C 246	9.2	43.8	28	8	AZ441205	AZ441205	1M0023B10	C 319	9.2	43.8	50	5	BX722422	BX722422
247	9.2	43.8	29	1	AJ674160	AJ674160	AR437050	C 320	9.2	43.8	50	7	CR437050	CR437050
248	9.2	43.8	29	1	AJ594026	AJ594026	Arabidops	C 321	9.2	43.8	50	9	BX977848	Forward s
249	9.2	43.8	29	9	AG198112	AG198112	Pan trogl	C 322	9.2	43.8	50	9	CR209280	Forward s
C 250	9.2	43.8	30	7	CF543220	CF543220	S014680-0	C 323	9.2	43.8	50	9	CL519142	SAG6G09 F
C 251	9.2	43.8	30	8	AZ431038	AZ431038	1M0215115	C 324	9	42.9	21	8	AZ592202	1M0402L19
C 252	9.2	43.8	30	8	BZ762449	BZ762449	SALK 1047	C 325	9	42.9	23	8	AZ818662	T. brucei
C 253	9.2	43.8	30	9	CG714388	CG714388	1119036D1	C 326	9	42.9	23	8	AZ818662	2M0088Q14
254	9.2	43.8	32	8	AZ765095	AZ765095	1M0561A22	C 327	9	42.9	23	8	AZ826455	2M0102P09
255	9.2	43.8	32	9	DME545578	DME545578		C 328	9	42.9	24	7	CO785230	BL282D.G0
256	9.2	43.8	34	1	AI125992	AI125992	QC46d12.x	C 329	9	42.9	25	8	AZ605844	1M0427022
C 257	9.2	43.8	34	8	BH907363	BH907363	SALK 0397	C 330	9	42.9	25	8	AZ655084	1M0529C20
C 258	9.2	43.8	34	8	BZ288240	BZ288240	SALK 0216	C 331	9	42.9	25	9	CG714033	1119034F0
C 259	9.2	43.8	35	8	AZ820699	AZ820699	2M0093102	C 332	9	42.9	25	9	CG723016	1119074D0
C 260	9.2	43.8	35	9	TA103A09Q	TA103A09Q		C 333	9	42.9	27	8	AZ831609	2M0111M19
C 261	9.2	43.8	37	9	DR108338	DR108338	Danio rer	C 334	9	42.9	27	9	AJ587528	Arabidops
C 262	9.2	43.8	38	1	AU260238	AU260238	AU260238	C 335	9	42.9	27	9	AJ587528	Arabidops
C 263	9.2	43.8	38	8	AZ659279	AZ659279	1M0536102	C 336	9	42.9	27	9	CG713831	T. brucei
C 264	9.2	43.8	39	8	BH809708	BH809708	SALK 0050	C 337	9	42.9	28	1	AI573848	uj17a12.x
C 265	9.2	43.8	39	8	BH908228	BH908228	SALK 0465	C 338	9	42.9	28	1	AJ795430	AJ795430
C 266	9.2	43.8	40	8	BZ589975	BZ589975	3590_1.73	C 339	9	42.9	28	8	AZ780159	2M0017C13
267	9.2	43.8	40	9	CL523373	CL523373	DAL2H04 F	C 340	9	42.9	29	8	BH846511	SALK 0085
C 268	9.2	43.8	41	1	AZ253540	AZ253540	SWMFCAL43	C 341	9	42.9	31	1	AI346598	qp51h06.x
C 269	9.2	43.8	41	8	AZ774470	AZ774470	2M0003P13	C 342	9	42.9	31	1	AU266417	AU266417
C 270	9.2	43.8	41	8	BZ765629	BZ765629	SALK 1319	C 343	9	42.9	31	6	CF335931	JMT--05-M
271	9.2	43.8	41	9	TA151G10Q	TA151G10Q		C 344	9	42.9	31	8	BZ382978	SALK 1192
272	9.2	43.8	42	8	AZ666806	AZ666806	1M0549N10	C 345	9	42.9	31	9	BX8931918	Arabidops
273	9.2	43.8	43	1	AA815634	AA815634	vt03d02.r	C 346	9	42.9	31	9	TA65G01Q	T. brucei
C 274	9.2	43.8	43	1	AA921653	AA921653	vy22d03.r	C 347	9	42.9	32	6	CD534487	39119 Ara
C 275	9.2	43.8	44	8	AZ646714	AZ646714	1M0512D21	C 348	9	42.9	32	8	AZ491344	1M0324B22
C 276	9.2	43.8	44	9	TA372A04P	TA372A04P		C 349	9	42.9	32	8	AZ799655	2M0057C15
277	9.2	43.8	45	9	CG892752	CG892752	0150617-0	C 350	9	42.9	32	8	BZ358744	SALK 1332
C 278	9.2	43.8	46	1	AI884160	AI884160	fc74e12.x	C 351	9	42.9	33	1	AJ590509	Arabidops
C 279	9.2	43.8	46	1	AA625631	AA625631	ad10d01.s	C 352	9	42.9	33	1	AJ647516	AJ647516
C 280	9.2	43.8	46	9	AJ591587	AJ591587	Arabidops	C 353	9	42.9	33	8	BH849814	SALK 0703
C 281	9.2	43.8	46	9	CR360032	CR360032	Arabidops	C 354	9	42.9	33	9	CG722737	1119073C0
C 282	9.2	43.8	47	4	BI089840	BI089840	602855085	C 355	9	42.9	33	8	BH251010	SALK 0108
C 283	9.2	43.8	47	8	AQ026076	AQ026076	1(2)k1420	C 356	9	42.9	35	8	BH253542	SALK 0150
C 284	9.2	43.8	47	8	BH813914	BH813914	SALK 0654	C 357	9	42.9	35	8	BH613670	SALK 0347
C 285	9.2	43.8	47	8	BH846892	BH846892		C 358	9	42.9	35	8	BH617331	SALK 0363
C 286	9.2	43.8	47	9	DME545407	DME545407		C 359	9	42.9	35	8	BH617681	SALK 0374
C 287	9.2	43.8	47	9	AG197950	AG197950	Pan trogl	C 360	9	42.9	35	8	BH618593	SALK 0393
C 288	9.2	43.8	48	4	BJ083470	BJ083470		C 361	9	42.9	35	8	BH751605	SALK 0503
C 289	9.2	43.8	48	9	CR358002	CR358002	Arabidops	C 362	9	42.9	35	8	BH753496	SALK 0292
C 290	9.2	43.8	49	1	AI109169	AI109169	mp38f04.x	C 363	9	42.9	35	8	BH854633	KG06875-5
C 291	9.2	43.8	49	4	BZ292262	BZ292262	602386710	C 364	9	42.9	35	9	TA248D1Q	T. brucei
C 292	9.2	43.8	49	4	BI760726	BI760726	603044726	C 365	9	42.9	36	7	T61825	Yp92a04.81
C 293	9.2	43.8	49	8	CC325828	CC325828	RRG292.Ba	C 366	9	42.9	36	8	BH751713	SALK 0505
C 294	9.2	43.8	49	9	CG779221	CG779221	1123032D0	C 367	9	42.9	36	9	CG713884	1119033H1
C 295	9.2	43.8	49	9	AG190566	AG190566	Pan trogl	C 368	9	42.9	36	9	CG714202	1119035E0
C 296	9.2	43.8	50	1	AI920149	AI920149	1679.Pine	C 369	9	42.9	36	9	CG714303	1119036A1
C 297	9.2	43.8	50	1	AU102923	AU102923		C 370	9	42.9	37	1	AU010468	AU010468
C 298	9.2	43.8	50	1	AU102930	AU102930		C 371	9	42.9	37	1	AU010469	AU010469
C 299	9.2	43.8	50	1	AU102933	AU102933		C 372	9	42.9	37	8	BH211687	SALK 0065
C 300	9.2	43.8	50	1	AU102934	AU102934		C 373	9	42.9	37	8	BH211761	SALK 0066
C 301	9.2	43.8	50	1	AU102935	AU102935		C 374	9	42.9	37	8	BH212711	SALK 0079
C 302	9.2	43.8	50	1	AU102936	AU102936		C 375	9	42.9	37	8	BH213109	SALK 0086
C 303	9.2	43.8	50	1	AU102937	AU102937		C 376	9	42.9	37	8	BH254171	SALK 0161
C 304	9.2	43.8	50	1	AU102947	AU102947		C 377	9	42.9	37	8	BH612755	SALK 0332
C 305	9.2	43.8	50	1	AU102948	AU102948		C 378	9	42.9	37	8	BH613685	SALK 0347
C 306	9.2	43.8	50	1	AU102954	AU102954		C 379	9	42.9	37	8	BH613909	SALK 0351
C 307	9.2	43.8	50	1	AU103589	AU103589		C 380	9	42.9	37	8	BH613940	SALK 0352
C 308	9.2	43.8	50	1	AU104153	AU104153		C 381	9	42.9	37	8	BH617568	SALK 0372
C 309	9.2	43.8	50	1	AU104179	AU104179		C 382	9	42.9	37	8	BH617569	SALK 0372
C 310	9.2	43.8	50	1	AU104207	AU104207		C 383	9	42.9	37	8	BH633214	SALK 0410
C 311	9.2	43.8	50	1	AU105472	AU105472		C 384	9	42.9	37	8	BH751779	SALK 0506
C 312	9.2	43.8	50	1	AU105473	AU105473		C 385	9	42.9	37	8	BH751802	SALK 0506
C 313	9.2	43.8	50	1	AU105474	AU105474		C 386	9	42.9	37	8	BH791757	SALK 0611
C 314	9.2	43.8	50	1	AU105475	AU105475		C 387	9	42.9	37	9	CG711288	1119020G1
C 315	9.2	43.8	50	1	AU105476	AU105476		C 388	9	42.9	37	9	CG7113746	1119033C0
C 316	9.2	43.8	50	1	AU105479	AU105479		C 389	9	42.9	37	9	CG722734	1119073C0

C 390	9	42.9	37	9	CG724536	CG724536	1119081F0	C 463	9	42.9	44	8	BH172646	BH172646	SALK_0059
C 391	9	42.9	38	4	BM400755	5009-0-78		C 464	9	42.9	44	8	BH172689	BH172689	SALK_0060
C 392	9	42.9	38	8	BH170263	BH170263	SALK_0026	C 465	9	42.9	44	8	BH173144	BH173144	SALK_0070
C 393	9	42.9	38	8	BH611224	SALK_0304		C 466	9	42.9	44	8	BH212259	BH212259	SALK_0073
C 394	9	42.9	38	8	BH612424	SALK_0326		C 467	9	42.9	44	8	BH212377	BH212377	SALK_0075
C 395	9	42.9	38	8	BH792093	SALK_0626		C 468	9	42.9	44	8	BH212514	BH212514	SALK_0076
C 396	9	42.9	38	9	EX287919	Arabidops		C 469	9	42.9	44	8	BH213282	BH213282	SALK_0090
C 397	9	42.9	38	9	CG729929	1119116E0		C 470	9	42.9	44	8	BH251475	BH251475	SALK_0116
C 398	9	42.9	39	4	BG112163	602283080		C 471	9	42.9	44	8	BH251575	BH251575	SALK_0118
C 399	9	42.9	39	4	BI660394	603302045		C 472	9	42.9	44	8	BH251615	BH251615	SALK_0121
C 400	9	42.9	39	4	BH212311	SALK_0074		C 473	9	42.9	44	8	BH251830	BH251830	SALK_0123
C 401	9	42.9	39	8	BH212359	SALK_0074		C 474	9	42.9	44	8	BH251946	BH251946	SALK_0128
C 402	9	42.9	39	8	BH751820	SALK_0506		C 475	9	42.9	44	8	BH252164	BH252164	SALK_0129
C 403	9	42.9	39	8	CG713665	1119032D0		C 476	9	42.9	44	8	BH252206	BH252206	SALK_0129
C 404	9	42.9	40	1	AI613042	ty06h09.x		C 477	9	42.9	44	8	BH252225	BH252225	SALK_0130
C 405	9	42.9	40	1	AI805437	tx96e03.x		C 478	9	42.9	44	8	BH252253	BH252253	SALK_0130
C 406	9	42.9	40	8	BH212182	SALK_0072		C 479	9	42.9	44	8	BH252260	BH252260	SALK_0130
C 407	9	42.9	40	8	BH212218	SALK_0072		C 480	9	42.9	44	8	BH252506	BH252506	SALK_0135
C 408	9	42.9	40	8	BH613805	SALK_0349		C 481	9	42.9	44	8	BH252718	BH252718	SALK_0137
C 409	9	42.9	40	8	BH751640	SALK_0504		C 482	9	42.9	44	8	BH252848	BH252848	SALK_0138
C 410	9	42.9	40	9	EX572583	Arabidops		C 483	9	42.9	44	8	BH252865	BH252865	SALK_0139
C 411	9	42.9	40	9	CG796357	SALK_1294		C 484	9	42.9	44	8	BH253523	BH253523	SALK_0150
C 412	9	42.9	40	9	CG729877	1119116B0		C 485	9	42.9	44	8	BH253838	BH253838	SALK_0155
C 413	9	42.9	41	1	AV834393	AV834393		C 486	9	42.9	44	8	BH254181	BH254181	SALK_0161
C 414	9	42.9	41	8	AQ025324	EP(X)0362		C 487	9	42.9	44	8	BH254446	BH254446	SALK_0165
C 415	9	42.9	41	8	AZ454047	1M0255015		C 488	9	42.9	44	8	BH254727	BH254727	SALK_0171
C 416	9	42.9	41	8	AZ475800	1M0294G10		C 489	9	42.9	44	8	BH611523	BH611523	SALK_0310
C 417	9	42.9	41	8	AZ773365	1M0584A20		C 490	9	42.9	44	8	BH611569	BH611569	SALK_0311
C 418	9	42.9	41	8	BH252552	SALK_0163		C 491	9	42.9	44	8	BH611657	BH611657	SALK_0315
C 419	9	42.9	41	8	BH254298	SALK_0163		C 492	9	42.9	44	8	BH611723	BH611723	SALK_0316
C 420	9	42.9	41	8	BH610796	SALK_0180		C 493	9	42.9	44	8	BH611974	BH611974	SALK_0319
C 421	9	42.9	41	8	BH611601	SALK_0312		C 494	9	42.9	44	8	BH612122	BH612122	SALK_0321
C 422	9	42.9	41	8	BH614048	SALK_0353		C 495	9	42.9	44	8	BH612168	BH612168	SALK_0322
C 423	9	42.9	41	8	BH749252	SALK_0475		C 496	9	42.9	44	8	BH612218	BH612218	SALK_0323
C 424	9	42.9	41	8	BH751659	SALK_0268		C 497	9	42.9	44	8	BH612350	BH612350	SALK_0325
C 425	9	42.9	41	8	BZ663233	SALK_0268		C 498	9	42.9	44	8	BH612910	BH612910	SALK_0334
C 426	9	42.9	41	8	DM547498	T. brucei		C 499	9	42.9	44	8	BH613025	BH613025	SALK_0336
C 427	9	42.9	41	9	TAL13C04P	AL465339		C 500	9	42.9	44	8	BH613027	BH613027	SALK_0336
C 428	9	42.9	42	8	BH611542	SALK_0311		C 501	9	42.9	44	8	BH613209	BH613209	SALK_0339
C 429	9	42.9	42	8	BH624495	SALK_0376		C 502	9	42.9	44	8	BH613323	BH613323	SALK_0339
C 430	9	42.9	42	8	BH750272	SALK_0306		C 503	9	42.9	44	8	BH613425	BH613425	SALK_0342
C 431	9	42.9	42	8	BH751578	SALK_0503		C 504	9	42.9	44	8	BH613572	BH613572	SALK_0342
C 432	9	42.9	42	8	AL765989	Arabidops		C 505	9	42.9	44	8	BH617039	BH617039	SALK_0358
C 433	9	42.9	42	9	CG729941	1119116F0		C 506	9	42.9	44	8	BH617095	BH617095	SALK_0359
C 434	9	42.9	42	9	CL705862	EY00848-3		C 507	9	42.9	44	8	BH617247	BH617247	SALK_0361
C 435	9	42.9	43	1	AA928331	OM76c12.s		C 508	9	42.9	44	8	BH617442	BH617442	SALK_0365
C 436	9	42.9	43	1	AI657864	fc14605.y		C 509	9	42.9	44	8	BH617453	BH617453	SALK_0365
C 437	9	42.9	43	1	AA241931	mx26a04.f		C 510	9	42.9	44	8	BH617506	BH617506	SALK_0371
C 438	9	42.9	43	1	AA549203	VK85Q08.s		C 511	9	42.9	44	8	BH617771	BH617771	SALK_0377
C 439	9	42.9	43	1	BH173048	SALK_0014		C 512	9	42.9	44	8	BH617921	BH617921	SALK_0381
C 440	9	42.9	43	8	BH254096	SALK_0159		C 513	9	42.9	44	8	BH617944	BH617944	SALK_0381
C 441	9	42.9	43	8	BH611286	SALK_0306		C 514	9	42.9	44	8	BH618166	BH618166	SALK_0386
C 442	9	42.9	43	8	BH611477	SALK_0309		C 515	9	42.9	44	8	BH618486	BH618486	SALK_0391
C 443	9	42.9	43	8	BH612999	SALK_0336		C 516	9	42.9	44	8	BH618549	BH618549	SALK_0392
C 444	9	42.9	43	8	BH613221	SALK_0339		C 517	9	42.9	44	8	BH618610	BH618610	SALK_0394
C 445	9	42.9	43	8	BH617226	SALK_0361		C 518	9	42.9	44	8	BH633222	BH633222	SALK_0410
C 446	9	42.9	43	8	BH617444	SALK_0365		C 519	9	42.9	44	8	BH634244	BH634244	SALK_0449
C 447	9	42.9	43	8	BH750703	SALK_0001		C 520	9	42.9	44	8	BH750166	BH750166	SALK_0371
C 448	9	42.9	44	8	BH168728	SALK_0002		C 521	9	42.9	44	8	BH750554	BH750554	SALK_0416
C 449	9	42.9	44	8	BH168811	SALK_0003		C 522	9	42.9	44	8	BH751355	BH751355	SALK_0500
C 450	9	42.9	44	8	BH168944	SALK_0004		C 523	9	42.9	44	8	BH752016	BH752016	SALK_0516
C 451	9	42.9	44	8	BH168955	SALK_0004		C 524	9	42.9	44	8	BH752121	BH752121	SALK_0517
C 452	9	42.9	44	8	BH169147	SALK_0007		C 525	9	42.9	44	8	BH752219	BH752219	SALK_0517
C 453	9	42.9	44	8	BH169189	SALK_0014		C 526	9	42.9	44	8	BH752319	BH752319	SALK_0140
C 454	9	42.9	44	8	BH169506	SALK_0019		C 527	9	42.9	44	8	BH752319	BH752319	SALK_0140
C 455	9	42.9	44	8	BH169809	SALK_0020		C 528	9	42.9	44	8	BH752350	BH752350	SALK_0141
C 456	9	42.9	44	8	BH169920	SALK_0029		C 529	9	42.9	44	8	BH752481	BH752481	SALK_0187
C 457	9	42.9	44	8	BH170451	SALK_0041		C 530	9	42.9	44	8	BH752619	BH752619	SALK_0189
C 458	9	42.9	44	8	BH171381	SALK_0041		C 531	9	42.9	44	8	BH908840	BH908840	SALK_0507
C 459	9	42.9	44	8	BH171826	SALK_0048		C 532	9	42.9	44	9	AL757126	AL757126	Arabidops
C 460	9	42.9	44	8	BH172056	SALK_0051		C 533	9	42.9	44	9	CG714300	CG714300	SALK_0516
C 461	9	42.9	44	8	BH172538	SALK_0058		C 534	9	42.9	44	9	CG724480	CG724480	SALK_0516
C 462	9	42.9	44	8	BH172538	SALK_0058		C 535	9	42.9	45	8	AZ815371	AZ815371	2M0083M04

C 536	9	42.9	45	8	BH168809	BH168809	SALK_0002	C 609	9	42.9	48	8	BH172074	BH172074	SALK_0052
C 537	9	42.9	45	8	BH169016	BH169016	SALK_0004	C 610	9	42.9	48	8	BH172483	BH172483	SALK_0057
C 538	9	42.9	45	8	BH169715	BH169715	SALK_0017	C 611	9	42.9	48	8	BH173104	BH173104	SALK_0013
C 539	9	42.9	45	8	BH170991	BH170991	SALK_0036	C 612	9	42.9	48	8	BH211911	BH211911	SALK_0068
C 540	9	42.9	45	8	BH171160	BH171160	SALK_0038	C 613	9	42.9	48	8	BH212124	BH212124	SALK_0071
C 541	9	42.9	45	8	BH172480	BH172480	SALK_0057	C 614	9	42.9	48	8	BH212192	BH212192	SALK_0072
C 542	9	42.9	45	8	BH251855	BH251855	SALK_0057	C 615	9	42.9	48	8	BH212362	BH212362	SALK_0074
C 543	9	42.9	45	8	BH252041	BH252041	SALK_0122	C 616	9	42.9	48	8	BH213362	BH213362	SALK_0091
C 544	9	42.9	45	8	BH252624	BH252624	SALK_0136	C 617	9	42.9	48	8	BH213445	BH213445	SALK_0092
C 545	9	42.9	45	8	BH253683	BH253683	SALK_0152	C 618	9	42.9	48	8	BH213559	BH213559	SALK_0093
C 546	9	42.9	45	8	BH610643	BH610643	SALK_0177	C 619	9	42.9	48	8	BH214012	BH214012	SALK_0100
C 547	9	42.9	45	8	BH613489	BH613489	SALK_0343	C 620	9	42.9	48	8	BH214058	BH214058	SALK_0101
C 548	9	42.9	45	8	BH617238	BH617238	SALK_0361	C 621	9	42.9	48	8	BH251827	BH251827	SALK_0121
C 549	9	42.9	45	8	BH617343	BH617343	SALK_0363	C 622	9	42.9	48	8	BH252179	BH252179	SALK_0128
C 550	9	42.9	45	8	BH617375	BH617375	SALK_0364	C 623	9	42.9	48	8	BH252272	BH252272	SALK_0130
C 551	9	42.9	45	8	BH617528	BH617528	SALK_0372	C 624	9	42.9	48	8	BH253038	BH253038	SALK_0143
C 552	9	42.9	45	8	BH618005	BH618005	SALK_0383	C 625	9	42.9	48	8	BH253184	BH253184	SALK_0145
C 553	9	42.9	45	8	BH618006	BH618006	SALK_0383	C 626	9	42.9	48	8	BH253291	BH253291	SALK_0147
C 554	9	42.9	45	8	BH618252	BH618252	SALK_0387	C 627	9	42.9	48	8	BH253306	BH253306	SALK_0147
C 555	9	42.9	45	8	BH619123	BH619123	SALK_0402	C 628	9	42.9	48	8	BH253358	BH253358	SALK_0148
C 556	9	42.9	45	8	BH749090	BH749090	SALK_0472	C 629	9	42.9	48	8	BH253833	BH253833	SALK_0155
C 557	9	42.9	45	8	BH790393	BH790393	SALK_0569	C 630	9	42.9	48	8	BH254186	BH254186	SALK_0161
C 558	9	42.9	46	1	A1735034	A1735034	as68H04.x	C 631	9	42.9	48	8	BH254463	BH254463	SALK_0165
C 559	9	42.9	46	1	A3399336	A3399336	zt49c12.x	C 632	9	42.9	48	8	BH254917	BH254917	SALK_0174
C 560	9	42.9	46	7	H55294	H55294	CHR220233.C	C 633	9	42.9	48	8	BH610731	BH610731	SALK_0179
C 561	9	42.9	46	8	BH168816	BH168816	SALK_0002	C 634	9	42.9	48	8	BH610835	BH610835	SALK_0181
C 562	9	42.9	46	8	BH169680	BH169680	SALK_0017	C 635	9	42.9	48	8	BH610916	BH610916	SALK_0182
C 563	9	42.9	46	8	BH212329	BH212329	SALK_0074	C 636	9	42.9	48	8	BH611306	BH611306	SALK_0306
C 564	9	42.9	46	8	BH212348	BH212348	SALK_0061	C 637	9	42.9	48	8	BH611439	BH611439	SALK_0309
C 565	9	42.9	46	8	BH213521	BH213521	SALK_0093	C 638	9	42.9	48	8	BH611499	BH611499	SALK_0310
C 566	9	42.9	46	8	BH252530	BH252530	SALK_0135	C 639	9	42.9	48	8	BH611861	BH611861	SALK_0318
C 567	9	42.9	46	8	BH611610	BH611610	SALK_0312	C 640	9	42.9	48	8	BH612357	BH612357	SALK_0325
C 568	9	42.9	46	8	BH618888	BH618888	SALK_0399	C 641	9	42.9	48	8	BH613342	BH613342	SALK_0341
C 569	9	42.9	46	8	BH641999	BH641999	1008052B0	C 642	9	42.9	48	8	BH614164	BH614164	SALK_0355
C 570	9	42.9	46	8	BH747763	BH747763	SALK_0340	C 643	9	42.9	48	8	BH617377	BH617377	SALK_0364
C 571	9	42.9	46	8	BH751055	BH751055	SALK_0487	C 644	9	42.9	48	8	BH617696	BH617696	SALK_0374
C 572	9	42.9	46	8	BH910540	BH910540	SALK_0601	C 645	9	42.9	48	8	BH633587	BH633587	SALK_0428
C 573	9	42.9	46	9	CC887473	CC887473	SALK_1502	C 646	9	42.9	48	8	BH748267	BH748267	SALK_0450
C 574	9	42.9	46	9	CG782542	CG782542	1123050H0	C 647	9	42.9	48	8	BH748292	BH748292	SALK_0451
C 575	9	42.9	47	8	AZ623246	AZ623246	1M0460C17	C 648	9	42.9	48	8	BH748882	BH748882	SALK_0469
C 576	9	42.9	47	8	AZ779546	AZ779546	2M0016C09	C 649	9	42.9	48	8	BH749772	BH749772	SALK_0302
C 577	9	42.9	47	8	BH169602	BH169602	SALK_0016	C 650	9	42.9	48	8	BH749892	BH749892	SALK_0303
C 578	9	42.9	47	8	BH172194	BH172194	SALK_0053	C 651	9	42.9	48	8	BH750103	BH750103	SALK_0347
C 579	9	42.9	47	8	BH172688	BH172688	SALK_0060	C 652	9	42.9	48	8	BH751416	BH751416	SALK_0501
C 580	9	42.9	47	8	BH213222	BH213222	SALK_0089	C 653	9	42.9	48	8	BH753224	BH753224	SALK_0199
C 581	9	42.9	47	8	BH213678	BH213678	SALK_0095	C 654	9	42.9	48	8	BH753678	BH753678	SALK_0294
C 582	9	42.9	47	8	BH214187	BH214187	SALK_0103	C 655	9	42.9	48	8	BH902361	BH902361	SALK_0917
C 583	9	42.9	47	8	BH252265	BH252265	SALK_0130	C 656	9	42.9	48	8	BZ382688	BZ382688	SALK_1186
C 584	9	42.9	47	8	BH252797	BH252797	SALK_0138	C 657	9	42.9	48	9	BX286631	BX286631	ArabiDops
C 585	9	42.9	47	8	BH253337	BH253337	SALK_0147	C 658	9	42.9	49	1	AA706582	AA706582	ah27b06.s
C 586	9	42.9	47	8	BH253852	BH253852	SALK_0155	C 659	9	42.9	49	1	AA726836	AA726836	vu94g12.r
C 587	9	42.9	47	8	BH611281	BH611281	SALK_0306	C 660	9	42.9	49	1	A1558595	A1558595	fb6a10.y
C 588	9	42.9	47	8	BH611531	BH611531	SALK_0310	C 661	9	42.9	49	1	A1584385	A1584385	fb92h12.x
C 589	9	42.9	47	8	BH612570	BH612570	SALK_0329	C 662	9	42.9	49	1	A1883392	A1883392	fc63c06.y
C 590	9	42.9	47	8	BH617563	BH617563	SALK_0372	C 663	9	42.9	49	1	AU013938	AU013938	AU013938
C 591	9	42.9	47	8	BH618704	BH618704	SALK_0395	C 664	9	42.9	49	5	BQ587334	BQ587334	E012340w-
C 592	9	42.9	47	8	BH747945	BH747945	SALK_0397	C 665	9	42.9	49	5	BQ587752	BQ587752	E012340-0
C 593	9	42.9	47	8	BH748581	BH748581	SALK_0461	C 666	9	42.9	49	7	X98140	X98140	MMEST49.Mou
C 594	9	42.9	47	8	BH752651	BH752651	SALK_0189	C 667	9	42.9	49	8	BH168986	BH168986	SALK_0004
C 595	9	42.9	47	8	BH753401	BH753401	SALK_0287	C 668	9	42.9	49	8	BH169475	BH169475	SALK_0014
C 596	9	42.9	47	8	BH851673	BH851673	SALK_0733	C 669	9	42.9	49	8	BH170166	BH170166	SALK_0034
C 597	9	42.9	47	9	AL946412	AL946412	ArabiDops	C 670	9	42.9	49	8	BH170234	BH170234	SALK_0035
C 598	9	42.9	47	9	CG714468	CG714468	1119036H0	C 671	9	42.9	49	8	BH172398	BH172398	SALK_0056
C 599	9	42.9	48	1	AV967257	AV967257	AV967257	C 672	9	42.9	49	8	BH212186	BH212186	SALK_0072
C 600	9	42.9	48	8	BH169127	BH169127	SALK_0006	C 673	9	42.9	49	8	BH212189	BH212189	SALK_0072
C 601	9	42.9	48	8	BH169913	BH169913	SALK_0020	C 674	9	42.9	49	8	BH213269	BH213269	SALK_0089
C 602	9	42.9	48	8	BH170421	BH170421	SALK_0028	C 675	9	42.9	49	8	BH251862	BH251862	SALK_0122
C 603	9	42.9	48	8	BH170455	BH170455	SALK_0029	C 676	9	42.9	49	8	BH252868	BH252868	SALK_0139
C 604	9	42.9	48	8	BH170532	BH170532	SALK_0030	C 677	9	42.9	49	8	BH253161	BH253161	SALK_0153
C 605	9	42.9	48	8	BH170799	BH170799	SALK_0033	C 678	9	42.9	49	8	BH253743	BH253743	SALK_0153
C 606	9	42.9	48	8	BH171310	BH171310	SALK_0040	C 679	9	42.9	49	8	BH253938	BH253938	SALK_0157
C 607	9	42.9	48	8	BH171340	BH171340	SALK_0041	C 680	9	42.9	49	8	BH614128	BH614128	SALK_0355
C 608	9	42.9	48	8	BH171719	BH171719	SALK_0047	C 681	9	42.9	49	8	BH748794	BH748794	SALK_0457

C 682	9	42.9	8	BH752698	SALK_0192	C 755	8.8	41.9	31	9	AG194290	Pan trogl
C 683	9	42.9	8	BH753750	SALK_0295	C 756	8.8	41.9	32	8	AZ485865	IM0313H02
C 684	9	42.9	8	AJ596083	Arabidops	C 757	8.8	41.9	32	8	AZ583239	IM0378K08
C 685	9	42.9	8	AL608178	Anopheles	C 758	8.8	41.9	32	8	BZ381666	SALK_1170
C 686	9	42.9	8	CNS0789C		C 759	8.8	41.9	32	8	BZ383892	SALK_1347
C 687	9	42.9	8	CR400023	Arabidops	C 760	8.8	41.9	32	9	BX656781	Arabidops
C 688	9	42.9	8	AL802196	AL802196	C 761	8.8	41.9	32	9	CR359094	Arabidops
C 689	9	42.9	8	AL802484	AU102484	C 762	8.8	41.9	32	9	CR359095	Arabidops
C 690	9	42.9	8	AU104254	AU104254	C 763	8.8	41.9	32	9	AJ545221	Drosophil
C 691	9	42.9	8	AU104296	AU105296	C 764	8.8	41.9	32	1	AV834380	AV834380
C 692	9	42.9	8	AU107262	AU107262	C 765	8.8	41.9	33	4	B1656215	603283594
C 693	9	42.9	8	AU107263	AU107263	C 766	8.8	41.9	33	7	T89682	Yd99f02_81
C 694	9	42.9	8	AU107510	AU107510	C 767	8.8	41.9	33	8	AZ316728	IM0035A15
C 695	9	42.9	8	AU107860	AU107860	C 768	8.8	41.9	33	8	BZ380694	SALK_1155
C 696	9	42.9	8	AU107968	AU107968	C 769	8.8	41.9	33	8	BZ382892	SALK_1190
C 697	9	42.9	8	AZ308799	IM0012112	C 770	8.8	41.9	33	8	CC049737	01S0506-0
C 698	9	42.9	8	BH211702	SALK_0065	C 771	8.8	41.9	33	9	AJ599957	Arabidops
C 699	9	42.9	8	BH213709	SALK_0096	C 772	8.8	41.9	34	8	BZ380603	SALK_1063
C 700	9	42.9	8	BH253148	SALK_0145	C 773	8.8	41.9	34	8	BZ380603	SALK_1153
C 701	9	42.9	8	BH611167	SALK_0299	C 774	8.8	41.9	34	8	CG723116	1119074G1
C 702	9	42.9	8	BH612727	SALK_0331	C 775	8.8	41.9	35	8	AZ838159	2M0133C15
C 703	9	42.9	8	BH617293	SALK_0362	C 776	8.8	41.9	35	8	BH847051	SALK_0129
C 704	9	42.9	8	BH617418	SALK_0364	C 777	8.8	41.9	35	8	BH852456	SALK_0746
C 705	9	42.9	8	BH750106	SALK_0169	C 778	8.8	41.9	35	8	BZ380621	SALK_1154
C 706	9	42.9	8	BH753469	SALK_0288	C 779	8.8	41.9	35	8	BZ380790	SALK_1156
C 707	9	42.9	8	BX572281	Arabidops	C 780	8.8	41.9	35	8	BZ383613	SALK_1341
C 708	9	42.9	8	CG547498	CH240_430	C 781	8.8	41.9	35	8	BZ763321	SALK_1162
C 709	9	42.9	8	CG711376	1119021B0	C 782	8.8	41.9	35	9	AL947040	Arabidops
C 710	9	42.9	8	CG713887	1119033H1	C 783	8.8	41.9	35	9	DR31314T	
C 711	8.8	41.9	20	1	AU258084	C 784	8.8	41.9	36	8	AQ073401	EP(2)2312
C 712	8.8	41.9	21	5	BX566484	C 785	8.8	41.9	36	8	BZ380578	SALK_1153
C 713	8.8	41.9	21	9	TA290E03P	C 786	8.8	41.9	36	9	TA126A03P	
C 714	8.8	41.9	22	9	TA290E03P	C 787	8.8	41.9	37	1	AA977326	0q72c02.s
C 715	8.8	41.9	22	9	CL438518	C 788	8.8	41.9	37	1	AA984865	am62b07.s
C 716	8.8	41.9	22	9	CL670198	C 789	8.8	41.9	37	1	AA142601	OK35d07.s
C 717	8.8	41.9	22	9	AG195487	C 790	8.8	41.9	37	1	AA458001	VF74910.r
C 718	8.8	41.9	23	8	AZ805705	C 791	8.8	41.9	37	2	BF122604	601760322
C 719	8.8	41.9	23	8	L32029	C 792	8.8	41.9	37	4	BJ049420	BJ049420
C 720	8.8	41.9	24	7	L32029	C 793	8.8	41.9	37	8	AZ653729	IM0527103
C 721	8.8	41.9	24	8	AZ469511	C 794	8.8	41.9	37	8	AZ653729	IM0527103
C 722	8.8	41.9	24	8	AZ475486	C 795	8.8	41.9	37	8	AZ789498	2M0037M16
C 723	8.8	41.9	25	1	AJ679528	C 796	8.8	41.9	37	8	AZ863572	2M0171B07
C 724	8.8	41.9	25	8	AZ654827	C 797	8.8	41.9	37	8	AZ863572	2M0171B07
C 725	8.8	41.9	26	1	AU011509	C 798	8.8	41.9	37	8	BZ377641	SALK_0986
C 726	8.8	41.9	26	8	AZ427547	C 799	8.8	41.9	37	8	BZ377654	SALK_0987
C 727	8.8	41.9	26	8	AZ623173	C 800	8.8	41.9	37	8	BZ377657	SALK_0987
C 728	8.8	41.9	26	8	AZ821460	C 801	8.8	41.9	37	8	BZ377658	SALK_0987
C 729	8.8	41.9	26	9	TA252D07Q	C 802	8.8	41.9	37	8	BZ377667	SALK_0987
C 730	8.8	41.9	27	8	AZ347928	C 803	8.8	41.9	37	8	BZ377667	SALK_0987
C 731	8.8	41.9	27	9	TA354A04Q	C 804	8.8	41.9	37	8	BZ377870	SALK_1063
C 732	8.8	41.9	28	1	A1076131	C 805	8.8	41.9	37	8	BZ378334	SALK_1079
C 733	8.8	41.9	28	8	AZ780159	C 806	8.8	41.9	37	8	BZ378377	SALK_1080
C 734	8.8	41.9	28	8	AZ783515	C 807	8.8	41.9	37	8	BZ378431	SALK_1080
C 735	8.8	41.9	28	8	AZ783515	C 808	8.8	41.9	37	8	BZ380232	SALK_1148
C 736	8.8	41.9	29	5	BQ595553	C 809	8.8	41.9	37	8	BZ380472	SALK_1151
C 737	8.8	41.9	29	8	AQ025252	C 810	8.8	41.9	37	8	BZ380541	SALK_1153
C 738	8.8	41.9	29	8	AZ775915	C 811	8.8	41.9	37	8	BZ380554	SALK_1153
C 739	8.8	41.9	29	8	BH906395	C 812	8.8	41.9	37	8	BZ380556	SALK_1153
C 740	8.8	41.9	29	8	BZ380586	C 813	8.8	41.9	37	8	BZ380556	SALK_1153
C 741	8.8	41.9	29	8	BZ380648	C 814	8.8	41.9	37	8	BZ380556	SALK_1153
C 742	8.8	41.9	29	8	BZ380770	C 815	8.8	41.9	37	8	BZ380556	SALK_1153
C 743	8.8	41.9	29	8	BZ384011	C 816	8.8	41.9	37	8	BZ380615	SALK_1154
C 744	8.8	41.9	30	9	BX289793	C 817	8.8	41.9	37	8	BZ380627	SALK_1154
C 745	8.8	41.9	31	1	AA781776	C 818	8.8	41.9	37	8	BZ380663	SALK_1154
C 746	8.8	41.9	31	1	A1078844	C 819	8.8	41.9	37	8	BZ380717	SALK_1155
C 747	8.8	41.9	31	1	AA590433	C 820	8.8	41.9	37	8	BZ380737	SALK_1155
C 748	8.8	41.9	31	1	AA590433	C 821	8.8	41.9	37	8	BZ380745	SALK_1156
C 749	8.8	41.9	31	7	CG432088	C 822	8.8	41.9	37	8	BZ380758	SALK_1156
C 750	8.8	41.9	31	7	CG782526	C 823	8.8	41.9	37	8	BZ380761	SALK_1156
C 751	8.8	41.9	31	8	AZ318049	C 824	8.8	41.9	37	8	BZ380781	SALK_1156
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C 830	8.8	41.9	37	8	BZ381722	BZ381722 SALK 1171	903	8.8	41.9	45	8	AL764750	Arabidops
C 831	8.8	41.9	37	8	BZ381723	BZ381723 SALK 1171	C 904	8.8	41.9	46	1	AV834157	AV834157
C 832	8.8	41.9	37	8	BZ381736	BZ381736 SALK 1171	C 905	8.8	41.9	46	1	AA616469	AA616469 vtn66d10.r
C 833	8.8	41.9	37	8	BZ381575	BZ381575 SALK 1341	C 906	8.8	41.9	46	8	BH861568	BH861568 SALK 0818
C 834	8.8	41.9	37	8	BZ383596	BZ383596 SALK 1341	C 907	8.8	41.9	46	8	BZ287326	BZ287326 SALK 0206
C 835	8.8	41.9	37	8	BZ383623	BZ383623 SALK 1341	C 908	8.8	41.9	46	8	BZ383801	BZ383801 SALK 1345
C 836	8.8	41.9	37	8	BZ383627	BZ383627 SALK 1341	C 909	8.8	41.9	46	9	AJ622642	Drosophil
C 837	8.8	41.9	37	8	BZ383631	BZ383631 SALK 1342	C 910	8.8	41.9	46	9	AJ758842	Arabidops
C 838	8.8	41.9	37	8	BZ383632	BZ383632 SALK 1342	C 911	8.8	41.9	47	6	CF329526	NAC1--04-
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C 847	8.8	41.9	38	8	BZ380646	BZ380646 SALK 1154	C 920	8.8	41.9	48	9	CG778060	1123025E0
C 848	8.8	41.9	38	8	BZ768853	BZ768853 SALK 1408	C 921	8.8	41.9	48	9	CG918667	01S0556-0
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C 850	8.8	41.9	38	9	BX287148	BX287148 Arabidops	C 923	8.8	41.9	49	1	AA657082	v823c09.r
C 851	8.8	41.9	38	9	AG217395	AG217395 Drosophil	C 924	8.8	41.9	49	1	AA948394	onS2b09.s
C 852	8.8	41.9	39	8	AZ595333	AZ595333 1M0407F23	C 925	8.8	41.9	49	1	A1004508	ot66g10.s
C 853	8.8	41.9	39	8	AZ773859	AZ773859 2M0001110	C 926	8.8	41.9	49	1	A1359268	qy27C06.x
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C 855	8.8	41.9	40	1	A1219362	A1219362 qtl4e08.x	C 928	8.8	41.9	49	1	A1638467	tt07d10.x
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C 858	8.8	41.9	40	8	AZ772376	AZ772376 1M0583011	C 931	8.8	41.9	49	6	CB337845	laa29h07.
C 859	8.8	41.9	40	8	BZ385044	BZ385044 SALK 1363	C 932	8.8	41.9	49	6	CD681046	tab7e02.
C 860	8.8	41.9	40	8	CC040316	CC040316 3591_1_13	C 933	8.8	41.9	49	8	AZ405394	1M0174N07
C 861	8.8	41.9	40	9	BX893447	BX893447 Arabidops	C 934	8.8	41.9	49	8	AQ254822	EP(2)1132
C 862	8.8	41.9	40	9	AG189131	AG189131 Pan trogl	C 935	8.8	41.9	49	8	BZ383782	SALK_1344
C 863	8.8	41.9	41	1	AU266348	AU266348 AU266348	C 936	8.8	41.9	49	8	CC045158	3591_1_17
C 864	8.8	41.9	41	7	CO732377	CO732377 L1LL01B01	C 937	8.8	41.9	49	8	CC060297	EY04028-5
C 865	8.8	41.9	41	7	H99001	H99001 Yw26b07.r1	C 938	8.8	41.9	49	9	AJ599619	Arabidops
C 866	8.8	41.9	41	7	H75667	T17567 mps v288 Th	C 939	8.8	41.9	49	9	CG718294	1119052D0
C 867	8.8	41.9	41	9	AJ600758	AJ600758 Arabidops	C 940	8.8	41.9	49	9	CG723873	1119073G1
C 868	8.8	41.9	41	9	AL756926	AL756926 Arabidops	C 941	8.8	41.9	49	9	CL213029	G030H04 G
C 869	8.8	41.9	41	9	DNE547050	AJ547050 Drosophil	C 942	8.8	41.9	50	1	AA116917	mq25g06.r
C 870	8.8	41.9	41	9	CC799936	CC799936 01S0783-0	C 943	8.8	41.9	50	1	AU102357	AU102357
C 871	8.8	41.9	41	9	CC884734	CC884734 SALK 1350	C 944	8.8	41.9	50	1	AU102880	AU102880
C 872	8.8	41.9	41	9	AB081895	AB081895 Drosophil	C 945	8.8	41.9	50	1	AU102957	AU102957
C 873	8.8	41.9	42	7	H07866	H07866 Y186b08.s1	C 946	8.8	41.9	50	1	AU103632	AU103632
C 874	8.8	41.9	42	8	BH000535	BH000535 2M0288B05	C 947	8.8	41.9	50	1	AU103633	AU103633
C 875	8.8	41.9	42	8	BH799740	BH799740 1008109H1	C 948	8.8	41.9	50	1	AU103997	AU103997
C 876	8.8	41.9	42	9	AL763435	AL763435 Arabidops	C 949	8.8	41.9	50	1	AU104135	AU104135
C 877	8.8	41.9	42	9	DNE545209	AJ545209 Drosophil	C 950	8.8	41.9	50	1	AU104175	AU104175
C 878	8.8	41.9	43	1	AA948203	AA948203 op99h09.s	C 951	8.8	41.9	50	1	AU104448	AU104448
C 879	8.8	41.9	43	1	AA976713	AA976713 q06d06.s	C 952	8.8	41.9	50	1	AU104485	AU104485
C 880	8.8	41.9	43	1	AA976713	AA976713 q06d06.s	C 953	8.8	41.9	50	1	AU104853	AU104853
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C 882	8.8	41.9	43	1	AJ666206	AJ666206 AJ666206	C 955	8.8	41.9	50	1	AU105325	AU105325
C 883	8.8	41.9	43	4	B1333375	B1333375 602996772	C 956	8.8	41.9	50	1	AU105434	AU105434
C 884	8.8	41.9	43	5	BX551512	BX551512 BX551512	C 957	8.8	41.9	50	1	AU105954	AU105954
C 885	8.8	41.9	43	5	CF321300	CF321300 HD--12-I0	C 958	8.8	41.9	50	1	AU106291	AU106291
C 886	8.8	41.9	43	7	W38487	W38487 zbl9p07.r1	C 959	8.8	41.9	50	1	AU107257	AU107257
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C 888	8.8	41.9	43	9	BX892893	BX892893 Arabidops	C 961	8.8	41.9	50	1	AU107260	AU107260
C 889	8.8	41.9	44	6	CF315888	CF315888 HD--04-P1	C 962	8.8	41.9	50	1	AU107261	AU107261
C 890	8.8	41.9	44	7	T17569	T17569 mps v3 The	C 963	8.8	41.9	50	1	AU107612	AU107612
C 891	8.8	41.9	44	8	BH905113	BH905113 SALK 1056	C 964	8.8	41.9	50	1	AU107636	AU107636
C 892	8.8	41.9	44	8	BZ384007	BZ384007 SALK 1349	C 965	8.8	41.9	50	1	AU107648	AU107648
C 893	8.8	41.9	44	8	BZ384717	BZ384717 SALK 1359	C 966	8.8	41.9	50	1	AU107652	AU107652
C 894	8.8	41.9	44	8	CC455081	CC455081 SALK 20476	C 967	8.8	41.9	50	1	AU107653	AU107653
C 895	8.8	41.9	44	9	CC795527	CC795527 SALK 0814	C 968	8.8	41.9	50	1	AU107654	AU107654
C 896	8.8	41.9	45	8	AZ345886	AZ345886 1M0080P17	C 969	8.8	41.9	50	1	AU107892	AU107892
C 897	8.8	41.9	45	8	AZ605963	AZ605963 1M0427A12	C 970	8.8	41.9	50	1	AU108020	AU108020
C 898	8.8	41.9	45	8	BH638406	BH638406 1008022D0	C 971	8.8	41.9	50	1	AU108057	AU108057
C 899	8.8	41.9	45	8	BH759240	BH759240 KG00542-3	C 972	8.8	41.9	50	1	AV836264	AV836264
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AL486921 T. brucei  
BM396768 5009-0-25  
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AZ806433 2M0068P24  
AJ588636 Arabidops

ALIGNMENTS

TA199C08P/c 32 bp DNA linear GSS 13-DEC-2000  
T. brucei sheared genomic DNA clone 199c08, forward sequence,  
genomic survey sequence.  
AL475986  
AL475986.1 GI:11842726  
GSS.  
Trypanosoma brucei  
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
Trypanosoma.  
1 (bases 1 to 32)  
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,  
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,  
Melville,S.E., Rajandream,M.A. and Barrell,B.G.  
Direct Submission  
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
nh@sanger.ac.uk  
Constructed at the Institute for Genomic Research (TIGR),  
Rockville, MD. Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
to give a tight size distribution (  
4 kb). The v + i method used for the library construction is  
described in detail in Smith, H. and Venter, J.C. (Making small  
insert libraries for whole genome shotgun sequencing projects. In  
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
Barrell, Oxford University Press, 1999).  
Email: nelsayed@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available  
at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).  
Location/Qualifiers  
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/organism="Trypanosoma brucei"  
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ORIGIN

Query Match 60.0%; Score 12.6; DB 9; Length 32;  
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Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 2 GGTCAATTAGACCGTACGCG 20  
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Db 25 GGTCAATTAGAAAGCAGCG 7

RESULT 2  
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LOCUS  
DEFINITION  
701550260 A. thaliana, Columbia Col-0, inflorescence-2 Arabidopsis  
thaliana cDNA clone 701550260, mRNA sequence.

ACCESSION  
AW004201  
VERSION  
AW004201.1 GI:5851230  
KEYWORDS  
SOURCE  
ORGANISM  
Arabidopsis thaliana (thale cress)

Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi  
1 (bases 1 to 50)  
Chen,J., Momiyama,M., Chan,E., Mooney,M., Carroon,B., Gilliland,D.,  
Wang,X., Hillman,J., Guegler,K., Kim,C., Doyle,M., Brzoka,P.,  
Gorgone,G., Burns,D., Griffin,J., Mouanoutoua,M., Nguyen,D.,  
Tan,R., Rose,M., Warren,B., Ton,B., Kastury,K., Borillo,C.,  
Carpio,T., Policky,J., Suzuki,G., Argentine,C., Shah,S.,  
Nobrega,A., Murry,L., Turner,C., Krikorian,S., Elder,L. and  
Hanson,D.

TITLE Arabidopsis thaliana Gene Expression MicroArray

Unpublished (1999)  
Contact: David Smoller, Ph.D.  
Genome Systems, Inc., a wholly owned subsidiary of Incyte  
Pharmaceuticals, Inc.  
4633 World Parkway Circle, St. Louis, MO 63134, USA  
Tel: 877-577-2733  
Fax: 314-427-3324  
Email: [service@genomesystems.com](mailto:service@genomesystems.com).

FEATURES

source  
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weeks. Plants were grown in 1:1:1 peat  
moss/vermiculite/perlite soil at 22 deg. C +/- 3 deg. C  
under constant light, and watered with fertilizer. cDNA  
synthesis was initiated using a NotI-oligo(dT) primer.  
Double-stranded cDNA was blunted, ligated to SalI  
adaptors, digested with NotI, size-selected, and cloned  
into the NotI and SalI sites of the pSPORT vector."

ORIGIN

Query Match 58.1%; Score 12.2; DB 1; Length 50;  
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Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
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Db 31 TCAATATACCGAGCG 47

RESULT 3

CF338319/c

LOCUS CF338319 33 bp mRNA linear EST 18-AUG-2003  
 DEFINITION RCL1--01-F04.g1 Regenerated callus lambda phage cDNA library (RCL1)  
 Orzya sativa (japonica cultivar-group) cDNA clone RCL1--01-F04,  
 mRNA sequence.  
 ACCESSION CF338319  
 VERSION CF338319.1 GI:33825024  
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 SOURCE Orzya sativa (japonica cultivar-group)  
 ORGANISM Orzya sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.  
 REFERENCE 1 (bases 1 to 33)  
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.  
 FEATURES  
 source  
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 /note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:  
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 induced on 2N6 media for 30 days and cultured for 36hrs on  
 regenerated media"  
 ORIGIN  
 Query Match 57.1%; Score 12; DB 6; Length 33;  
 Best Local Similarity 75.0%; Pred. No. 7.3e+04;  
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
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 Db 27 GGTATTAGACACTACTTGA 8  
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 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris  
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.  
 REFERENCE 1 (bases 1 to 36)  
 AUTHORS Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,  
 Drungowski, M., Stahl, D., Wruick, W., Menze, A., O'Brien, J., Lehrach, H.  
 and Radelof, U.  
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 JOURNAL Plant J. 32 (5), 845-857 (2002)  
 MEDLINE 22362189

12472698  
 CONTACT: Weishaar B  
 ADIS DNA core facility at MP1Z  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@mpiz-koeln.mpg.de  
 Insert Length: 36 Std Error: 0.00  
 Plate: 20 row: N column: 04  
 Seq primer: SP6; CATACGATTGAGTGCACACTATAG.  
 FEATURES  
 source  
 1. .36  
 Location/Qualifiers  
 /organism="Beta vulgaris"  
 /mol\_type="mRNA"  
 /cultivar="KWS2320 (double haploid, monogerm breeding  
 line)"  
 /db\_xref="GABI:190371"  
 /db\_xref="taxon:161934"  
 /clone="024-020-N04"  
 /tissue\_type="developing root"  
 /lab\_host="EMDH10B"  
 /clone\_lib="MP1Z-ADIS-024-developing root"  
 /note="Vector: pCMVSPORT6; Site 1: SstI; Site 2: NotI;  
 cDNA library from sugar beet, library provided by KWS  
 Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:  
 b.schulz@kws.de; cloning sites SstI-NotI, primer sites and  
 orientation:  
 SP6-SstI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-Beet  
 Project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: http://gabi.rzpd.de"  
 ORIGIN  
 Query Match 55.2%; Score 11.6; DB 5; Length 36;  
 Best Local Similarity 77.8%; Pred. No. 1.2e+05;  
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 Qy 3 GTCATTAGACCGTACGCG 20  
 ||| ||||| ||| ||  
 Db 22 GTATAAATCGTACGCG 5  
 ||| ||||| ||| ||  
 RESULT 5  
 BH903257/c  
 LOCUS BH903257 43 bp DNA linear GSS 04-SEP-2002  
 DEFINITION SALK\_102332.18.30.x Arabidopsis thaliana TDNA insertion lines  
 Arabidopsis thaliana genomic clone SALK\_102332.18.30.x, genomic  
 survey sequence.  
 ACCESSION BH903257  
 VERSION BH903257.1 GI:22714417  
 KEYWORDS GSS.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
 REFERENCE 1 (bases 1 to 43)  
 AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,  
 Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,  
 Shinn, P., Zimmerman, J. and Eckert, J.R.  
 TITLE A Sequence-Indexed Library of Insertion Mutations in the  
 Arabidopsis Genome  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Joseph R. Ecker  
 Salk Institute Genomic Analysis Laboratory (SIGAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752  
 Fax: 858 558 6379  
 Email: ecker@salk.edu  
 This is single pass sequence recovered from the left border of  
 TDNA.



Class: TDNA tagged.  
Location/Qualifiers  
1. .43  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/ecotype="Col-0"  
/db\_xref="taxon:3702"  
/clone="SALK 10232.18.30.x"  
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

ORIGIN  
Query Match 55.2%; Score 11.6; DB 8; Length 43;  
Best Local Similarity 77.8%; Pred. No. 1.2e+05;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGTTCATTAGACCGTACGC 19  
|||||  
Db 30 GGTATACAGACCAACGC 13

RESULT 6  
CL660557/c 29 bp DNA linear GSS 09-JUL-2004  
LOCUS  
DEFINITION  
PRI0137b H04 - PRI0137b.B21 (29) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.  
ACCESSION  
CL660557 GI:50146000  
VERSION  
CL660557.1  
SOURCE  
Pristionchus pacificus  
ORGANISM  
Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.  
REFERENCE  
1 (bases 1 to 29)  
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J. AppaDB: an Acedb database for the nematode satellite organism Pristionchus pacificus  
Nucleic Acids Res. 32 (1), D421-D422 (2004)  
JOURNAL  
Contact: Sommer RJ  
COMMENT  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.  
Seq primer: 17  
Class: fosmid ends.  
Location/Qualifiers  
1. .29  
/organism="Pristionchus pacificus"  
/mol\_type="genomic DNA"  
/strain="California"  
/db\_xref="taxon:54126"  
/clone\_lib="Mixed stage fosmid library of P. pacificus var. California"  
/note="Vector: pBpifos-5 Fosmid vector"

ORIGIN  
Query Match 54.3%; Score 11.4; DB 9; Length 29;  
Best Local Similarity 92.3%; Pred. No. 1.6e+05;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GTCATTAGACCGT 15  
|||||  
Db 28 GTCATTAGATCGT 16

RESULT 7  
CL293866 39 bp DNA linear GSS 12-FEB-2004  
LOCUS  
DEFINITION  
02S0349-08A1-E04 UniformMu MUTAIL Library Zea mays genomic clone  
02S0349-08A1-E04, genomic survey sequence.  
ACCESSION  
CL293866 GI:42541995  
VERSION  
CL293866.1  
KEYWORDS  
GSS.  
SOURCE  
Zea mays  
ORGANISM  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE  
1 (bases 1 to 39)  
Latshaw,S., Tan,B.-C., Settles,A.M. and McCarty,D.R. Sequence tagged transposon insertions from the UniformMu maize population  
Unpublished (2003)  
JOURNAL  
Contact: Donald R. McCarty  
COMMENT  
Plant Molecular and Cellular Biology Program  
University of Florida  
PO 110690 Gainesville, FL 32611-0690, USA  
Tel: 352-392-1928 x322  
Email: drmc@ufl.edu  
Sequence flanking probable Mu insertion site in UniformMu line:  
02S0349-08, Primer set: A  
Class: transposon insertion site.  
Location/Qualifiers  
1. .39  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="W22 (ACR, bz1-m9)"  
/cultivar="UniformMu"  
/db\_xref="taxon:4577"  
/clone="02S0349-08A1-E04"  
/clone\_lib="UniformMu MUTAIL Library"  
/note="Vector: TOPO-PCR4; DNA flanking Mu transposon insertions in Mu inactive lines were extracted from the UniformMu maize population by the thermo asymmetric intercalated PCR (TAIL) protocol using primers specific for the Mu terminal inverted repeat and a set of 16 arbitrary primers. Amplicons were size enriched using Sepharose 400 spin columns and cloned into the TOPO PCR4 vector."

ORIGIN  
Query Match 54.3%; Score 11.4; DB 9; Length 39;  
Best Local Similarity 71.4%; Pred. No. 1.6e+05;  
Matches 15; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CGGTTCATTAGACCGTACCGCA 21  
|||||  
Db 14 CGGGGATTATACCGGAGTGA 34

RESULT 8  
AU106620 50 bp mRNA linear EST 28-JAN-2004  
LOCUS  
DEFINITION  
AU106620 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone KAT06186, mRNA sequence.  
ACCESSION  
AU106620 GI:13556141  
VERSION  
AU106620.1  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 50)  
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Oka,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S. Diverse transcriptional initiation revealed by fine, large-scale





REFERENCE 1 (bases 1 to 43)  
 AUTHORS Hansen, J., Floss, T., van Sloun, P., Fuchtbauer, E.M., Vauti, F., Arnold, H.H., Schnutgen, F., Wurst, W., Von Melchner, H. and Ruiz, P.  
 TITLE A large-scale, gene-driven mutagenesis approach for the functional analysis of the mouse genome  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)  
 MEDLINE 22810117  
 PUBMED 12904583  
 COMMENT On Jun 30, 2004 this sequence version replaced gi:42744159.  
 Contact: GGTC  
 German Genetrap Consortium (GGTC)  
 Email: info@genetrap.de  
 pribeageo gene trap. Sequence tag generated by 5'RACE. Additional sequence information can be found at:  
 'http://genetrap.gsf.de/project/web\_new/database/result\_clone.html?clone\_id=W130C02'. ES cell line harboring insertion mutation of target gene is available at:  
 'http://genetrap.gsf.de/project/web\_new/order\_clones/howtoorder.htm  
 1' Inhouse Sequence Identifier: 08816  
 Class: Gene Trap.

#### FEATURES

source Location/Qualifiers  
 1..43  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="129 Sv"  
 /db\_xref="taxon:10090"  
 /clone="W130C02"  
 /sex="Male"  
 /cell\_type="Embryonic stem cell"  
 /cell\_line="ES cells 129S2 (formerly 129/SvPas)"  
 /clone\_lib="GGTC Gene Trap Library GV03C04"  
 /note="Vector: pTribetageo"

#### ORIGIN

Query Match 53.3%; Score 11.2; DB 9; Length 43;  
 Best Local Similarity 72.2%; Pred. No. 2.1e+05;  
 Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCGGTATTAGACCGTACG 18  
 ||||| ||||| |||||  
 Db 21 CCGGTTTTTANNACGTACG 38

RESULT 12  
 BX287629/c  
 LOCUS BX287629.1 GI:28886625  
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-403C11-017864, genomic survey sequence.  
 ACCESSION BX287629.1 GI:28886625  
 VERSION BX287629.1  
 KEYWORDS GSS.  
 ORGANISM Arabidopsis thaliana (thale cress)  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1  
 Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weissshaar, B.  
 GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana  
 Bioinformatics 19 (11), 1441-1442 (2003)  
 MEDLINE 22755823  
 PUBMED 12874060  
 2  
 Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weissshaar, B.  
 An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics  
 Plant Mol. Biol. 53 (1-2), 247-259 (2003)  
 JOURNAL 23117147  
 MEDLINE

#### REFERENCE

14756321  
 3  
 Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and Weissshaar, B.  
 High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines  
 Biotechniques 35 (6), 1164-1168 (2003)  
 JOURNAL 14682050  
 PUBMED 14682050  
 4 (bases 1 to 45)  
 Rosso, M.G., Li, Y., Strizhov, N. and Weissshaar, B.  
 Direct Submission  
 Submitted (31-MAR-2004) Weissshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
 It indicates an insertion within the locus defined by BAC clone T12C14. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

#### FEATURES

source Location/Qualifiers  
 1..45  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="GK-403C11-017864"  
 /clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
 /ecotype="Col-0"  
 /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AU537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

#### ORIGIN

Query Match 53.3%; Score 11.2; DB 9; Length 45;  
 Best Local Similarity 81.2%; Pred. No. 2.1e+05;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 ATTAGACCGTACGCGA 21  
 ||||| ||||| |||||  
 Db 38 AGTAGACGCTACCGCA 23

#### RESULT 13

BX650703/c  
 LOCUS BX650703.1 GI:37607091  
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-551H04-022301, genomic survey sequence.  
 ACCESSION BX650703  
 VERSION BX650703.1  
 KEYWORDS GSS.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1  
 Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weissshaar, B.  
 GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana  
 Bioinformatics 19 (11), 1441-1442 (2003)  
 MEDLINE 22755829  
 PUBMED 12874060  
 2  
 Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weissshaar, B.  
 An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for

flanking sequence tag-based reverse genetics  
Plant Mol. Biol. 53 (1-2), 247-259 (2003)  
23117147  
PUBMED  
14756321  
REFERENCE  
3  
AUTHORS  
Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and  
Weisshaar,B.  
TITLE  
High-throughput generation of sequence indexes from T-DNA  
mutagenized Arabidopsis thaliana lines  
Biotechniques 35 (6), 1164-1168 (2003)  
14682050  
PUBMED  
4 (bases 1 to 45)  
AUTHORS  
Rosso,M.G., Li,Y., Strizhov,N. and Weisshaar,B.  
JOURNAL  
Direct Submission  
TITLE  
Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer  
Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
COMMENT  
This sequence has been recovered from the left border of the T-DNA.  
It indicates an insertion close to or within gene At3g53580.  
Details on the protocols used for generation of the sequence are  
described in References 1-3. The sequences are generated at the MPI  
for Plant Breeding Research in the context of the GABI-Kat project.  
GABI-Kat is part of the German Plant Genomics program designated  
'GABI'. Information on line availability can be found at:  
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.  
FEATURES  
Location/Qualifiers  
1..45  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
/ecotype="Col-0"  
/note="PCR was performed on DNA from Arabidopsis thaliana  
plants (T1) which were transformed with the T-DNA from  
vector PAC161 (GenBank accession number: AJ537514). The  
lines contain one or more T-DNA insertions. The DNA  
fragment(s) resulting from the PCR were directly sequenced  
to determine the genomic sequence flanking the insertion.  
T-DNA derived sequences were removed."  
ORIGIN  
Query Match 53.3%; Score 11.2; DB 9; Length 45;  
Best Local Similarity 81.2%; Pred. No. 2.1e+05;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 5 CATTAGACCTATCGC 20  
|||||  
Db 28 CATTAGACCTATCGC 13  
|||||  
RESULT 14  
AZ583945/c  
LOCUS  
AZ583945 46 bp DNA linear GSS 13-DEC-2000  
DEFINITION  
IM0388107F Mouse 10kb plasmid UUC1M library Mus musculus genomic  
clone UUC1M0388107 F, genomic survey sequence.  
ACCESSION  
AZ583945  
VERSION  
AZ583945.1 GI:11704336  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1. (bases 1 to 46)  
REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0388 row: I column: 07  
Seq primer: CGTTGTAACACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 46.  
FEATURES  
Location/Qualifiers  
1..46  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUC1M0388107"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 [gi|4732114|gb|AF129072.1|, a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."  
ORIGIN  
Query Match 53.3%; Score 11.2; DB 8; Length 46;  
Best Local Similarity 81.2%; Pred. No. 2.1e+05;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 CGGTCATTAGACCGTA 16  
|||||  
Db 19 CTGTCATTAGTCCCTA 4  
|||||  
RESULT 15  
CG774856  
LOCUS  
CG774856 49 bp DNA linear GSS 29-OCT-2003  
DEFINITION  
1123021C02.1EL\_xl 1123 - RescueMu.Grid L Zea mays genomic, genomic  
survey sequence.  
ACCESSION  
CG774856  
VERSION  
CG774856.1 GI:38031309  
KEYWORDS  
GSS.  
SOURCE  
Zea mays  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1. (bases 1 to 49)  
REFERENCE  
AUTHORS  
Walbot,V.  
TITLE  
Maize genomic sequences found using engineered RescueMu transposon  
Unpublished (2001)  
JOURNAL  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227

Fax: 650 725 8221  
Email: walbot@stanford.edu  
Very probable ligation site of ends cut by single endonuclease.  
Reverse complemented post-ligation sequence from source sequence.  
Plate: 1123021 row: 16  
Class: transposon-tagged.

Location/Qualifiers

FEATURES

source

1..49

/organism="Zea mays"

/mol\_type="genomic DNA"

/cultivar="mixed background W23/A188/B73/K55"

/db\_xref="taxon:4577"

/tissue\_type="leaf"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="1123 - RescueMu Grid L"

/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid L was grown in Molokai in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 53.3%; Score 11.2; DB 9; Length 49;  
Best Local Similarity 81.2%; Pred. No. 2.1e+05;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TCATTAGACCGTACGC 19  
|||||  
Db 21 TTATTCGACCATACGC 36

RESULT 16  
AL754718/c 42 bp DNA linear GSS 01-APR-2004  
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-055D02-012479,  
genomic survey sequence.  
DEFINITION Arabidopsis thaliana (thale cress)  
ACCESSION AL754718.1 GI:21487216  
VERSION GSS  
KEYWORDS Arabidopsis thaliana  
SOURCE Arabidopsis thaliana  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
1  
Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weissshaar, B.  
GABI-Kat SimpleSearch: a flanking sequence tag (PST) database for  
the identification of T-DNA insertion mutants in Arabidopsis  
thaliana  
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)  
MEDLINE 22755829  
PUBMED 12874060  
REFERENCE 2  
Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and  
Weissshaar, B.  
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for  
flanking sequence tag-based reverse genetics  
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)  
MEDLINE 23117147  
PUBMED 14756321  
REFERENCE 3  
Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and  
Weissshaar, B.  
High-throughput generation of sequence indexes from T-DNA  
mutagenized Arabidopsis thaliana lines

BioTechniques 35 (6), 1164-1168 (2003)

14682050

4 (bases 1 to 42)

Li, Y., Rosso, M.G., Strizhov, N. and Weissshaar, B.  
Direct Submission  
Submitted (31-MAR-2004) Weissshaar B., Max-Planck-Institut fuer  
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
This sequence has been recovered from the left border of the T-DNA.  
It indicates an insertion close to or within gene Atlg78560.  
Details on the protocols used for generation of the sequence are  
described in References 1-3. The sequences are generated at the MPI  
for Plant Breeding Research in the context of the GABI-Kat project.  
GABI-Kat is part of the German Plant Genomics program designated  
'GABI'. Information on line availability can be found at:  
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

Location/Qualifiers

1..42

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="GK-055D02-012479"

/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"

/ecotype="Col-0"

/note="PCR was performed on DNA from Arabidopsis thaliana  
plants (Ti) which were transformed with the T-DNA from  
vector PAC161 (GenBank accession number: AJ537514). The  
lines contain one or more T-DNA insertions. The DNA  
fragment(s) resulting from the PCR were directly sequenced  
to determine the genomic sequence flanking the insertion.  
T-DNA derived sequences were removed."

ORIGIN

Query Match 52.4%; Score 11; DB 9; Length 42;  
Best Local Similarity 73.7%; Pred. No. 2.7e+05;  
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GTCATTAGACCGTACGCCA 21  
|||||  
Db 29 GTCATTAGATAGCAATCCA 11

RESULT 17  
AL939959/c 47 bp DNA linear GSS 01-APR-2004  
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-243C02-014389,  
genomic survey sequence.  
DEFINITION Arabidopsis thaliana (thale cress)  
ACCESSION AL939959.1 GI:24396408  
VERSION GSS  
KEYWORDS Arabidopsis thaliana  
SOURCE Arabidopsis thaliana  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
1  
Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weissshaar, B.  
GABI-Kat SimpleSearch: a flanking sequence tag (PST) database for  
the identification of T-DNA insertion mutants in Arabidopsis  
thaliana  
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)  
MEDLINE 22755829  
PUBMED 12874060  
REFERENCE 2  
Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and  
Weissshaar, B.  
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for  
flanking sequence tag-based reverse genetics  
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)  
MEDLINE 23117147  
PUBMED 14756321  
REFERENCE 3  
Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and



## ORIGIN

Query Match 51.4%; Score 10.8; DB 4; Length 32;  
 Best Local Similarity 85.7%; Pred. No. 3.6e+05;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 TTAGACCGTACCGG 20  
 || |||||  
 DB 17 TTGCACCGTACCGG 4

RESULT 20  
BH810122/c

LOCUS BH810122 36 bp DNA linear GSS 02-MAY-2002  
 DEFINITION SALK\_040987 Arabidopsis thaliana TDNA insertion lines Arabidopsis  
 thaliana genomic clone SALK\_040987, genomic survey sequence.

ACCESSION BH810122  
 VERSION BH810122.1 GI:20387940

## KEYWORDS

SOURCE Arabidopsis thaliana (thale cress)

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 36)

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
 Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,  
 Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA.

Class: TDNA tagged.

## FEATURES

source

Location/Qualifiers  
 1..36  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /ecotype="Col-0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_040987"  
 /clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
 /note="PCR was performed on Arabidopsis thaliana lines  
 each of which contains one or more TDNA insertion  
 elements. The resultant fragment for each line was  
 directly sequenced to determine the genomic sequence at  
 the site of insertion. Details of the protocols used can  
 be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

## ORIGIN

Query Match 51.4%; Score 10.8; DB 8; Length 36;  
 Best Local Similarity 85.7%; Pred. No. 3.6e+05;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GTCATTAGACCGTA 16  
 || |||||  
 DB 22 GTTATTATACCGTA 9

## RESULT 21

BH810143/c

LOCUS BH810143 36 bp DNA linear GSS 02-MAY-2002  
 DEFINITION SALK\_041377 Arabidopsis thaliana TDNA insertion lines Arabidopsis  
 thaliana genomic clone SALK\_041377, genomic survey sequence.

ACCESSION BH810143

VERSION BH810143.1 GI:20387961

## KEYWORDS

SOURCE Arabidopsis thaliana (thale cress)

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

## REFERENCE

1 (bases 1 to 36)

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
 Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,  
 Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA.

Class: TDNA tagged.

## FEATURES

source

Location/Qualifiers  
 1..36  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /ecotype="Col-0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_041377"  
 /clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
 /note="PCR was performed on Arabidopsis thaliana lines  
 each of which contains one or more TDNA insertion  
 elements. The resultant fragment for each line was  
 directly sequenced to determine the genomic sequence at  
 the site of insertion. Details of the protocols used can  
 be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

## ORIGIN

Query Match 51.4%; Score 10.8; DB 8; Length 36;  
 Best Local Similarity 85.7%; Pred. No. 3.6e+05;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GTCATTAGACCGTA 16  
 || |||||  
 DB 22 GTTATTATACCGTA 9

## RESULT 22

CR360542

LOCUS CR360542

DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-821B07-025531,  
 genomic survey sequence.

ACCESSION CR360542

VERSION CR360542.1 GI:45543464

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

## REFERENCE

1

Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weisshaar,B.  
 GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for  
 the identification of T-DNA insertion mutants in Arabidopsis  
 thaliana

JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)

MEDLINE 22755829

PUBMED 12874060

## REFERENCE

2

Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and

Weisshaar,B.

AUTHORS

TITLE

An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for

```

flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
23117147
14756321
PUBMED
AUTHORS
Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and
Weishaar, B.
TITLE
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
Biotechniques 35 (6), 1164-1168 (2003)
14682050
4 (bases 1 to 36)
Strizhov, N., Rosso, M.G., Li, Y. and Weishaar, B.
Direct Submission
TITLE
Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
It indicates an insertion close to or within gene Atg10350.
Details on the protocols used for generation of the sequence are
described in References 1-3. The sequences are generated at the MPI
for Plant Breeding Research in the context of the GABI-Kat project.
GABI-Kat is part of the German Plant Genomics program designated
'GABI'. Information on line availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES
source
Location/Qualifiers
1..36
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector PAC106 (GenBank accession number: AJ537513). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."
ORIGIN
Query Match 51.4%; Score 10.8; DB 9; Length 36;
Best Local Similarity 85.7%; Pred. No. 3.6e+05;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 GTCATTAGACCGTA 16
|||||
Db 23 GTCATTGAGCGTA 36

RESULT 23
CL524591 44 bp DNA linear GSS 02-APR-2004
LOCUS DAA2H11 Flanking Sequence Tag of Oryza sativa T-DNA insertion lines
DEFINITION Oryza sativa (japonica cultivar-group) genomic, genomic survey
sequence.
CL524591
ACCESSION CL524591.1 GI:46151391
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 44)
Sallaud, C., Gay, C., Larmande, P., Bes, M., Piffanelli, P., Piegou, B.,
Droc, G., Regad, F., Bourgeois, E., Meynard, D., Perin, C.,
Ghesquiere, A., Delseny, M., Glaszmann, J.C. and Guiderdoni, E.
High throughput T-DNA insertion mutagenesis in rice: A first step
towards in silico reverse genetics
Plant J. (2004) In press
Contact: Guiderdoni

flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
23117147
14756321
PUBMED
AUTHORS
Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and
Weishaar, B.
TITLE
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
Biotechniques 35 (6), 1164-1168 (2003)
14682050
4 (bases 1 to 36)
Strizhov, N., Rosso, M.G., Li, Y. and Weishaar, B.
Direct Submission
TITLE
Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
It indicates an insertion close to or within gene Atg10350.
Details on the protocols used for generation of the sequence are
described in References 1-3. The sequences are generated at the MPI
for Plant Breeding Research in the context of the GABI-Kat project.
GABI-Kat is part of the German Plant Genomics program designated
'GABI'. Information on line availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES
source
Location/Qualifiers
1..36
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector PAC106 (GenBank accession number: AJ537513). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."
ORIGIN
Query Match 51.4%; Score 10.8; DB 9; Length 36;
Best Local Similarity 85.7%; Pred. No. 3.6e+05;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 GTCATTAGACCGTA 16
|||||
Db 23 GTCATTGAGCGTA 36

RESULT 24
AG192385/c 45 bp DNA linear GSS 06-MAR-2004
LOCUS Pan troglodytes DNA, clone: RP43-068014.TJ, genomic survey
sequence.
AG192385
ACCESSION AG192385.1 GI:45224561
VERSION
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
BAC end sequences of Library RP-43
REFERENCE
2 (bases 1 to 45)
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
Direct Submission
TITLE
Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC) ;
52, Oun-dong, Yuseong-gu, Daejeon 305-333, Korea
(E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
Tel:82-42-866-7181, Fax:82-42-860-4409)
Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: TJ
LIBRARY
Vector : pBACe3.6
R.Site 1 : ECOR1
R.Site 2 : ECOR1.

```



FEATURES	Location/Qualifiers	survey sequence.
source	1..45	BZ358744
	/organism="Pan troglodytes"	GI:24951173
	/mol_type="genomic DNA"	GSS.
	/db_xref="taxon:9598"	Arabidopsis thaliana (thale cress)
	/clone="RP43-068014.TJ"	Arabidopsis thaliana
	/sex="male"	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
	/cell_type="lymphocytes"	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
	/clone_lib="RP-43 Chimpanzee Male BAC Library"	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
ORIGIN		
Query Match	51.4%; Score 10.8; DB 9; Length 45;	Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Best Local Similarity	85.7%; Pred. No. 3.6e+05;	Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Matches	12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	Shinn,P., Zimmerman,J. and Ecker,J.R.
QY	7 TTATACCGGTACGCG 20	A Sequence-indexed Library of Insertion Mutations in the
		Arabidopsis Genome
Db	15 TTATACCGGTATGCG 2	Unpublished (2001)
		Contact: Joseph R. Ecker
RESULT 25		Salk Institute Genomic Analysis Laboratory (SIGAL)
LOCUS	AU102564 50 bp mRNA linear EST 28-JAN-2004	The Salk Institute for Biological Studies
DEFINITION	AU102564 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone	10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
ACCESSION	HEP07440, mRNA sequence.	Tel: 858 453 4100 x1752
VERSION	AU102564.1 GI:13552085	Fax: 858 558 6379
KEYWORDS	EST.	Email: ecker@salk.edu
SOURCE	Homo sapiens (human)	This is single pass sequence recovered from the left border of
ORGANISM	Homo sapiens	TDNA.
REFERENCE		Class: TDNA tagged.
AUTHORS		Location/Qualifiers
		1..32
		/organism="Arabidopsis thaliana"
		/mol_type="genomic DNA"
		/ecotype="Col-0"
		/db_xref="taxon:3702"
		/clone="SALK_133243.27.05.x"
		/clone_lib="Arabidopsis thaliana TDNA insertion lines"
		/note="PCR was performed on Arabidopsis thaliana lines
		each of which contains one or more TDNA insertion
		elements. The resultant fragment for each line was
		directly sequenced to determine the genomic sequence at
		the site of insertion. Details of the protocols used can
		be found at <a href="http://signal.salk.edu/tdna_protocols.html">http://signal.salk.edu/tdna_protocols.html</a> "
JOURNAL		
MEDLINE		
PUBMED		
COMMENT		
	Contact: Yutaka Suzuki	Query Match
	Department of Virology	Best Local Similarity
	Institute of Medical Science, University of Tokyo	Matches
	4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan	13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
	Email: <a href="mailto:ysuzuki@ims.u-tokyo.ac.jp">ysuzuki@ims.u-tokyo.ac.jp</a>	
	Suzuki,Y., Yoshimoto-Nakagawa,K., Maruyama,K., Suyama,A. and	QY
	Sugano,S. Construction and characterization of a full	2 GGTCAATTAGACCGTACG 18
	length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),	
	149-156 (1997).	Db
		28 GCTCATGTGTCGGTACG 12
FEATURES	Location/Qualifiers	
source	1..50	
	/organism="Homo sapiens"	
	/mol_type="mRNA"	
	/db_xref="taxon:9606"	
	/clone="HEP07440"	
	/clone_lib="Sugano Homo sapiens cDNA library"	
ORIGIN		
Query Match	51.4%; Score 10.8; DB 1; Length 50;	
Best Local Similarity	85.7%; Pred. No. 3.6e+05;	
Matches	12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	4 TCATTAGACCGGTAC 17	
Db	2 TCATTAGACCGGTGC 15	
RESULT 26		
BZ358744/c		
LOCUS	BZ358744 32 bp DNA linear GSS 14-NOV-2002	
DEFINITION	SALK 133243.27.05.x Arabidopsis thaliana TDNA insertion lines	
	Arabidopsis thaliana genomic clone SALK 133243.27.05.x, genomic	



University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunne@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0326 row: D column: 24  
Seq primer: CACACAGGAAACAGCATGACC  
Class: plasmid ends  
High quality sequence stop: 38.

## FEATURES

source  
1...38  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clones="UUC1M0326D24"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 50.5%; Score 10.6; DB 8; Length 38;  
Best Local Similarity 76.5%; Pred. No. 4.7e+05;  
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 TCATTAGACCTGACGG 20  
|||||  
Db 18 TCATTAGAGTGACGGG 34

## ORIGIN

Query Match 50.5%; Score 10.6; DB 8; Length 38;  
Best Local Similarity 76.5%; Pred. No. 4.7e+05;  
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 TCATTAGACCTGACGG 20  
|||||  
Db 18 TCATTAGAGTGACGGG 34

## RESULT 28

DME545378/c  
LOCUS 39 bp DNA linear GSS 24-FEB-2003  
DEFINITION Drosophila melanogaster flanking sequence of RS P element insertion P[RS]5-SZ-3505, clone library P[RS]5, genomic survey sequence.  
ACCESSION AJ545378  
VERSION AJ545378.1 GI:28553187  
KEYWORDS GSS; genome survey sequence.  
SOURCE Drosophila melanogaster (fruit fly)  
ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

## REFERENCE

1  
AUTHORS Ryder, E.J., Ashburner, M., Baguna, J., Blows, F., Bucheton, A., Coulson, D., Dickson, B., Drummond, J., Glover, D., Gunton, N., Hafen, E., Hall, S., Heisenberg, M., Lepesant, J.A., Maroy, P., Mechler, B., O'Kane, C., Pflugfelder, G., Rasmuson-Lestander, A., Reuter, G., Roote, J., Sridonya, J., Wang, S., Webster, J. and Russell, S.  
TITLE Mapping of RS P element insertions in *Drosophila melanogaster* for the DrosDel second generation deficiency kit

## JOURNAL REFERENCE

2 (bases 1 to 39)  
AUTHORS Ryder, E.J.

TITLE Direct Submission

JOURNAL Submitted (17-FEB-2003) Ryder E.J., Department of Genetics, University of Cambridge, Downing Street, CB2 3EH, UNITED KINGDOM

COMMENT The insertion point of the P element is before base 1 of the sequence. Further information about this P element insertion line can be found at <http://www.flyseq.org.uk> and <http://www.drosdel.org.uk>.

## FEATURES

source  
1...39  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/chromosome="3L"  
/clone="P[RS]5-SZ-3505"  
/clone\_lib="P[RS]5"  
/note="read=5' end"

misc\_feature  
1...39  
/note="P element insertion in the 5' to 3' orientation"

## ORIGIN

Query Match 50.5%; Score 10.6; DB 9; Length 39;  
Best Local Similarity 76.5%; Pred. No. 4.6e+05;  
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 TCATTAGACCTGACGG 20  
|||||  
Db 18 TCATTAAACATTACGTG 2

## RESULT 29

BH213213/c  
LOCUS 43 bp DNA linear GSS 24-OCT-2001  
DEFINITION SALK\_008917 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK\_008917, genomic survey sequence.  
ACCESSION BH213213  
VERSION BH213213.1 GI:16394927  
KEYWORDS GSS.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

1 (bases 1 to 43)  
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.  
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome  
Unpublished (2001)  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGnAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.  
Location/Qualifiers  
1...43  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/ecotype="Col-0"  
/db\_xref="taxon:3702"  
/clones="SALK\_008917"  
/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was

## JOURNAL REFERENCE

2 (bases 1 to 39)  
AUTHORS Ryder, E.J.

TITLE Direct Submission

JOURNAL Submitted (17-FEB-2003) Ryder E.J., Department of Genetics, University of Cambridge, Downing Street, CB2 3EH, UNITED KINGDOM

COMMENT The insertion point of the P element is before base 1 of the sequence. Further information about this P element insertion line can be found at <http://www.flyseq.org.uk> and <http://www.drosdel.org.uk>.

## FEATURES

source  
1...39  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/chromosome="3L"  
/clone="P[RS]5-SZ-3505"  
/clone\_lib="P[RS]5"  
/note="read=5' end"

misc\_feature  
1...39  
/note="P element insertion in the 5' to 3' orientation"

## ORIGIN

Query Match 50.5%; Score 10.6; DB 9; Length 39;  
Best Local Similarity 76.5%; Pred. No. 4.6e+05;  
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 TCATTAGACCTGACGG 20  
|||||  
Db 18 TCATTAAACATTACGTG 2

## RESULT 29

BH213213/c  
LOCUS 43 bp DNA linear GSS 24-OCT-2001  
DEFINITION SALK\_008917 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK\_008917, genomic survey sequence.  
ACCESSION BH213213  
VERSION BH213213.1 GI:16394927  
KEYWORDS GSS.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

1 (bases 1 to 43)  
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.  
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome  
Unpublished (2001)  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGnAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.  
Location/Qualifiers  
1...43  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/ecotype="Col-0"  
/db\_xref="taxon:3702"  
/clones="SALK\_008917"  
/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)

```

ORIGIN
Query Match          50.5%; Score 10.6; DB 8; Length 43;
Best Local Similarity 76.5%; Pred. No. 4.6e+05;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 TCATTAGCGGTACGCG 20
    ||||| ||||| |||||
Db 41 TCATTATAGGCACGCG 25

RESULT 30
AA441847
LOCUS
DEFINITION
zw62c04.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
IMAGE:774630 5' similar to TR:G558458 G558458 ACIDIC 82 KDA
PROTEIN. i, mRNA sequence.
ACCESSION
AA441847
VERSION
AA441847.1 GI:2153731
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 46)
AUTHORS
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
TITLE
Contact: Wilson RK
JOURNAL
Washington University School of Medicine
COMMENT
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estowatson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.
FEATURES
Location/Qualifiers
1..46
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:774630"
/dev_stage="8-9 weeks"
/lab_host="PH10B"
/clone_lib="Soares total fetus Nb2HF8_9w"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(GT) primer [5'
TGTTCACCATCTAGATGGAGCGCGCTTAATTTTATTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Facima Bonaldo."

ORIGIN
Query Match          50.5%; Score 10.6; DB 1; Length 46;
Best Local Similarity 76.5%; Pred. No. 4.6e+05;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGGTATTAGCGGTAC 17
    ||||| ||||| |||||

```

```

Db 27 CGTCATTACACCTGAC 43

RESULT 31
AZ769367/c
LOCUS
DEFINITION
1M0569021R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0569021 R, genomic survey sequence.
ACCESSION
AZ769367
VERSION
AZ769367.1 GI:12889428
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 46)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
TITLE
Contact: Robert B. Weiss
JOURNAL
University of Utah Genome Center
COMMENT
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0569 row: 0 column: 21
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 46.
FEATURES
Location/Qualifiers
1..46
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0569021"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match          50.5%; Score 10.6; DB 8; Length 46;
Best Local Similarity 76.5%; Pred. No. 4.6e+05;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 CATTAGACCGTACGCGA 21
    || ||||| ||||| |||||

```

21 CAGAGACGCCACGCCA 5

Db

RESULT 32

BZ379971/c

LOCUS

DEFINITION

Arabidopsis thaliana genomic clone SALK\_114399.18.50.x, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BZ379971

BZ379971.1 GI:25472355

GSS

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 46)

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmermann, J., and Ecker, J.R.

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At4g03070.

Class: TDNA tagged.

FEATURES

source

1..46

Location/Qualifiers

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/ecotype="Col-0"

/db\_xref="taxon:3702"

/clone="SALK\_114399.18.50.x"

/clone\_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)."

ORIGIN

Query Match 50.5%; Score 10.6; DB 8; Length 46;

Best Local Similarity 76.5%; Pred. No. 4.6e+05;

Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY

5 CATTAGACCGTACGCCA 21

|||||

Db

39 CATATTACCTTACGCCA 23

|||||

RESULT 33

AL753413

LOCUS

DEFINITION

Arabidopsis thaliana T-DNA flanking sequence GK-049H07-013871, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AL753413

AL753413.1 GI:21485911

GSS

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1

Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P., and Weisshaar, B. GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana

Bioinformatics 19 (11), 1441-1442 (2003)

22755829

PUBMED

12874060

REFERENCE

2

ROSSO, M.G., LI, Y., STRIZHOV, N., REISS, B., DEKKER, K. and WEISSHAAR, B.

An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics

Plant Mol. Biol. 53 (1-2), 247-259 (2003)

23117147

PUBMED

14756321

REFERENCE

3

STRIZHOV, N., LI, Y., ROSSO, M.G., VIEHOEVER, P., DEKKER, K.A. and WEISSHAAR, B.

High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines

BioTechniques 35 (6), 1164-1168 (2003)

14682050

PUBMED

4 (bases 1 to 46)

Li, Y., Rosso, M.G., Strizhov, N. and Weisshaar, B.

Direct Submission

Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone F2605. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

Location/Qualifiers

1..46

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="GK-049H07-013871"

/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"

/ecotype="Col-0"

/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Query Match 50.5%; Score 10.6; DB 9; Length 46;

Best Local Similarity 76.5%; Pred. No. 4.6e+05;

Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY

4 TCATTAGACCGTACCGC 20

|||||

Db

24 TCATTAAACGTAACG 40

|||||

RESULT 34

H50401

LOCUS

DEFINITION

Y029h01.r1 Soares adult brain N25HB55Y Homo sapiens cDNA clone IMAGE:179377 5', similar to SP:A45072 A45072 TYPE L K+ CHANNEL, KV3.1 - HUMAN ;, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

H50401

H50401.1 GI:990242

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 49)

Hilliet.L., Clark.N., Dubuque.T., Elliston.K., Hawkins.M., Holman.M., Hultman.M., Kucaba.T., Le.M., Lennon.G., Marra.M., Parsons.J., Rifkin.L., Rohlfing.T., Soares.M., Tan.F., Trevaskis.B., Waterston.R., Williamson.A., Wohldmann.P. and Wilson.R.

The WashU-Merck EST Project

Unpublished (1995)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 1530

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Insert length: 1530 Std Error: 0.00

Seq primer: M13RP1

High quality sequence stop: 1.

Location/Qualifiers

1. .49

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:3841573"

/db\_xref="taxon:9606"

/clone="IMAGE:179377"

/sex="Male"

/dev\_stage="55-year old"

/lab\_host="PH10B (ampicillin resistant)"

/clone\_lib="Soares adult brain N25HB55Y"

/note="Organ: brain; Vector: pT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TTTTACCATCTGAGTGGACGCCGCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 53. Library constructed by Bento Soares and M.Fatima Ronaldo. The adult brain RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of a ruptured aortic aneurysm. RNA was prepared from a pool of tissues representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, subcortical white matter, basal ganglia, thalamus, cerebellum, midbrain, pons and medulla."

Query Match 50.5%; Score 10.6; DB 7; Length 49;

Best Local Similarity 65.0%; Pred. No. 4.6e+05;

Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 GGTCTATTAGACCGTACGCGA 21

|||||

Db 10 GNTCATTGGCTGTGCNCA 29

|||||

RESULT 35

AW004243

LOCUS

DEFINITION

25 bp mRNA linear EST 08-SEP-1999

AW004243

701552628 A. thaliana, Columbia Col-0, root-2 Arabidopsis thaliana

cdna clone 701552628, mRNA sequence.

ACCESSION

AW004243

VERSION

AW004243.1

GI:5951272

EST.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 25)

Chen,J., Momiyama,M., Chan,E., Mooney,M., Carroon,B., Gilliland,D., Wang,X., Hillman,J., Guegler,K., Kim,C., Doyle,M., Brzoska,P., Gorgone,G., Burns,D., Griffin,J., Mouanoutoua,M., Nguyen,D., Tan,R., Rose,M., Warren,B., Ton,B., Kastyur,K., Borillo,C., Carpio,T., Policky,J., Suzuki,G., Argentine,C., Shah,S., Nobrega,A., Murry,L., Turner,C., Krikorian,S., Elder,L. and Hanson,D.

Arabidopsis thaliana Gene Expression Microarray

Unpublished (1999)

Contact: David Smoller, Ph.D.

Genome Systems, Inc., a wholly owned subsidiary of Incyte Pharmaceuticals, Inc.

4633 World Parkway Circle, St. Louis, MO 63134, USA

Tel: 877-577-2733

Fax: 314-427-3324

Email: service@genomesystems.com.

Location/Qualifiers

1. .25

/organism="Arabidopsis thaliana"

/mol\_type="mRNA"

/ecotype="Col-0"

/db\_xref="taxon:3702"

/clone="701552628"

/tissue\_type="root"

/dev\_stage="4 - 7 weeks"

/clone\_lib="A. thaliana, Columbia Col-0, root-2"

/note="Vector: pSPORT; Site 1: NotI; Site 2: SalI; cdna library was derived from untreated root tissue from Arabidopsis thaliana, Columbia Col-0, at 4 - 7 weeks. Plants were grown in 1:1:1 peat moss/vermiculite/perlite soil at 22 deg. C +/- 3 deg. C under constant light, and watered with fertilizer. cDNA synthesis was initiated using a NotI-oligo(dT) primer. Double-stranded cDNA was blunted, ligated to SalI adaptors, digested with NotI, size-selected, and cloned into the NotI and SalI sites of the pSPORT vector."

Query Match 49.5%; Score 10.4; DB 1; Length 25;

Best Local Similarity 70.0%; Pred. No. 6.1e+05;

Matches 14; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CGGTCTATTAGACCGTACGCG 20

|||||

Db 3 CGGAACACACCGGACGCG 22

|||||

RESULT 36

AZ317845/c

LOCUS

DEFINITION

30 bp DNA linear GSS 29-SEP-2000

1M0036K16R Mouse 10kb plasmid UUGCLM library Mus musculus genomic clone UUGCLM0036K16 R, genomic survey sequence.

ACCESSION

AZ317845

VERSION

AZ317845.1

GI:10367047

GSS.

KEYWORDS

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 30)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10Kb

AW004243.1

GI:5951272

EST.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 25)

Chen,J., Momiyama,M., Chan,E., Mooney,M., Carroon,B., Gilliland,D., Wang,X., Hillman,J., Guegler,K., Kim,C., Doyle,M., Brzoska,P., Gorgone,G., Burns,D., Griffin,J., Mouanoutoua,M., Nguyen,D., Tan,R., Rose,M., Warren,B., Ton,B., Kastyur,K., Borillo,C., Carpio,T., Policky,J., Suzuki,G., Argentine,C., Shah,S., Nobrega,A., Murry,L., Turner,C., Krikorian,S., Elder,L. and Hanson,D.

Arabidopsis thaliana Gene Expression Microarray

Unpublished (1999)

Contact: David Smoller, Ph.D.

Genome Systems, Inc., a wholly owned subsidiary of Incyte Pharmaceuticals, Inc.

4633 World Parkway Circle, St. Louis, MO 63134, USA

Tel: 877-577-2733

Fax: 314-427-3324

Email: service@genomesystems.com.

Location/Qualifiers

1. .25

/organism="Arabidopsis thaliana"

/mol\_type="mRNA"

/ecotype="Col-0"

/db\_xref="taxon:3702"

/clone="701552628"

/tissue\_type="root"

/dev\_stage="4 - 7 weeks"

/clone\_lib="A. thaliana, Columbia Col-0, root-2"

/note="Vector: pSPORT; Site 1: NotI; Site 2: SalI; cdna library was derived from untreated root tissue from Arabidopsis thaliana, Columbia Col-0, at 4 - 7 weeks. Plants were grown in 1:1:1 peat moss/vermiculite/perlite soil at 22 deg. C +/- 3 deg. C under constant light, and watered with fertilizer. cDNA synthesis was initiated using a NotI-oligo(dT) primer. Double-stranded cDNA was blunted, ligated to SalI adaptors, digested with NotI, size-selected, and cloned into the NotI and SalI sites of the pSPORT vector."

Query Match 49.5%; Score 10.4; DB 1; Length 25;

Best Local Similarity 70.0%; Pred. No. 6.1e+05;

Matches 14; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CGGTCTATTAGACCGTACGCG 20

|||||

Db 3 CGGAACACACCGGACGCG 22

|||||

RESULT 36

AZ317845/c

LOCUS

DEFINITION

30 bp DNA linear GSS 29-SEP-2000

1M0036K16R Mouse 10kb plasmid UUGCLM library Mus musculus genomic clone UUGCLM0036K16 R, genomic survey sequence.

ACCESSION

AZ317845

VERSION

AZ317845.1

GI:10367047

GSS.

KEYWORDS

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 30)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10Kb

plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0036 row: K column: 16  
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/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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## COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-r@mail.nih.gov  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality  
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## FEATURES

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## ORIGIN

Query Match 49.5%; Score 10.4; DB 1; Length 37;  
 Best Local Similarity 70.0%; Pred. No. 6.1e+05;  
 Matches 14; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY

1 CGCTCATTAGACCGTACGCG 20

Db

14 CGCTCGCATGACCGTACGCG 33

RESULT 39

BZ377768/c

LOCUS

DEFINITION BZ377768 37 bp DNA linear GSS 26-NOV-2002  
 SALK\_106163.28.55.n Arabidopsis thaliana TDNA insertion lines  
 Arabidopsis thaliana genomic clone SALK\_106163.28.55.n, genomic survey sequence.

ACCESSION

BZ377768

VERSION

BZ377768.1

KEYWORDS

GSS.

SOURCE

Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 37)

REFERENCE

AUTHORS

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,

Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,

Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@alk.edu

This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of AT2g25610.

Class: TDNA tagged.

Location/Qualifiers

source

1. .37

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/mol\_type="genomic DNA"

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/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

## ORIGIN

Query Match 49.5%; Score 10.4; DB 8; Length 37;

Best Local Similarity 91.7%; Pred. No. 6.1e+05;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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4 TCATTAGACCGT 15

Db

24 TCATTAGACCGT 13

RESULT 40

BZ383634/c

LOCUS

DEFINITION

BZ383634 37 bp DNA linear GSS 26-NOV-2002

SALK\_134205.28.00.n Arabidopsis thaliana TDNA insertion lines

Arabidopsis thaliana genomic clone SALK\_134205.28.00.n, genomic survey sequence.

ACCESSION

BZ383634

VERSION

BZ383634.1

KEYWORDS

GSS.

SOURCE

Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 37)

REFERENCE

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Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,

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Query Match 49.5%; Score 10.4; DB 8; Length 37;  
 Best Local Similarity 91.7%; Pred. NO. 6.1e+05;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCATTAGACCGT 15  
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 Db 24 TCATTAGACCGT 13

Search completed: November 23, 2004, 22:25:16  
 Job time : 1007.82 secs

**This Page Blank (uspto)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:50:22 ; Search time 504.21 Seconds  
(without alignments)  
2626.113 Million cell updates/sec

Title: US-10-087-631B-7  
Perfect score: 28  
Sequence: 1 gcaagcaccctatcaggcagtcaccacaa 28

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 1785872

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_hgt.\*
- 3: gb\_in.\*
- 4: gb\_on.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	28	100.0	28	6	AR094138 Sequence
3	28	100.0	28	6	BD181368 A method
4	28	100.0	28	6	AX147022 Sequence
5	28	100.0	28	6	AX523948 Sequence
6	28	100.0	28	6	AX524846 Sequence
c 7	28	100.0	47	6	AR204716 Sequence
c 8	28	100.0	47	6	AX284180 Sequence
9	27	96.4	27	6	AR054577 Sequence
10	27	96.4	27	6	AR411541 Sequence
11	27	96.4	27	6	BD000267 Sequence
c 12	27	96.4	29	6	BD183052 Sequence
13	25	89.3	40	6	E17189 Partial seq
14	24	85.7	28	6	AR094374 Sequence
15	24	85.7	33	6	AR004397 Sequence
16	24	85.7	33	6	AR064936 Sequence
17	24	85.7	33	6	AR097189 Sequence
18	24	85.7	33	6	AR130687 Sequence
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118	17	60.7	28	6	AX282437	AX282437 Sequence	191	15	53.6	20	6	E17190	E17190 A reverse p
119	17	60.7	30	6	AR428912	AR428912 Sequence	192	15	53.6	20	6	AR222518	AR222518 Sequence
120	17	60.7	30	6	AR488115	AR488115 Sequence	193	15	53.6	22	6	E07366	E07366 PCR primer
121	17	60.7	30	6	AX472308	AX472308 Sequence	194	15	53.6	25	6	AR400913	AR400913 Sequence
122	17	60.7	30	6	AX696020	AX696020 Sequence	195	15	53.6	25	6	AR400922	AR400922 Sequence
123	17	60.7	30	6	AX720384	AX720384 Sequence	196	15	53.6	25	6	AR411543	AR411543 Sequence
124	17	60.7	30	6	AX720388	AX720388 Sequence	197	15	53.6	25	6	BD000247	BD000247 Oligonuc
125	17	60.7	30	6	AX814299	AX814299 Sequence	198	15	53.6	25	6	BD000256	BD000256 Oligonuc
126	17	60.7	30	6	AX814302	AX814302 Sequence	199	15	53.6	25	6	BD000269	BD000269 Oligonuc
127	16.8	60.0	21	6	AX003961	AX003961 Sequence	200	15	53.6	30	6	BD161083	BD161083 RNA molec
128	16.8	60.0	21	6	AX021583	AX021583 Sequence	201	15	53.6	30	6	BD161084	BD161084 RNA molec
129	16.8	60.0	21	6	AX021640	AX021640 Sequence	202	14.8	52.9	22	6	E07372	E07372 PCR primer
130	16.8	60.0	21	6	BD138680	BD138680 Specific	203	14.6	52.1	20	6	AX003970	AX003970 Sequence
131	16.4	58.6	33	6	BD177933	BD177933 Sequence	204	14.6	52.1	20	6	AX021592	AX021592 Sequence
132	16.4	58.6	33	6	AR351581	AR351581 Sequence	205	14.6	52.1	20	6	AX021648	AX021648 Sequence
133	16.4	58.6	33	6	AX492891	AX492891 Sequence	206	14.6	52.1	20	6	BD138688	BD138688 Specific
134	16.4	58.6	34	6	AR351583	AR351583 Sequence	207	14.6	52.1	20	6	AR090031	AR090031 Sequence
135	16.4	58.6	34	6	AX492893	AX492893 Sequence	208	14.6	52.1	30	6	AR197066	AR197066 Sequence
136	16.4	58.6	34	6	AX492893	AX492893 Sequence	209	14.6	52.1	30	6	AR259220	AR259220 Sequence
137	16.4	58.6	48	9	HS249814	HS249814 Homo sapi	210	14.6	52.1	30	6	E03834	E03834 DNA encodin
138	16	57.1	16	6	AR285662	AR285662 Sequence	211	14.4	51.4	30	6	AX021657	AX021657 Sequence
139	16	57.1	16	6	AR397653	AR397653 Sequence	212	14.4	51.4	31	6	AX021601	AX021601 Sequence
140	16	57.1	18	6	BD185893	BD185893 A stabili	213	14.4	51.4	31	6	AX021597	AX021597 Sequence
141	16	57.1	45	6	BD004847	BD004847 Method fo	214	14.4	51.4	31	6	AX021597	AX021597 Sequence
142	15.8	56.4	18	6	AX003973	AX003973 Sequence	215	14.4	51.4	31	6	AX003975	AX003975 Sequence
143	15.8	56.4	18	6	AX021595	AX021595 Sequence	216	14.4	51.4	31	6	AX003979	AX003979 Sequence
144	15.8	56.4	18	6	BD138691	BD138691 Specific	217	14.2	50.7	18	6	AX021597	AX021597 Sequence
145	15.8	56.4	18	6	AX003963	AX003963 Sequence	218	14.2	50.7	18	6	AX021597	AX021597 Sequence
146	15.8	56.4	20	6	AX021586	AX021586 Sequence	219	14.2	50.7	18	6	AX021597	AX021597 Sequence
147	15.8	56.4	20	6	AX021642	AX021642 Sequence	220	14.2	50.7	18	6	AX021597	AX021597 Sequence
148	15.8	56.4	20	6	BD138682	BD138682 Specific	221	14.2	50.7	18	6	AX021597	AX021597 Sequence
149	15.8	56.4	20	6	S86440	S86440 TCR V beta	222	14.2	50.7	18	6	BD138693	BD138693 Specific
150	15.8	56.4	36	10	S86440	S86440 TCR V beta	223	14.2	50.7	18	6	BD138697	BD138697 Specific
151	15.6	55.7	21	6	AX003968	AX003968 Sequence	224	14.2	50.7	18	6	AX003966	AX003966 Sequence
152	15.4	55.0	22	6	AR381924	AR381924 Sequence	225	14.2	50.7	20	6	AX021589	AX021589 Sequence
153	15.4	55.0	22	6	AX165783	AX165783 Sequence	226	14.2	50.7	20	6	AX021589	AX021589 Sequence
154	15.4	55.0	24	6	E06775	E06775 Primer to d	227	14.2	50.7	20	6	AX021645	AX021645 Sequence
155	15.2	54.3	21	6	AX003964	AX003964 Sequence	228	14.2	50.7	20	6	BD138685	BD138685 Specific
156	15.2	54.3	21	6	AX021587	AX021587 Sequence	229	14.2	50.7	20	6	AX021645	AX021645 Sequence
157	15.2	54.3	21	6	AX021643	AX021643 Sequence	230	14.2	50.7	20	6	BD138685	BD138685 Specific
158	15.2	54.3	21	6	BD138683	BD138683 Specific	231	14.2	50.7	20	6	AX021645	AX021645 Sequence
159	15	53.6	15	6	A70975	A70975 Sequence 29	232	14.2	50.7	20	6	BD138685	BD138685 Specific
160	15	53.6	15	6	AR033247	AR033247 Sequence	233	14	50.0	16	6	AX021645	AX021645 Sequence
161	15	53.6	15	6	AR033248	AR033248 Sequence	234	14	50.0	16	6	AX021645	AX021645 Sequence
162	15	53.6	15	6	AR113069	AR113069 Sequence	235	14	50.0	18	6	AX021645	AX021645 Sequence
163	15	53.6	15	6	AR113070	AR113070 Sequence	236	14	50.0	19	6	AX021645	AX021645 Sequence
164	15	53.6	15	6	BD206980	BD206980 Enzymatic	237	14	50.0	26	6	AX021645	AX021645 Sequence
165	15	53.6	15	6	BD206981	BD206981 Enzymatic	238	14	50.0	26	6	AX021645	AX021645 Sequence

c 239	14	50.0	30	6	AR036104	Sequence	312	12.8	45.7	26	6	AR215087	Sequence
c 240	14	50.0	30	6	AR037033	Sequence	c 313	12.8	45.7	26	6	AR215089	Sequence
c 241	14	50.0	30	6	AR071738	Sequence	314	12.8	45.7	26	6	BD073565	Novel Pic
c 242	14	50.0	41	6	AX514331	Sequence	c 315	12.8	45.7	26	6	BD073567	Novel Pic
c 243	14	50.0	41	6	AX519898	Sequence	316	12.8	45.7	29	6	BD259030	Regulation
c 244	14	50.0	43	6	AX697252	Sequence	317	12.8	45.7	31	6	AR217198	Sequence
c 245	14	50.0	44	6	AX397949	Sequence	318	12.8	45.7	31	6	AR217204	Sequence
c 246	14	50.0	44	6	AX397961	Sequence	319	12.8	45.7	31	6	AX088379	Sequence
c 247	14	50.0	46	6	BD175036	Method fo	c 320	12.8	45.7	31	6	AX088385	Sequence
c 248	14	50.0	46	6	BD102536	Method fo	321	12.8	45.7	47	6	AR291109	Sequence
c 249	14	50.0	50	6	CQ003036	Sequence	322	12.8	45.7	47	6	AX612137	Sequence
c 250	14	50.0	50	6	CQ008879	Sequence	323	12.8	45.7	48	6	CQ654228	Sequence
c 251	14	50.0	50	6	AX397948	Sequence	c 324	12.8	45.7	50	6	CQ007050	Sequence
c 252	14	50.0	50	6	AX397960	Sequence	325	12.8	45.7	50	6	AR218541	Sequence
c 253	13.8	49.3	30	6	AX026567	Sequence	326	12.8	45.7	50	6	AR218542	Sequence
c 254	13.8	49.3	40	6	AX026567	Sequence	327	12.8	45.7	50	6	AX657047	Sequence
c 255	13.6	48.6	40	6	BD185267	Method fo	328	12.8	45.7	50	6	AX657048	Sequence
c 256	13.6	48.6	20	6	AX3564	Sequence 2	329	12.8	45.7	50	6	AX657049	Sequence
c 257	13.6	48.6	21	6	AR129461	Sequence	330	12.6	45.0	19	6	CQ776067	Sequence
c 258	13.6	48.6	26	6	BD134691	Human mal	331	12.6	45.0	19	6	CQ779508	Sequence
c 259	13.6	48.6	39	6	AX769755	Sequence	332	12.6	45.0	24	6	AS8796	Sequence 7
c 260	13.6	48.6	48	5	OMY517942	AJ517942 Oncorhync	333	12.6	45.0	24	6	AR304628	Sequence
c 261	13.6	48.6	48	6	AX156818	Sequence	c 334	12.6	45.0	24	6	AX447057	Sequence
c 262	13.6	48.6	50	6	AX156820	Sequence	c 335	12.6	45.0	25	6	AX448487	Sequence
c 263	13.4	47.9	30	6	BD133378	Method fo	c 336	12.6	45.0	25	6	AX078473	Sequence
c 264	13.4	47.9	40	6	AX538429	Sequence	337	12.6	45.0	30	6	AX084173	Sequence
c 265	13.4	47.9	44	6	CQ760654	Sequence	c 338	12.6	45.0	30	6	AX791282	Sequence
c 266	13.4	47.9	49	6	AX614097	Sequence	c 339	12.6	45.0	35	6	AX167070	Sequence
c 267	13.4	47.9	50	10	Y03355S05	AX033559 Mus muscu	340	12.6	45.0	36	6	AR077793	Sequence
c 268	13.2	47.1	20	6	AR085562	Sequence	341	12.6	45.0	36	6	BD227160	Protease
c 269	13.2	47.1	20	6	AR085563	Sequence	342	12.6	45.0	36	6	AR368738	Sequence
c 270	13.2	47.1	20	6	AR216082	Sequence	343	12.6	45.0	36	6	AR392693	Sequence
c 271	13.2	47.1	20	6	AR216083	Sequence	344	12.6	45.0	38	6	AR330466	Sequence
c 272	13.2	47.1	25	6	AX196917	Sequence	345	12.6	45.0	38	6	AR333324	Sequence
c 273	13.2	47.1	25	6	BD206483	Enzymatic	346	12.6	45.0	38	6	AX219621	Sequence
c 274	13.2	47.1	27	6	AX3853	Sequence 1	347	12.6	45.0	38	6	AX228363	Sequence
c 275	13.2	47.1	29	6	BD200428	Method an	c 348	12.6	45.0	39	6	AX108742	Sequence
c 276	13.2	47.1	29	6	AR200602	Sequence	c 349	12.6	45.0	40	6	AI3294	Sequence
c 277	13.2	47.1	29	6	AX662636	Sequence	c 350	12.6	45.0	40	6	E32723	Small tripl
c 278	13.2	47.1	29	6	AX081549	Sequence	c 351	12.6	45.0	40	6	AX000279	Sequence
c 279	13.2	47.1	30	6	AX084172	Sequence	c 352	12.6	45.0	41	6	A20761	Promoterreg
c 280	13.2	47.1	31	6	BD002450	Gene comp	c 353	12.6	45.0	41	6	AR051798	Sequence
c 281	13.2	47.1	33	6	AX361202	Sequence	354	12.6	45.0	41	6	AX516884	Sequence
c 282	13.2	47.1	37	6	AX183784	Sequence	355	12.6	45.0	41	6	AX519394	Sequence
c 283	13.2	47.1	38	6	AX82703	Sequence 48	c 356	12.6	45.0	42	6	AR195542	Sequence
c 284	13.2	47.1	42	6	AX694662	Sequence	357	12.6	45.0	45	10	MMH2RNA	X60855 M.mueculus
c 285	13.2	47.1	43	6	AR079783	Sequence	358	12.6	45.0	49	6	CQ654308	Sequence
c 286	13.2	47.1	43	6	AR081313	Sequence	359	12.6	45.0	50	6	CQ004215	Sequence
c 287	13.2	47.1	43	6	AR170673	Sequence	c 360	12.6	45.0	50	6	CQ008709	Sequence
c 288	13.2	47.1	48	6	BD007251	Novel flt	c 361	12.6	45.0	50	6	AX589636	Sequence
c 289	13.2	47.1	48	6	BD022525	BD022525 Multi-fun	c 362	12.4	44.3	18	6	AR048544	Sequence
c 290	13	46.4	19	6	E06600	E06600 PCR primer	c 363	12.4	44.3	18	6	AR051905	Sequence
c 291	13	46.4	19	6	BD004751	BD004751 Method fo	c 364	12.4	44.3	18	6	AR075933	Sequence
c 292	13	46.4	20	6	E06778	E06778 Primer to d	c 365	12.4	44.3	24	6	AR048537	Sequence
c 293	13	46.4	24	6	AR011821	AR011821 Sequence	c 366	12.4	44.3	24	6	AR075926	Sequence
c 294	13	46.4	24	6	I77144	I77144 Sequence 16	367	12.4	44.3	25	6	AX609288	Sequence
c 295	13	46.4	31	6	AX248123	Sequence	368	12.4	44.3	26	6	A31651	A31651 Synthetic P
c 296	13	46.4	31	6	AX248843	Sequence	369	12.4	44.3	30	6	AR3158	AR3158 Sequence 8
c 297	13	46.4	31	14	SV4EV14A	K01538 SV40 varian	370	12.4	44.3	30	6	AR207271	Sequence
c 298	13	46.4	35	6	BD186553	BD186553 Gene tran	371	12.4	44.3	32	6	AR065300	Sequence
c 299	13	46.4	35	6	BD092072	BD092072 Vector fo	c 372	12.4	44.3	32	6	AR065301	Sequence
c 300	13	46.4	36	6	BD209503	Enzymatic	c 373	12.4	44.3	38	6	AR329804	Sequence
c 301	13	46.4	38	6	AR332574	Sequence	c 374	12.4	44.3	38	6	AR331552	Sequence
c 302	13	46.4	38	6	AR333916	Sequence	c 375	12.4	44.3	38	6	AR334273	Sequence
c 303	13	46.4	40	6	AX514976	Sequence	c 376	12.4	44.3	38	6	AX219528	Sequence
c 304	13	46.4	40	6	AX517322	Sequence	c 377	12.4	44.3	38	6	AX273695	Sequence
c 305	13	46.4	42	9	S68042	S68042 hemoglobin	c 378	12.4	44.3	38	6	AX273729	Sequence
c 306	13	46.4	45	6	AR157675	AR157675 Sequence	c 379	12.4	44.3	39	6	AR009887	Sequence
c 307	13	46.4	45	6	AR157676	AR157676 Sequence	380	12.4	44.3	41	6	AX710963	Sequence
c 308	12.8	45.7	17	6	AX727750	AX727750 Sequence	381	12.4	44.3	41	6	BD001104	Method an
c 309	12.8	45.7	18	6	AR437453	Sequence	382	12.4	44.3	41	6	BD001533	Method an
c 310	12.8	45.7	21	6	BD142103	BD142103 A method	383	12.4	44.3	45	6	AR168078	Sequence
c 311	12.8	45.7	21	6	BD142139	BD142139 A method	384	12.4	44.3	45	6	AR204849	Sequence

385	12.4	44.3	45	10	MM3AR5RNA	X60903 M.musculus	458	12	42.9	33	6	AX280443	AX280443 Sequence
386	12.4	44.3	46	5	OMV517921	AJ517921 Oncorhync	c 459	12	42.9	34	6	AX384900	AX384900 Sequence
387	12.4	44.3	46	6	AX040127	AX040127 Sequence	460	12	42.9	36	6	AR001578	AR001578 Sequence
388	12.4	44.3	47	6	AR289042	AR289042 Sequence	461	12	42.9	37	6	AR211686	AR211686 Sequence
389	12.4	44.3	47	6	AR292084	AR292084 Sequence	462	12	42.9	38	6	AR332085	AR332085 Sequence
390	12.4	44.3	48	6	AR076783	AR076783 Sequence	463	12	42.9	38	6	AX218427	AX218427 Sequence
391	12.2	43.6	20	6	AR226034	AR226034 Sequence	464	12	42.9	38	6	AX218653	AX218653 Sequence
392	12.2	43.6	22	6	AR073920	AR073920 Sequence	465	12	42.9	38	6	AX219590	AX219590 Sequence
393	12.2	43.6	22	6	AR176064	AR176064 Sequence	466	12	42.9	38	6	AX222811	AX222811 Sequence
394	12.2	43.6	25	6	AX110464	AX110464 Sequence	467	12	42.9	38	6	AX580579	AX580579 Sequence
395	12.2	43.6	25	6	AX110487	AX110487 Sequence	c 468	12	42.9	39	6	AX299895	AX299895 Sequence
396	12.2	43.6	28	6	E05106	E05106 PCR primer	c 469	12	42.9	39	6	AX611632	AX611632 Sequence
397	12.2	43.6	29	6	A17131	A17131 Oligonucleo	c 470	12	42.9	40	6	E32724	E32724 Small tripl
398	12.2	43.6	29	6	AR027515	AR027515 Sequence	c 471	12	42.9	40	6	AX000280	AX000280 Sequence
399	12.2	43.6	32	6	A17130	A17130 Oligonucleo	c 472	12	42.9	40	6	AX538428	AX538428 Sequence
400	12.2	43.6	32	6	AR027514	AR027514 Sequence	c 473	12	42.9	41	6	AX514947	AX514947 Sequence
401	12.2	43.6	34	6	I04231	I04231 Sequence 3	c 474	12	42.9	41	6	AX514948	AX514948 Sequence
402	12.2	43.6	36	6	AR078502	AR078502 Sequence	c 475	12	42.9	41	6	AX515169	AX515169 Sequence
403	12.2	43.6	36	6	AX030041	AX030041 Sequence	c 476	12	42.9	41	6	AX517295	AX517295 Sequence
404	12.2	43.6	36	6	AX030042	AX030042 Sequence	c 477	12	42.9	41	6	AX517961	AX517961 Sequence
405	12.2	43.6	36	6	A05043	A05043 Oligonucleo	c 478	12	42.9	41	6	BD205021	BD205021 Gene enco
406	12.2	43.6	38	6	A05057	A05057 NOR-361 oli	c 479	12	42.9	42	6	BD205022	BD205022 Gene enco
407	12.2	43.6	38	6	A08153	A08153 Oligonucleo	c 480	12	42.9	42	6	AX014772	AX014772 Sequence
408	12.2	43.6	38	6	A13254	A13254 oligonucleo	c 481	12	42.9	42	6	AX014773	AX014773 Sequence
409	12.2	43.6	38	6	A29677	A29677 NOR-361 oli	c 482	12	42.9	42	6	AX014773	AX014773 Sequence
410	12.2	43.6	38	6	AR045842	AR045842 Sequence	c 483	12	42.9	45	3	DR0COPCIS	K02191 D. melanoga
411	12.2	43.6	38	6	I33204	I33204 Sequence 27	c 484	12	42.9	47	6	AR288546	AR288546 Sequence
412	12.2	43.6	38	6	I40183	I40183 Sequence 27	c 485	12	42.9	49	6	C0828092	C0828092 Sequence
413	12.2	43.6	38	6	I40415	I40415 Sequence 27	c 486	12	42.9	49	6	BD141204	BD141204 Fungal ce
414	12.2	43.6	38	6	I52894	I52894 Sequence 63	c 487	12	42.9	50	6	AR252548	AR252548 Sequence
415	12.2	43.6	39	6	A05042	A05042 Oligonucleo	c 488	12	42.9	50	6	AX403364	AX403364 Sequence
416	12.2	43.6	39	6	A05056	A05056 NOR-360 oli	c 489	12	42.9	50	9	HUMUR1	K03097 Human (HeLa
417	12.2	43.6	39	6	A08152	A08152 Oligonucleo	c 490	11.8	42.1	17	6	AX724658	AX724658 Sequence
418	12.2	43.6	39	6	A13253	A13253 Oligonucleo	c 491	11.8	42.1	18	6	A59327	A59327 Sequence 14
419	12.2	43.6	39	6	A29676	A29676 NOR-360 oli	c 492	11.8	42.1	18	6	AX838076	AX838076 Sequence
420	12.2	43.6	39	6	I33203	I33203 Sequence 26	c 493	11.8	42.1	18	6	AX838302	AX838302 Sequence
421	12.2	43.6	39	6	I40182	I40182 Sequence 26	c 494	11.8	42.1	20	6	AR165946	AR165946 Sequence
422	12.2	43.6	39	6	I40414	I40414 Sequence 26	c 495	11.8	42.1	20	6	BD013359	BD013359 Primer fo
423	12.2	43.6	39	6	AX769757	AX769757 Sequence	c 496	11.8	42.1	21	6	AX095891	AX095891 Sequence
424	12.2	43.6	40	6	AX538442	AX538442 Sequence	c 497	11.8	42.1	21	6	AX146004	AX146004 Sequence
425	12.2	43.6	41	6	AR109150	AR109150 Sequence	c 498	11.8	42.1	22	6	AR404938	AR404938 Sequence
426	12.2	43.6	41	6	BD217553	BD217553 Glucoamyl	c 499	11.8	42.1	22	6	AR404961	AR404961 Sequence
427	12.2	43.6	41	6	AR198433	AR198433 Sequence	c 500	11.8	42.1	22	6	AX441284	AX441284 Sequence
428	12.2	43.6	41	6	AR200805	AR200805 Sequence	c 501	11.8	42.1	22	6	AX441307	AX441307 Sequence
429	12.2	43.6	42	6	AR031539	AR031539 Sequence	c 502	11.8	42.1	22	6	BD161566	BD161566 Base sequ
430	12.2	43.6	42	6	AX059013	AX059013 Sequence	c 503	11.8	42.1	22	6	BD171607	BD171607 Method fo
431	12.2	43.6	43	6	AX426331	AX426331 Sequence	c 504	11.8	42.1	23	6	AX663305	AX663305 Sequence
432	12.2	43.6	48	9	HSBOM1B	X72102 H.septiens (	c 505	11.8	42.1	23	10	MMU459714	AJ459714 Mus muscu
433	12.2	43.6	49	6	CQ654493	CQ654493 Sequence	c 506	11.8	42.1	24	6	CQ816789	CQ816789 Sequence
434	12.2	43.6	50	6	BD274559	BD274559 Different	c 507	11.8	42.1	24	6	AX447216	AX447216 Sequence
435	12.2	43.6	50	6	CQ002459	CQ002459 Sequence	c 508	11.8	42.1	24	6	BD143469	BD143469 Human lhx
436	12.2	43.6	50	6	AX073412	AX073412 Sequence	c 509	11.8	42.1	25	6	AR474227	AR474227 Sequence
437	12.2	43.6	50	6	AX645652	AX645652 Sequence	c 510	11.8	42.1	25	6	AX043261	AX043261 Sequence
438	12.2	42.9	18	6	A52658	A52658 Sequence 3	c 511	11.8	42.1	25	6	AX825359	AX825359 Sequence
439	12.2	42.9	20	6	AR066820	AR066820 Sequence	c 512	11.8	42.1	25	6	AX825359	AX825359 Sequence
440	12.2	42.9	20	6	AX295758	AX295758 Sequence	c 513	11.8	42.1	26	6	AX240247	AX240247 Sequence
441	12.2	42.9	21	6	AX459913	AX459913 Sequence	c 514	11.8	42.1	27	6	AX066363	AX066363 Sequence
442	12.2	42.9	22	6	E07368	E07368 PCR primer	c 515	11.8	42.1	27	6	AX317744	AX317744 Sequence
443	12.2	42.9	22	6	AX802837	AX802837 Sequence	c 516	11.8	42.1	28	6	AR096214	AR096214 Sequence
444	12.2	42.9	24	6	AX291125	AX291125 Sequence	c 517	11.8	42.1	28	6	CQ787532	CQ787532 Sequence
445	12.2	42.9	24	6	AX445781	AX445781 Sequence	c 518	11.8	42.1	28	6	I33133	I33133 Sequence 3
446	12.2	42.9	25	6	AR487008	AR487008 Sequence	c 519	11.8	42.1	28	6	AX224559	AX224559 Sequence
447	12.2	42.9	25	6	AX149583	AX149583 Sequence	c 520	11.8	42.1	28	6	AX814770	AX814770 Sequence
448	12.2	42.9	25	6	AX197036	AX197036 Sequence	c 521	11.8	42.1	28	6	AX825677	AX825677 Sequence
449	12.2	42.9	27	6	AX109741	AX109741 Sequence	c 522	11.8	42.1	28	6	BD080283	BD080283 Transgeni
450	12.2	42.9	28	6	AX203856	AX203856 Sequence	c 523	11.8	42.1	30	6	A97525	A97525 Sequence 25
451	12.2	42.9	29	6	AR432056	AR432056 Sequence	c 524	11.8	42.1	30	6	AR125877	AR125877 Sequence
452	12.2	42.9	29	6	BD091724	BD091724 Novel deo	c 525	11.8	42.1	30	6	I24244	I24244 Sequence 31
453	12.2	42.9	30	6	BD196555	BD196555 Prostatic	c 526	11.8	42.1	30	6	AR428173	AR428173 Sequence
454	12.2	42.9	30	6	AR308682	AR308682 Sequence	c 527	11.8	42.1	30	6	AX791290	AX791290 Sequence
455	12.2	42.9	30	6	AX65232	AX65232 Sequence	c 528	11.8	42.1	31	6	AR195890	AR195890 Sequence
456	12.2	42.9	31	6	AX248570	AX248570 Sequence	c 529	11.8	42.1	31	6	AX248470	AX248470 Sequence
457	12.2	42.9	33	6	AR275363	AR275363 Sequence	c 530	11.8	42.1	31	6		

531	11.8	42.1	31	6	AX249351	Sequence	AX249351	Sequence	AX249351	Sequence	604	11.6	41.4	21	6	BD074379	Method of
c 532	11.8	42.1	31	6	AX249453	Sequence	AX249453	Sequence	AX249453	Sequence	605	11.6	41.4	22	6	E13354	Primer, 4/1
c 533	11.8	42.1	32	6	AX053463	Sequence	AX053463	Sequence	AX053463	Sequence	606	11.6	41.4	22	12	AB069597	AB069597 Synthetic
c 534	11.8	42.1	32	6	AR091088	Sequence	AR091088	Sequence	AR091088	Sequence	607	11.6	41.4	23	6	BD143681	Method of
c 535	11.8	42.1	32	6	BD206156	Human ant	BD206156	Human ant	BD206156	Human ant	608	11.6	41.4	24	6	AR438465	Sequence
c 536	11.8	42.1	32	6	BD206159	Human ant	BD206159	Human ant	BD206159	Human ant	609	11.6	41.4	24	6	AR447115	Sequence
c 537	11.8	42.1	32	6	BD206160	Human ant	BD206160	Human ant	BD206160	Human ant	610	11.6	41.4	24	6	AX447313	Sequence
c 538	11.8	42.1	32	6	AR198123	Sequence	AR198123	Sequence	AR198123	Sequence	611	11.6	41.4	25	6	AR106305	Sequence
c 539	11.8	42.1	32	6	AR260277	Sequence	AR260277	Sequence	AR260277	Sequence	612	11.6	41.4	25	6	AR126275	Sequence
c 540	11.8	42.1	33	6	AR078514	Sequence	AR078514	Sequence	AR078514	Sequence	613	11.6	41.4	25	6	AR136171	Sequence
c 541	11.8	42.1	34	6	BD185265	Method fo	BD185265	Method fo	BD185265	Method fo	614	11.6	41.4	25	6	BD230368	Total gen
c 542	11.8	42.1	35	6	AR075190	Sequence	AR075190	Sequence	AR075190	Sequence	615	11.6	41.4	25	6	AX475954	Sequence
543	11.8	42.1	36	6	AX077856	Sequence	AX077856	Sequence	AX077856	Sequence	616	11.6	41.4	25	6	AX475955	Sequence
544	11.8	42.1	36	6	I73341	Sequence 5	I73341	Sequence 5	I73341	Sequence 5	617	11.6	41.4	25	6	AX475956	Sequence
545	11.8	42.1	36	6	I82500	Sequence 5	I82500	Sequence 5	I82500	Sequence 5	618	11.6	41.4	25	6	AX475957	Sequence
546	11.8	42.1	36	6	AR287820	Sequence 5	AR287820	Sequence 5	AR287820	Sequence 5	619	11.6	41.4	25	6	AX475958	Sequence
547	11.8	42.1	39	6	A59196	Sequence	A59196	Sequence	A59196	Sequence	620	11.6	41.4	25	6	AX475959	Sequence
548	11.8	42.1	39	6	AR149879	Sequence	AR149879	Sequence	AR149879	Sequence	621	11.6	41.4	25	6	AX475960	Sequence
c 549	11.8	42.1	39	6	AR404972	Sequence	AR404972	Sequence	AR404972	Sequence	622	11.6	41.4	25	6	AX475961	Sequence
c 550	11.8	42.1	39	6	AX441318	Sequence	AX441318	Sequence	AX441318	Sequence	623	11.6	41.4	26	6	AX512394	Sequence
c 551	11.8	42.1	39	6	BD171619	Method fo	BD171619	Method fo	BD171619	Method fo	624	11.6	41.4	27	6	AR143800	Sequence
552	11.8	42.1	40	6	E13039	Genomic RNA	E13039	Genomic RNA	E13039	Genomic RNA	625	11.6	41.4	27	6	AR185076	Sequence
c 553	11.8	42.1	40	6	AX538405	Sequence	AX538405	Sequence	AX538405	Sequence	626	11.6	41.4	28	6	AR064482	Sequence
554	11.8	42.1	41	6	AX059990	Sequence	AX059990	Sequence	AX059990	Sequence	627	11.6	41.4	28	6	AR143244	Sequence
555	11.8	42.1	41	6	AX514591	Sequence	AX514591	Sequence	AX514591	Sequence	628	11.6	41.4	28	6	AR300637	Sequence
556	11.8	42.1	41	6	AX514969	Sequence	AX514969	Sequence	AX514969	Sequence	629	11.6	41.4	28	6	AR448670	Sequence
557	11.8	42.1	41	6	AX515447	Sequence	AX515447	Sequence	AX515447	Sequence	630	11.6	41.4	28	6	AX473148	Sequence
c 558	11.8	42.1	41	6	AX516321	Sequence	AX516321	Sequence	AX516321	Sequence	631	11.6	41.4	28	6	BD085787	Alpha-amy
559	11.8	42.1	41	6	AX517315	Sequence	AX517315	Sequence	AX517315	Sequence	632	11.6	41.4	29	6	BD190754	Secreted
560	11.8	42.1	41	6	AX520201	Sequence	AX520201	Sequence	AX520201	Sequence	633	11.6	41.4	29	6	BD200040	Method an
c 561	11.8	42.1	41	6	AX520351	Sequence	AX520351	Sequence	AX520351	Sequence	634	11.6	41.4	29	6	BD252278	Regulatio
562	11.8	42.1	41	6	AX520533	Sequence	AX520533	Sequence	AX520533	Sequence	635	11.6	41.4	29	6	BD271406	Molecular
563	11.8	42.1	41	6	AX520995	Sequence	AX520995	Sequence	AX520995	Sequence	636	11.6	41.4	29	6	AX049247	Sequence
c 564	11.8	42.1	41	6	AX838902	Sequence	AX838902	Sequence	AX838902	Sequence	637	11.6	41.4	29	6	AX049852	Sequence
c 565	11.8	42.1	42	6	AR306673	Sequence	AR306673	Sequence	AR306673	Sequence	638	11.6	41.4	29	6	AX050850	Sequence
c 566	11.8	42.1	42	6	AR340108	Sequence	AR340108	Sequence	AR340108	Sequence	639	11.6	41.4	29	6	AX099575	Sequence
c 567	11.8	42.1	42	6	AR412177	Sequence	AR412177	Sequence	AR412177	Sequence	640	11.6	41.4	29	6	AX329104	Sequence
c 568	11.8	42.1	43	9	HSLAS125A	Sequence	HSLAS125A	Sequence	HSLAS125A	Sequence	641	11.6	41.4	29	6	AX511133	Sequence
c 569	11.8	42.1	45	6	AR242793	Sequence	AR242793	Sequence	AR242793	Sequence	642	11.6	41.4	29	6	AX805628	Sequence
c 570	11.8	42.1	45	10	NMTCRA25	Sequence	NMTCRA25	Sequence	NMTCRA25	Sequence	643	11.6	41.4	30	6	A41516	Sequence 9
c 571	11.8	42.1	47	6	AR289403	Sequence	AR289403	Sequence	AR289403	Sequence	644	11.6	41.4	30	6	AR145006	Sequence
c 572	11.8	42.1	47	6	AR290690	Sequence	AR290690	Sequence	AR290690	Sequence	645	11.6	41.4	30	6	BD184302	Method an
c 573	11.8	42.1	47	6	AR291603	Sequence	AR291603	Sequence	AR291603	Sequence	646	11.6	41.4	30	6	E59827	GMP synthas
574	11.8	42.1	47	6	AR292041	Sequence	AR292041	Sequence	AR292041	Sequence	647	11.6	41.4	30	6	AR359120	Sequence
575	11.8	42.1	49	6	BD233641	Neisseria	BD233641	Neisseria	BD233641	Neisseria	648	11.6	41.4	30	6	AX742449	Sequence
576	11.8	42.1	49	6	AR476052	Sequence	AR476052	Sequence	AR476052	Sequence	649	11.6	41.4	30	6	AX791080	Sequence
c 577	11.8	42.1	50	6	CQ002433	Sequence	CQ002433	Sequence	CQ002433	Sequence	650	11.6	41.4	30	6	AX799992	Sequence
c 578	11.8	42.1	50	6	CQ005423	Sequence	CQ005423	Sequence	CQ005423	Sequence	651	11.6	41.4	31	6	BD185685	2,6-Pyrid
579	11.8	42.1	50	6	AR366381	Sequence	AR366381	Sequence	AR366381	Sequence	652	11.6	41.4	31	6	CQ800756	Sequence
580	11.8	42.1	50	6	AR435577	Sequence	AR435577	Sequence	AR435577	Sequence	653	11.6	41.4	31	6	AX248364	Sequence
581	11.8	42.1	50	6	AX157594	Sequence	AX157594	Sequence	AX157594	Sequence	654	11.6	41.4	31	6	AX248761	Sequence
582	11.8	42.1	50	6	AX199710	Sequence	AX199710	Sequence	AX199710	Sequence	655	11.6	41.4	32	6	AR066465	Sequence
583	11.8	42.1	50	6	AX199712	Sequence	AX199712	Sequence	AX199712	Sequence	656	11.6	41.4	32	6	AX375484	Sequence
584	11.8	42.1	50	6	AX199713	Sequence	AX199713	Sequence	AX199713	Sequence	657	11.6	41.4	32	6	AX805691	Sequence
585	11.8	42.1	50	6	AX899629	Sequence	AX899629	Sequence	AX899629	Sequence	658	11.6	41.4	33	6	AR152566	Sequence
c 586	11.8	42.1	50	6	AX951977	Sequence	AX951977	Sequence	AX951977	Sequence	659	11.6	41.4	33	6	I86635	Sequence 14
c 587	11.8	42.1	50	6	AX952571	Sequence	AX952571	Sequence	AX952571	Sequence	660	11.6	41.4	33	6	AX280457	Sequence
588	11.8	42.1	50	6	BD035162	Sequence	BD035162	Sequence	BD035162	Sequence	661	11.6	41.4	34	6	AX009755	Sequence
c 589	11.6	41.4	19	6	BD230626	Total gen	BD230626	Total gen	BD230626	Total gen	662	11.6	41.4	35	6	E13948	PCR primer
c 590	11.6	41.4	19	6	CQ768777	Sequence	CQ768777	Sequence	CQ768777	Sequence	663	11.6	41.4	35	11	C75896	Homo sapien
c 591	11.6	41.4	19	6	CQ778373	Sequence	CQ778373	Sequence	CQ778373	Sequence	664	11.6	41.4	36	6	A08048	Oligonucleo
c 592	11.6	41.4	20	6	AR085544	Sequence	AR085544	Sequence	AR085544	Sequence	665	11.6	41.4	36	6	A14247	REP sequenc
593	11.6	41.4	20	6	AR104211	Sequence	AR104211	Sequence	AR104211	Sequence	666	11.6	41.4	36	6	A19271	oligonucleo
c 594	11.6	41.4	20	6	AR216064	Sequence	AR216064	Sequence	AR216064	Sequence	667	11.6	41.4	36	6	AR033997	Sequence
c 595	11.6	41.4	20	6	AR272072	Sequence	AR272072	Sequence	AR272072	Sequence	668	11.6	41.4	36	6	AR124006	Sequence
c 596	11.6	41.4	20	6	AR293463	Sequence	AR293463	Sequence	AR293463	Sequence	669	11.6	41.4	36	6	AR236453	Sequence
c 597	11.6	41.4	20	6	AX226216	Sequence	AX226216	Sequence	AX226216	Sequence	670	11.6	41.4	36	6	AR349977	Sequence
598	11.6	41.4	20	6	BD086295	G protein	BD086295	G protein	BD086295	G protein	671	11.6	41.4	36	6	AR408657	Sequence
c 599	11.6	41.4	21	4	DOGSP3001	L15646 Dog (Clone)	DOGSP3001	L15646 Dog (Clone)	DOGSP3001	L15646 Dog (Clone)	672	11.6	41.4	36	6	BD102119	Method of
c 600	11.6	41.4	21	6	BD230834	Total gen	BD230834	Total gen	BD230834	Total gen	673	11.6	41.4	36	6	BD105763	Ciliary n
c 601	11.6	41.4	21	6	BD235619	Gene, 7/2	BD235619	Gene, 7/2	BD235619	Gene, 7/2	674	11.6	41.4	37	6	CQ759419	Sequence
602	11.6	41.4	21	6	E64450	Peptide hav	E64450	Peptide hav	E64450	Peptide hav	675	11.6	41.4	38	6	AR125937	Sequence
c 603	11.6	41.4	21	6	AX000318	Sequence	AX000318	Sequence	AX000318	Sequence	676	11.6	41.4	38	6	BD263783	Adeno-ass

C 677	11.6	41.4	38	6	I24304	I24304 Sequence 91	C 750	11.6	41.4	42	6	AR198296	AR198296 Sequence
C 678	11.6	41.4	38	6	I49650	I49650 Sequence 2	C 751	11.6	41.4	42	6	AX469989	AX469989 Sequence
C 679	11.6	41.4	38	6	I56644	I56644 Sequence 2	C 752	11.6	41.4	42	9	S81405	S81405 T cell anti
C 680	11.6	41.4	38	6	AR236456	AR236456 Sequence	C 753	11.6	41.4	43	6	AR070510	AR070510 Sequence
C 681	11.6	41.4	38	6	AR236459	AR236459 Sequence	C 754	11.6	41.4	43	6	AR070526	AR070526 Sequence
C 682	11.6	41.4	38	6	AR236463	AR236463 Sequence	C 755	11.6	41.4	43	6	AR070530	AR070530 Sequence
C 683	11.6	41.4	38	6	AR236465	AR236465 Sequence	C 756	11.6	41.4	43	6	AR070534	AR070534 Sequence
C 684	11.6	41.4	38	6	AR236468	AR236468 Sequence	C 757	11.6	41.4	43	6	BD260002	BD260002 Polynucle
C 685	11.6	41.4	38	6	AX048269	AX048269 Sequence	C 758	11.6	41.4	43	6	AX045488	AX045488 Sequence
C 686	11.6	41.4	38	6	AX580618	AX580618 Sequence	C 759	11.6	41.4	44	6	AX483447	AX483447 Sequence
C 687	11.6	41.4	38	6	AX580618	AX580618 Sequence	C 760	11.6	41.4	44	6	AR051584	AR051584 Sequence
C 688	11.6	41.4	38	6	AX581172	AX581172 Sequence	C 761	11.6	41.4	44	6	AR088305	AR088305 Sequence
C 689	11.6	41.4	39	6	A26290	A26290 Subtilisin	C 762	11.6	41.4	44	6	AR112413	AR112413 Sequence
C 690	11.6	41.4	39	6	A26922	A26922 Oligonucleo	C 763	11.6	41.4	44	6	AR140204	AR140204 Sequence
C 691	11.6	41.4	39	6	AR022568	AR022568 Sequence	C 764	11.6	41.4	44	6	CQ779278	CQ779278 Sequence
C 692	11.6	41.4	39	6	AR037583	AR037583 Sequence	C 765	11.6	41.4	44	6	CO822734	CO822734 Sequence
C 693	11.6	41.4	39	6	AR083834	AR083834 Sequence	C 766	11.6	41.4	44	6	AR198563	AR198563 Sequence
C 694	11.6	41.4	39	6	AR138230	AR138230 Sequence	C 767	11.6	41.4	44	6	AR280488	AR280488 Sequence
C 695	11.6	41.4	39	6	AR140195	AR140195 Sequence	C 768	11.6	41.4	44	6	BD088442	BD088442 Fibroblas
C 696	11.6	41.4	39	6	AR140300	AR140300 Sequence	C 769	11.6	41.4	45	6	AR028569	AR028569 Sequence
C 697	11.6	41.4	39	6	AR150850	AR150850 Sequence	C 770	11.6	41.4	45	6	AR083215	AR083215 Sequence
C 698	11.6	41.4	39	6	AR173274	AR173274 Sequence	C 771	11.6	41.4	45	6	AR146461	AR146461 Sequence
C 699	11.6	41.4	39	6	AR178041	AR178041 Sequence	C 772	11.6	41.4	45	6	AR146531	AR146531 Sequence
C 700	11.6	41.4	39	6	I43379	I43379 Sequence 8	C 773	11.6	41.4	47	6	CO816919	CO816919 Sequence
C 701	11.6	41.4	39	6	I65730	I65730 Sequence 90	C 774	11.6	41.4	47	6	AR290076	AR290076 Sequence
C 702	11.6	41.4	39	6	I67962	I67962 Sequence 88	C 775	11.6	41.4	47	6	AR290518	AR290518 Sequence
C 703	11.6	41.4	39	6	I90181	I90181 Sequence	C 776	11.6	41.4	48	6	AR012090	AR012090 Sequence
C 704	11.6	41.4	39	6	AR236457	AR236457 Sequence	C 777	11.6	41.4	48	6	AR146457	AR146457 Sequence
C 705	11.6	41.4	39	6	AR255791	AR255791 Sequence	C 778	11.6	41.4	48	6	AR146457	AR146457 Sequence
C 706	11.6	41.4	39	6	AR275353	AR275353 Sequence	C 779	11.6	41.4	48	6	CO654096	CO654096 Sequence
C 707	11.6	41.4	39	6	AR344740	AR344740 Sequence	C 780	11.6	41.4	48	6	AR306678	AR306678 Sequence
C 708	11.6	41.4	39	6	BD074819	BD074819 Homolog o	C 781	11.6	41.4	48	6	AR340113	AR340113 Sequence
C 709	11.6	41.4	39	6	BD087227	BD087227 Mammalian	C 782	11.6	41.4	48	6	AR412182	AR412182 Sequence
C 710	11.6	41.4	40	6	AR022573	AR022573 Sequence	C 783	11.6	41.4	48	6	AX006263	AX006263 Sequence
C 711	11.6	41.4	40	6	AR024250	AR024250 Sequence	C 784	11.6	41.4	48	6	BD073398	BD073398 Respirato
C 712	11.6	41.4	40	6	AR026918	AR026918 Sequence	C 785	11.6	41.4	48	9	HS224216	HS224216 Homo sapi
C 713	11.6	41.4	40	6	AR037588	AR037588 Sequence	C 786	11.6	41.4	49	6	AR146496	AR146496 Sequence
C 714	11.6	41.4	40	6	AR045103	AR045103 Sequence	C 787	11.6	41.4	49	6	AR170484	AR170484 Sequence
C 715	11.6	41.4	40	6	AR091804	AR091804 Sequence	C 788	11.6	41.4	50	6	AI6122	AI6122 Synthetic p
C 716	11.6	41.4	40	6	AR146464	AR146464 Sequence	C 789	11.6	41.4	50	6	A38858	A38858 Sequence 12
C 717	11.6	41.4	40	6	AR146513	AR146513 Sequence	C 790	11.6	41.4	50	6	A73047	A73047 Sequence 23
C 718	11.6	41.4	40	6	AR157712	AR157712 Sequence	C 791	11.6	41.4	50	6	A73139	A73139 Sequence 23
C 719	11.6	41.4	40	6	AR166574	AR166574 Sequence	C 792	11.6	41.4	50	6	AR013763	AR013763 Sequence
C 720	11.6	41.4	40	6	AR178046	AR178046 Sequence	C 793	11.6	41.4	50	6	AR103941	AR103941 Sequence
C 721	11.6	41.4	40	6	CO819845	CO819845 Sequence	C 794	11.6	41.4	50	6	AR103942	AR103942 Sequence
C 722	11.6	41.4	40	6	E05394	E05394 DNA sequence	C 795	11.6	41.4	50	6	AR126943	AR126943 Sequence
C 723	11.6	41.4	40	6	E11592	E11592 PCR primer.	C 796	11.6	41.4	50	6	AR174688	AR174688 Sequence
C 724	11.6	41.4	40	6	E43797	E43797 ChimERIC an	C 797	11.6	41.4	50	6	CO003432	CO003432 Sequence
C 725	11.6	41.4	40	6	AR236455	AR236455 Sequence	C 798	11.6	41.4	50	6	CO005043	CO005043 Sequence
C 726	11.6	41.4	40	6	AR236458	AR236458 Sequence	C 799	11.6	41.4	50	6	CO005573	CO005573 Sequence
C 727	11.6	41.4	40	6	AR236462	AR236462 Sequence	C 800	11.6	41.4	50	6	CO005574	CO005574 Sequence
C 728	11.6	41.4	40	6	AR364170	AR364170 Sequence	C 801	11.6	41.4	50	6	CO005885	CO005885 Sequence
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C 738	11.6	41.4	41	6	AX518676	AX518676 Sequence	C 811	11.6	41.4	50	6	AX160640	AX160640 Sequence
C 739	11.6	41.4	41	6	AX519407	AX519407 Sequence	C 812	11.6	41.4	50	6	AX160888	AX160888 Sequence
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ALIGNMENTS

RESULT 1  
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LOCUS Sequence 2 from patent US 5837442.  
DEFINITION AR054576  
ACCESSION AR054576  
VERSION AR054576.1 GI:5980153  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 28)  
AUTHORS Tsang,S.Yen.  
TITLE Oligonucleotide primers for amplifying HCV nucleic acid  
JOURNAL Patent: US 5837442-A 2 17-NOV-1998;  
FEATURES Location/Qualifiers  
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RESULT 2  
AR094138 28 bp DNA linear PAT 08-SEP-2000  
LOCUS Sequence 4 from patent US 6001611.  
DEFINITION AR094138  
ACCESSION AR094138  
VERSION AR094138.1 GI:10020883  
KEYWORDS

SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 28)  
AUTHORS Will,S.Gordon.  
TITLE Modified nucleic acid amplification primers  
JOURNAL Patent: US 6001611-A 4 14-DEC-1999;  
FEATURES Location/Qualifiers  
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/organism="unknown"  
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Best Local Similarity 100.0%; Pred. No. 0.23; 0; Indels 0; Gaps 0;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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BD181368 28 bp DNA linear PAT 15-MAY-2003  
LOCUS A method for determination of a nucleic acid using a control.  
DEFINITION BD181368  
ACCESSION BD181368  
VERSION BD181368.1 GI:30792286  
KEYWORDS JP 2002335981-A/7.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 28)  
AUTHORS Jaeger,S.  
TITLE A method for determination of a nucleic acid using a control  
JOURNAL Patent: JP 2002335981-A 7 26-NOV-2002;  
COMMENT F HOFFMANN LA ROCHE AG  
OS Artificial Sequence  
PN JP 2002335981-A/7  
PD 26-NOV-2002  
PF 04-MAR-2002 JP 2002057515  
PR 02-MAR-2001 EP 01105172.9  
PI STEPHAN JAEGER  
PC C12N15/09,C12Q1/68,G01N33/50,G01N33/53,G01N33/566,G01N33/58,  
PC C12N15/00  
CC Description of Artificial Sequence: ST778 HCV-specific Primer-  
CC sequence  
FH Key Location/Qualifiers  
FT source 1..28  
FT /organism='Artificial Sequence'.  
FEATURES Location/Qualifiers  
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AX147022 28 bp DNA linear PAT 08-JUN-2001  
LOCUS Sequence 16 from Patent WO0137291.  
DEFINITION AX147022  
ACCESSION AX147022  
VERSION AX147022.1 GI:14346293  
KEYWORDS



SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences

REFERENCE 1  
AUTHORS Weindel, K., Riedling, M. and Geiger, A.  
TITLE Magnetic glass particles, method for their preparation and uses  
JOURNAL thereof  
Patent: WO 0137291-A 16 25-MAY-2001;  
Roche Diagnostics GmbH (DE)  
FEATURES Location/Qualifiers  
source 1..28  
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DEFINITION Sequence 7 from Patent EP1236804.  
ACCESSION AX523948  
VERSION AX523948.1 GI:25168879  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences

REFERENCE 1  
AUTHORS Jaeger, S.  
TITLE A method for determination of a nucleic acid using a control  
JOURNAL Patent: EP 1236804-A 7 04-SEP-2002;  
Roche Diagnostics GmbH (DE); F. Hoffmann-La Roche AG (CH)  
FEATURES Location/Qualifiers  
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Db 1 GCAAGCACCTTATCAGGCAGTACCACAA 28

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DEFINITION Sequence 7 from Patent EP1236805.  
ACCESSION AX524846  
VERSION AX524846.1 GI:25169940  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences

REFERENCE 1  
AUTHORS Jaeger, S.

TITLE A method for the determination of a nucleic acid using a control  
JOURNAL Patent: EP 1236805-A 7 04-SEP-2002;  
Roche Diagnostics GmbH (DE); F. Hoffmann-La Roche AG (CH)  
FEATURES Location/Qualifiers  
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DEFINITION Sequence 1 from patent US 6368801.  
ACCESSION AR204716  
VERSION AR204716.1 GI:21502113  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 47)  
AUTHORS Faruqi, A. Fawad.  
TITLE Detection and amplification of RNA using target-mediated ligation  
of DNA by RNA ligase  
JOURNAL Patent: US 6368801-A 1 09-APR-2002;  
FEATURES Location/Qualifiers  
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RESULT 8  
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DEFINITION Sequence 1 from Patent WO0179420.  
ACCESSION AX284180  
VERSION AX284180.1 GI:17044868  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Faruqi, A. F.  
TITLE Detection and amplification of rna using target-mediated ligation  
of dna by rna ligase  
JOURNAL Patent: WO 0179420-A 1 25-OCT-2001;  
MOLECULAR STAGING, INC. (US)  
FEATURES Location/Qualifiers  
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QY 1 GCAAGCACCTATCAGGCGAGTACCACAA 28
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Db 36 GCAAGCACCTATCAGGCGAGTACCACAA 9

RESULT 9
LOCUS AR054577 27 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5837442.
ACCESSION AR054577
VERSION AR054577.1 GI:5980154
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 27)
AUTHORS Tsang,S.Yen.
TITLE Oligonucleotide primers for amplifying HCV nucleic acid
JOURNAL Patent: US 5837442-A 3 17-NOV-1998;
FEATURES Location/Qualifiers
source 1..27
/mol_type="unknown"
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Query Match      96.4%; Score 27; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCTATCAGGCGAGTACCACAA 27
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Db 1 GCAAGCACCTATCAGGCGAGTACCACAA 27

RESULT 10
LOCUS AR411541 27 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 5 from patent US 6638714.
ACCESSION AR411541
VERSION AR411541.1 GI:40163885
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 27)
AUTHORS Linnen,J.M. and Gorman,K.M.
TITLE Oligonucleotide primers for efficient detection of hepatitis C
JOURNAL Patent: US 6638714-A 5 28-OCT-2003;
FEATURES Location/Qualifiers
source 1..27
/mol_type="unknown"
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Query Match      96.4%; Score 27; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCTATCAGGCGAGTACCACAA 27
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Db 1 GCAAGCACCTATCAGGCGAGTACCACAA 27

RESULT 11
LOCUS BD000267 27 bp DNA linear PAT 31-JAN-2002
DEFINITION Oligonucleotide primers for efficient detection of hepatitis C
virus (HCV) and methods of use thereof.
Accession BD000267.1 GI:18623346
Keywords JP 2000279200-A/5.
Source synthetic construct
Organism artificial sequences.
Reference 1 (bases 1 to 27)
Authors Linnen,J.M. and Gorman,K.M.
Title Oligonucleotide primers for efficient detection of hepatitis C
virus (HCV) and methods of use thereof
Journal Patent: JP 2000279200-A 5 10-OCT-2000;
Comment ORTHO CLINICAL DIAGNOSTICS INC
OS Artificial Sequence
PN JP 2000279200-A/5
PD 10-OCT-2000
PF 03-FEB-2000 JP 2000032656
PR 03-FEB-1999 US 60/118497
PI JEFFREY M LYNEN,KEVIN M GORMAN
PC C12Q1/68,C12N15/09//(C12N15/09,C12R1:92),C12N15/00,(C12N15/00,
CC C12R1:92)
FH Key Location/Qualifiers
FT source 1..27
/mol_type="synthetic construct"
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Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCTATCAGGCGAGTACCACAA 27
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Db 1 GCAAGCACCTATCAGGCGAGTACCACAA 27

RESULT 12
LOCUS BD183052/c 29 bp DNA linear PAT 17-JUN-2003
DEFINITION Nucleic acids for grouping hepatitis C virus and method for group
ing hepatitis C virus using the same.
Accession BD183052
Version BD183052.1 GI:31875252
Keywords JP 2002345467-A/24.
Source synthetic construct
Organism artificial sequences.
Reference 1 (bases 1 to 29)
Authors Mukaide,M., Tsunoda,K. and Hikiji,K.
Title Nucleic acids for grouping hepatitis C virus and method for group
ing hepatitis C virus using the same
Journal Patent: JP 2002345467-A 24 03-DEC-2002;
SRL INC
OS Artificial Sequence
PN JP 2002345467-A/24
PD 03-DEC-2002
PF 17-APR-2001 JP 2001118810
PI MASAKAZU MUKAIDE,KOICHI TSUNODA,KAZUMASA HIKIJI PC
C12N15/09,C12Q1/68,G01N33/53,G01N33/566,C12N15/00 CC Nucleic Acid
Used as signal-amplifying probe which hybridizes CC
with a
region in HCV 5'-UTR region
FH Key Location/Qualifiers
FT source 1..29
/mol_type="synthetic construct"

ORIGIN
Query Match      96.4%; Score 27; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCTATCAGGCGAGTACCACAA 27
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Db 1 GCAAGCACCTATCAGGCGAGTACCACAA 27

RESULT 11
LOCUS BD000267 27 bp DNA linear PAT 31-JAN-2002
DEFINITION Oligonucleotide primers for efficient detection of hepatitis C
virus (HCV) and methods of use thereof.
Accession BD000267.1 GI:18623346
Keywords JP 2000279200-A/5.
Source synthetic construct
Organism artificial sequences.
Reference 1 (bases 1 to 27)
Authors Linnen,J.M. and Gorman,K.M.
Title Oligonucleotide primers for efficient detection of hepatitis C
virus (HCV) and methods of use thereof
Journal Patent: JP 2000279200-A 5 10-OCT-2000;
Comment ORTHO CLINICAL DIAGNOSTICS INC
OS Artificial Sequence
PN JP 2000279200-A/5
PD 10-OCT-2000
PF 03-FEB-2000 JP 2000032656
PR 03-FEB-1999 US 60/118497
PI JEFFREY M LYNEN,KEVIN M GORMAN
PC C12Q1/68,C12N15/09//(C12N15/09,C12R1:92),C12N15/00,(C12N15/00,
CC C12R1:92)
FH Key Location/Qualifiers
FT source 1..27
/mol_type="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match      96.4%; Score 27; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCTATCAGGCGAGTACCACAA 27
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Db 1 GCAAGCACCTATCAGGCGAGTACCACAA 27
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Best Local Similarity 100.0%; Pred.No.14;					
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	GCAAGCACCCCTATCAGGCAGTACC	24		
Db	5	GCAAGCACCCCTATCAGGCAGTACC	28		
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AR004397		33 bp DNA linear PAT 04-DEC-1998			
LOCUS					
DEFINITION		Sequence 51 from patent US 5747244.			
ACCESSION		AR004397			
VERSION		AF004397.1 GI:3965276			
KEYWORDS					
SOURCE		Unknown.			
ORGANISM		Unclassified.			
REFERENCE		1 (bases 1 to 33)			
AUTHORS		Sheridan,P., Chang,C.-A., Running,J. and Urdea,M.S.			
TITLE		Nucleic acid probes immobilized on polystyrene surfaces			
JOURNAL		Patent: US 5747244-A 51 05-MAY-1998;			
<b>FEATURES</b>					
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	GCAAGCACCCCTATCAGGCAGTACC	24		
Db	10	GCAAGCACCCCTATCAGGCAGTACC	33		
<b>RESULT 16</b>					
AR064936		33 bp DNA linear PAT 29-SEP-1999			
LOCUS					
DEFINITION		Sequence 61 from patent US 5849481.			
ACCESSION		AR064936			
VERSION		AR064936.1 GI:5995152			
KEYWORDS					
SOURCE		Unknown.			
ORGANISM		Unclassified.			
REFERENCE		1 (bases 1 to 33)			
AUTHORS		Urdea,M.S.; Horn,T., Chang,C.-A., Warner,B. and Fultz,T.J.			
TITLE		Nucleic acid hybridization assays employing large comb-type branched polynucleotides			
JOURNAL		Patent: US 5849481-A 61 15-DEC-1998;			
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Best Local Similarity 100.0%; Pred.No.13;					
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	GCAAGCACCCCTATCAGGCAGTACC	24		
Db	10	GCAAGCACCCCTATCAGGCAGTACC	33		

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RESULT 17
LOCUS AR097189 33 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 127 from patent US 6071693.
ACCESSION AR097189
VERSION AR097189.1 GI:12805919
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Cha,T.-A., Beall,E., Irvine,B., Kolberg,J. and Urdea,M.S.
TITLE HCV genomic sequences for diagnostics and therapeutics
JOURNAL Patent: US 6071693-A 127 06-JUN-2000;
FEATURES
source Location/Qualifiers
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCCCTATCAGGCAGTACC 24
Db 10 GCAAGCACCCCTATCAGGCAGTACC 33

RESULT 20
LOCUS BD189153 33 bp DNA linear PAT 17-JUL-2003
DEFINITION HCV Genomic Sequences For Diagnostics And Therapeutics.
ACCESSION BD189153
VERSION BD189153.1 GI:32998892
KEYWORDS JP 2003009891-A/127.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 33)
AUTHORS Adair,M.S., Irvine,B., Kolberg,J., Beal,E. and Cha,T.
TITLE HCV Genomic Sequences For Diagnostics And Therapeutics
JOURNAL Patent: JP 2003009891-A 127 14-JAN-2003;
COMMENT Chiron Corporation
OS Artificial Sequence
PN JP 2003009891-A/127
PD 14-JAN-2003
PF 10-MAY-2002 JP 2002134997
PR 08-MAY-1991 US 697326
PI michael s adair,bruce irvine,janice kolberg,eileen beal,tai-ann cha
PI ann cha
CC synthetic construct
FH Key Location/Qualifiers
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/mol_type="synthetic construct"
/db_xref="taxon:32630"

FEATURES
source Location/Qualifiers
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/mol_type="synthetic construct"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCCCTATCAGGCAGTACC 24
Db 10 GCAAGCACCCCTATCAGGCAGTACC 33

RESULT 21
LOCUS BD189300 33 bp DNA linear PAT 17-JUL-2003
DEFINITION HCV Genomic Sequences For Diagnostics And Therapeutics.
ACCESSION BD189300
VERSION BD189300.1 GI:32999039
KEYWORDS JP 2003009892-A/127.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 33)
AUTHORS Adair,M.S., Cha,T., Irvine,B., Kolberg,J. and Beal,E.
TITLE HCV Genomic Sequences For Diagnostics And Therapeutics
JOURNAL Patent: JP 2003009892-A 127 14-JAN-2003;
COMMENT Chiron Corporation
OS Artificial Sequence
PN JP 2003009892-A/127
PD 14-JAN-2003
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RESULT 18
LOCUS AR130687 33 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 127 from patent US 6190864.
ACCESSION AR130687
VERSION AR130687.1 GI:14119012
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Cha,T.-A., Beall,E., Irvine,B., Kolberg,J. and Urdea,M.S.
TITLE HCV genomic sequences for diagnostics and therapeutics
JOURNAL Patent: US 6190864-A 127 20-FEB-2001;
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source Location/Qualifiers
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ORIGIN
Query Match 85.7%; Score 24; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCCCTATCAGGCAGTACC 24
Db 10 GCAAGCACCCCTATCAGGCAGTACC 33

RESULT 19
LOCUS AR172036 33 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 127 from patent US 6297370.
ACCESSION AR172036
VERSION AR172036.1 GI:17910986
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Cha,T.-A., Beall,E., Irvine,B., Kolberg,J. and Urdea,M.S.
TITLE HCV genomic sequences for diagnostics and therapeutics
JOURNAL Patent: US 6297370-A 127 02-OCT-2001;
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PF 10-MAY-2002 JP 2002134999  
PR 08-MAY-1991 US 697326  
PI michael s adair,tai-ann cha,bruce irvine,janice kolberg,eileen  
CC synthetic construct  
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Best Local Similarity 100.0%; Pred. No. 13;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GCAAGCACCTATCAGGCAGTACC 24  
Db 10 GCAAGCACCTATCAGGCAGTACC 33  
RESULT 22  
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LOCUS HCV Genomic Sequences For Diagnostics And Therapeutics. 33 bp. DNA linear PAT 17-JUL-2003  
DEFINITION  
ACCESSION BD189447  
VERSION BD189447.1 GI:32999186  
KEYWORDS JP 2003009893-A/127.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 33)  
AUTHORS Adair,M.S.; Cha,T.; Beal,E.; Irvine,B. and Kolberg,J.  
TITLE HCV Genomic Sequences For Diagnostics And Therapeutics  
JOURNAL Patent: JP 2003009893-A 127 14-JAN-2003;  
COMMENT Chiron Corporation  
OS Artificial Sequence  
PN JP 2003009893-A/127  
PD 14-JAN-2003  
PF 10-MAY-2002 JP 2002135000  
PR 08-MAY-1991 US 697326  
PI michael s adair,tai-ann cha,eileen beal,bruce irvine,janice  
CC kolberg  
CC synthetic construct  
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GCAAGCACCTATCAGGCAGTACC 24  
Db 10 GCAAGCACCTATCAGGCAGTACC 33  
RESULT 23  
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LOCUS I82872 Sequence 51 from patent US 5712389. 33 bp. DNA linear PAT 10-JUN-1998  
DEFINITION  
ACCESSION I82872  
VERSION I82872.1 GI:3211169  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 33)  
AUTHORS Sheridan,P.; Chang,C.-A.; Running,J. and Urdea,M.S.  
TITLE Process for immobilizing nucleic acid probes on polystyrene surfaces  
JOURNAL Patent: US 5712383-A 51 27-JAN-1998;  
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Best Local Similarity 100.0%; Pred. No. 13;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GCAAGCACCTATCAGGCAGTACC 24  
Db 10 GCAAGCACCTATCAGGCAGTACC 33  
RESULT 24  
AX250665  
LOCUS AX250665 24 bp. DNA linear PAT 06-OCT-2001  
DEFINITION Sequence 61 from Patent WO0168921.  
ACCESSION AX250665  
VERSION AX250665.1 GI:15984409  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1  
AUTHORS Koshinsky,H.; Zwick,M.S. and Mccue,K.F.  
TITLE Compositions and methods for simultaneous detection of multiple biological entities  
JOURNAL Patent: WO 0168921-A 61 20-SEP-2001;  
FEATURES  
source  
Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 38;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GCAAGCACCTATCAGGCAGTACC 23  
Db 2 GCAAGCACCTATCAGGCAGTACC 24  
RESULT 25  
AX202931  
LOCUS AX202931 27 bp. DNA linear PAT 30-AUG-2001  
DEFINITION Sequence 6 from Patent WO0152612.  
ACCESSION AX202931  
VERSION AX202931.1 GI:15392394  
KEYWORDS unidentified  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1  
AUTHORS Elaisari,A.; Mandrand,B.; Delair,T.; Spencer,D. and Arkis,A.  
TITLE Method for isolating proteins or protein and nucleic acid associations, or particle and protein complexes, reagent and uses  
JOURNAL Patent: WO 0152612-A 6 26-JUL-2001;  
FEATURES  
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Query Match      82.1%; Score 23; DB 6; Length 27;
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Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCTATCAGGCAGTAC 23
    |||||
DB 5 GCAAGCACCTATCAGGCAGTAC 27
    |||||

RESULT 26
LOCUS AX202933 27 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 8 from Patent WO0152612.
ACCESSION AX202933
VERSION AX202933.1 GI:15392396
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Elaissari, A., Mandrand, B., Delair, T., Spencer, D. and Arkis, A.
TITLE Method for isolating proteins or protein and nucleic acid
JOURNAL associations, or particle and protein complexes, reagent and uses
PATENT: WO 0152612-A 8 26-JUL-2001;
BIO MERIEUX (FR)
FEATURES
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ORIGIN
Query Match      82.1%; Score 23; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCTATCAGGCAGTAC 23
    |||||
DB 5 GCAAGCACCTATCAGGCAGTAC 27
    |||||

RESULT 27
LOCUS AR411542 27 bp DNA linear PAT 19-DEC-2003
DEFINITION Sequence 6 from patent US 6638714.
ACCESSION AR411542
VERSION AR411542.1 GI:40163886
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Linnen, J.M. and Gorman, K.M.
TITLE Oligonucleotide primers for efficient detection of hepatitis C
JOURNAL virus (HCV) and methods of use thereof
PATENT: US 6638714-A 6 28-OCT-2003;
FEATURES
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    Location/Qualifiers
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ORIGIN
Query Match      78.6%; Score 22; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCTATCAGGCAGTAC 22
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/db_xref="taxon:32644"
/note="Origine de la sequence :AMORCE"

ORIGIN
Query Match      82.1%; Score 23; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCTATCAGGCAGTAC 23
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DB 5 GCAAGCACCTATCAGGCAGTAC 27
    |||||

RESULT 28
LOCUS AX282438 27 bp RNA linear PAT 02-NOV-2001
DEFINITION Sequence 10 from Patent WO0166721.
ACCESSION AX282438
VERSION AX282438.1 GI:16609569
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Usman, N., Mcswiggen, J.A., Zinnen, S., Seiwert, S., Haeberli, P.,
Chowrira, B. and Blatt, L.
TITLE Nucleic acid sensor molecules
JOURNAL Patent: WO 0166721-A 10 13-SEP-2001;
RIBOZYME PHARMACEUTICALS, INC. (US)
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        /organism="synthetic construct"
        /mol_type="unassigned RNA"
        /db_xref="taxon:32630"
        /note="Synthetic target signaling sequence"

ORIGIN
Query Match      78.6%; Score 22; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCTATCAGGCAGTAC 22
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DB 22 GCAAGCACCTATCAGGCAGTAC 1
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RESULT 29
LOCUS BD000268 27 bp DNA linear PAT 31-JAN-2002
DEFINITION Oligonucleotide primers for efficient detection of hepatitis C
virus (HCV) and methods of use thereof.
ACCESSION BD000268
VERSION BD000268.1 GI:18623347
KEYWORDS JP 2000279200-A/6.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 27)
AUTHORS Linnen, J.M. and Gorman, K.M.
TITLE Oligonucleotide primers for efficient detection of hepatitis C
JOURNAL virus (HCV) and methods of use thereof
PATENT: JP 2000279200-A 6 10-OCT-2000;
ORTHOClinical Diagnostics Inc
COMMENT OS Artificial Sequence
PN JP 2000279200-A/6
PD 10-OCT-2000
PF 03-FEB-2000 JP 2000032656
PR 03-FEB-1999 US 60/118497
PI JEFFREY M LYNEN, KEVIN M GORMAN
PC C12Q1/68, C12N15/09, C12R1:92, C12N15/00, (C12N15/00,
CC C12R1:92)
FT Key
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FEATURES
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        /mol_type="genomic DNA"
        /db_xref="taxon:32630"

ORIGIN
Query Match      78.6%; Score 22; DB 6; Length 27;
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Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCAGTA 22
Db 6 GCAAGCACCTATCAGGCAGTA 27

RESULT 30
E58845
LOCUS E58845 46 bp DNA linear PAT 31-JAN-2002
DEFINITION Method for detecting ribonucleic acid.
ACCESSION E58845
VERSION JP 2000333699-A/1
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Fujii,T., Goda,H., Tsuruoka,M. and Karube,M.
TITLE Method for detecting ribonucleic acid
JOURNAL Patent: JP 2000333699-A 1 05-DEC-2000;
COMMENT MASAO KARUBE MAKOTO TSURUOKA, TOWA KAGAKU KK
OS Artificial Sequence
PN JP 2000333699-A/1
PD 05-DEC-2000
PF 31-MAY-1999 JP 1999152109
PR
PI TAKAKI FUJII, HIROSHI GODA, MAKOTO TSURUOKA, MASAO KARUBE PC
C12Q1/68, C12N15/09, G01N21/64, G01N33/50, G01N33/566, PC
G01N33/58,
PC C12N15/00
CC
FH Key Location/Qualifiers
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Query Match 78.6%; Score 22; DB 6; Length 46;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCAGTA 22
Db 25 GCAAGCACCTATCAGGCAGTA 46

RESULT 31
AR124661
LOCUS AR124661 21 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 4 from patent US 6172046.
ACCESSION AR124661
VERSION AR124661.1 GI:14110022
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Albrecht,J.K.
TITLE Combination therapy for eradicating detectable HCV-RNA in patients
having chronic Hepatitis C infection
JOURNAL Patent: US 6172046-A 4 09-JAN-2001;
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Db 1 CCCTATCAGGCAGTACCACAA 21

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AR167000
LOCUS AR167000 21 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 17 from patent US 6284458.
ACCESSION AR167000
VERSION AR167000.1 GI:16243416
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Anderson,K.P., Hanecak,R.C., Hoshiko,K., Nozaki,C., Nishihara,T.,
Nakatake,H., Hamada,F., Eto,T. and Furukawa,S.
TITLE Compositions and methods for treatment of hepatitis C
virus-associated diseases
JOURNAL Patent: US 6284458-A 17 04-SEP-2001;
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Db 1 CCCTATCAGGCAGTACCACAA 21

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AR210655
LOCUS AR210655 21 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 17 from patent US 6391542.
ACCESSION AR210655
VERSION AR210655.1 GI:21513440
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Anderson,K.P., Hanecak,R.C., Hoshiko,K., Nozaki,C., Nishihara,T.,
Nakatake,H., Hamada,F., Eto,T., Furukawa,S., Furasako,S.,
Bruice,T.W. and Iima,W.F.
TITLE Compositions and methods for treatment of Hepatitis C
virus-associated diseases
JOURNAL Patent: US 6391542-A 17 21-MAY-2002;
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Best Local Similarity 100.0%; Pred. No. 3e+02;
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Db 1 CCCTATCAGGCAGTACCACAA 21

RESULT 34
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AR242414  
LOCUS AR242414 21 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 4 from patent US 6472373.  
ACCESSION AR242414  
VERSION AR242414.1 GI:27288683  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Albrecht J.K.  
TITLE Combination therapy for eradicating detectable HCV-RNA in antiviral treatment naive patients having chronic hepatitis C infection  
JOURNAL Patent: US 6472373-A 4 29-OCT-2002;  
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RESULT 35  
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DEFINITION Sequence 4 from Patent WO0232414.  
ACCESSION AX540625  
VERSION AX540625.1 GI:25273610  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1  
AUTHORS Albrecht J.  
TITLE Ribavirin-pegylated interferon alfa hcv combination therapy  
JOURNAL Patent: WO 0232414-A 4 25-APR-2002;  
Schering Corporation (US)  
FEATURES  
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RESULT 36  
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DEFINITION Sequence 25 from patent US 5686272.  
ACCESSION I73294  
VERSION I73294.1 GI:3009433  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 23)  
AUTHORS Marshall, R.L., Carrino, J.J. and Sustacheck, J.C.

TITLE Amplification of RNA sequences using the ligase chain reaction  
JOURNAL Patent: US 5686272-A 25 11-NOV-1997;  
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Db 3 GCAAGCACCCCTATCAGGCAGT 23

RESULT 37  
A68286  
LOCUS A68286 24 bp DNA linear PAT 06-MAY-1999  
DEFINITION Sequence 7 from Patent WO9746716.  
ACCESSION A68286  
VERSION A68286.1 GI:4759407  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Bosio, P., Strumia, C. and Clemenza, F.  
TITLE METHOD TO DETECT HCV SPECIFIC NUCLEIC ACIDS  
JOURNAL Patent: WO 9746716-A 7 11-DEC-1997;  
WARCO B V (NL)  
COMMENT Other publication IT RM960404 19971209.  
FEATURES  
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Db 4 GCAAGCACCCCTATCAGGCAGT 24

RESULT 38  
AR011642/c  
LOCUS AR011642 24 bp DNA linear PAT 04-DEC-1998  
DEFINITION Sequence 51 from patent US 5763159.  
ACCESSION AR011642  
VERSION AR011642.1 GI:3969632  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Simmonds, P., Chan, S.-W. and Yap, P. Lee.  
TITLE Hepatitis-C virus testing  
JOURNAL Patent: US 5763159-A 51 09-JUN-1998;  
FEATURES  
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RESULT 39

LOCUS AR054579 24 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 5 from patent US 5837442.  
ACCESSION AR054579

VERSION AR054579.1 GI:5980156  
KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 24)

AUTHORS Tsang, S.Yen.

TITLE Oligonucleotide primers for amplifying HCV nucleic acid

JOURNAL Patent: US 5837442-A 5 17-NOV-1998;

FEATURES Location/Qualifiers

source 1..24

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Db 4 GCAAGCACCCCTATCAGGCAGT 24

RESULT 40

LOCUS BD183045 24 bp DNA linear PAT 17-JUN-2003  
DEFINITION Nucleic acids for grouping hepatitis C virus and method for group  
ing hepatitis C virus using the same.

ACCESSION BD183045

VERSION BD183045.1 GI:31875245

KEYWORDS JP 2002345467-A/17.

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 24)

AUTHORS Mukaide, M., Tsunoda, K. and Hikiji, K.

TITLE Nucleic acids for grouping hepatitis C virus and method for group

ing hepatitis C virus using the same

JOURNAL Patent: JP 2002345467-A 17 03-DEC-2002;

COMMENT SRL INC

OS Artificial Sequence

PN JP 2002345467-A/17

PD 03-DEC-2002

PF 17-APR-2001 JP 200118810

PI MASAKAZU MUKAIDE, KOICHI TSUNODA, KAZUMASA HIKIJI PC

C12N15/09, C12Q1/68, G01N33/53, G01N33/566, C12N15/00 CC Nucleic Acid

Used as Primer amplifying a region in 5'-UTR of CC

Hepatitis C

CC virus

FH Key

FT source 1..24

Location/Qualifiers

1..24

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Search completed: November 23, 2004, 18:47:19  
Job time : 507.21 secs

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9	27	96.4	29	10	ADC54073	HCV 5'-UTR
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c 257	16	57.1	17	12	AD182820	Ad182820 HCV DNaz	330	15	53.6	20	3	AAZ88591	Aaz88591 Nucleotid
c 258	16	57.1	17	12	AD182817	Ad182817 HCV DNaz	331	15	53.6	20	3	AAZ88591	Aaz88591 Nucleotid
259	16	57.1	18	10	ABT23637	Abt23637 Stabilisi	332	15	53.6	21	2	AAV35209	Aav35209 Hepatitis
260	16	57.1	19	10	AD552133	Ad552133 Hepatitis	333	15	53.6	21	2	AAV41667	Aav41667 Nucleotid
261	16	57.1	19	10	AD552124	Ad552124 Hepatitis	334	15	53.6	22	2	AAQ00298	Aax00298 PCR prime
c 262	16	57.1	19	10	AD552124	Ad552124 Hepatitis	335	15	53.6	22	2	AAQ67618	Aaq67618 Primer fo
c 263	16	57.1	19	10	AD551428	Ad551428 Hepatitis	336	15	53.6	25	3	AAQ96561	Aaq96561 Reverse p
c 264	16	57.1	19	10	AD551437	Ad551437 Hepatitis	337	15	53.6	25	3	AAQ96561	Aaq96561 Reverse p
c 265	16	57.1	22	3	AAZ72996	Aaz72996 Hepatitis	c 338	15	53.6	25	3	AAZ72996	Aaz72996 HCV-speci
c 266	15.8	56.4	30	4	AAZ95136	Aaz95136 Hepatitis	c 339	15	53.6	25	9	ACH56987	ACH56987 DNA targe
267	15.4	55.0	22	5	AAZ86010	Aaz86010 Internal	c 340	15	53.6	30	6	ABK89627	Abk89627 Chimeric
268	15.4	55.0	24	2	AAQ44488	Aaq44488 HCV virus	c 341	15	53.6	30	6	ABK89627	Abk89627 Chimeric
269	15.2	54.3	23	8	AAZ56617	Aaz56617 Oligonucle	342	14.8	52.9	31	8	ACD17034	AcD17034 Sample pr
c 270	15.2	54.3	23	8	AAZ56617	Aaz56617 Oligonucle	343	14.8	52.9	31	8	ACD17034	AcD17034 Sample pr
c 271	15	53.6	15	3	AAZ62402	Aaz62402 Substrate	344	14.6	52.1	22	2	AAQ67624	Aaq67624 Primer fo
c 272	15	53.6	15	3	AAZ62402	Aaz62402 Substrate	345	14.6	52.1	25	9	ACI36544	ACI36544 Human mic
c 273	15	53.6	15	3	AAZ29446	Aaz29446 Hepatitis	346	14.6	52.1	25	9	ACI36544	ACI36544 Human mic
c 274	15	53.6	15	6	ABX00259	Abx00259 Hepatitis	c 347	14.6	52.1	30	6	ABK66063	Abk66063 Human gen
c 275	15	53.6	15	6	ABX01758	Abx01758 Hepatitis	c 348	14.6	52.1	48	2	AAQ27825	Aaq27825 Thrombomo
c 276	15	53.6	15	6	ABX01756	Abx01756 Hepatitis	c 349	14.6	52.1	50	10	ADD01487	AdD01487 Human adu
c 277	15	53.6	15	6	ABX01757	Abx01757 Hepatitis	c 350	14.4	51.4	25	9	ACI65494	ACI65494 Human mic
c 278	15	53.6	15	6	ABX00258	Abx00258 Hepatitis	351	14.4	51.4	25	12	ADP14075	AdP14075 Renal cel
c 279	15	53.6	15	6	ABX00258	Abx00258 Hepatitis	c 352	14.4	51.4	30	2	AAQ06963	Aaq06963 Pestiviru
c 280	15	53.6	15	6	ABX01825	Abx01825 Hepatitis	c 353	14.2	50.7	31	2	AAV71016	Aav71016 PCR prime
c 281	15	53.6	15	6	ABX01825	Abx01825 Hepatitis	c 354	14.2	50.7	20	8	ACC42196	Acc42196 Human GAT
c 282	15	53.6	15	8	ACD66205	AcD66205 Hepatitis	c 355	14.2	50.7	25	9	ACH52589	ACH52589 DNA targe
c 283	15	53.6	15	8	ACD66281	AcD66281 Anti-HCV	c 356	14.2	50.7	40	9	ACD32830	AcD32830 Synthetic
c 284	15	53.6	15	8	ACD66281	AcD66281 Anti-HCV	c 357	14.2	50.7	50	12	ADH08314	AdH08314 Probe for
c 285	15	53.6	15	8	ACD65978	AcD65978 Anti-HCV	c 358	14.2	50.7	50	12	ADH08314	AdH08314 Probe for
c 286	15	53.6	15	8	ACD65979	AcD65979 Anti-HCV	c 359	14.2	50.7	50	12	ADH08314	AdH08314 Probe for
c 287	15	53.6	15	8	ACD66190	AcD66190 Anti-HCV	c 360	14.2	50.7	14	3	AAZ64683	Aaz64683 Substrate
c 288	15	53.6	15	8	ACD66204	AcD66204 Anti-HCV	c 361	14.2	50.7	14	3	AAZ64683	Aaz64683 Substrate
c 289	15	53.6	15	8	ACD66257	AcD66257 Anti-HCV	c 362	14.2	50.7	14	3	ABX01754	Abx01754 Hepatitis
c 290	15	53.6	15	8	ACD66191	AcD66191 Anti-HCV	c 363	14.2	50.7	17	8	ACD56921	AcD56921 HCV DNaz
c 291	15	53.6	15	12	AD187710	Ad187710 Anti-HCV	c 364	14.2	50.7	17	8	ACD56916	AcD56916 HCV DNaz
c 292	15	53.6	15	12	AD187686	Ad187686 Anti-HCV	c 365	14.2	50.7	17	12	ADI82821	AdI82821 HCV DNaz
c 293	15	53.6	15	12	AD187547	Ad187547 Anti-HCV	c 366	14.2	50.7	17	12	ADI82821	AdI82821 HCV DNaz
c 294	15	53.6	15	12	AD187655	Ad187655 Anti-HCV	c 367	14.2	50.7	18	2	AAV41664	Aav41664 Nucleotid
c 295	15	53.6	15	12	AD187548	Ad187548 Anti-HCV	c 368	14.2	50.7	18	2	AAV41664	Aav41664 Nucleotid
c 296	15	53.6	15	12	AD187669	Ad187669 Anti-HCV	c 369	14.2	50.7	19	3	AAA38182	Aaa38182 Primer us
c 297	15	53.6	15	12	AD187654	Ad187654 Anti-HCV	c 370	14.2	50.7	19	3	AAA38182	Aaa38182 Primer us
c 298	15	53.6	15	12	AD187668	Ad187668 Anti-HCV	c 371	14.2	50.7	19	3	AAA38182	Aaa38182 Primer us
c 299	15	53.6	15	12	AD187685	Ad187685 Anti-HCV	c 372	14.2	50.7	20	2	AAZ58050	Aaz58050 PCR prime
300	15	53.6	17	8	ACD65753	AcD65753 HCV minus	c 373	14.2	50.7	20	2	AAZ58050	Aaz58050 PCR prime
301	15	53.6	17	8	ACD65749	AcD65749 HCV minus	c 374	14.2	50.7	21	3	AAZ88380	Aaz88380 Oligonucle
302	15	53.6	17	12	AD187247	Ad187247 HCV DNaz	c 375	14.2	50.7	21	10	AD552990	Ad552990 Hepatitis
303	15	53.6	17	12	AD187243	Ad187243 HCV DNaz	c 376	14.2	50.7	21	10	AD552932	Ad552932 Hepatitis
304	15	53.6	18	2	AAV70447	Aav70447 HCV targe	c 377	14.2	50.7	21	10	AD552981	Ad552981 Hepatitis
305	15	53.6	18	6	AB146057	Ab146057 Hepatitis	c 378	14.2	50.7	23	10	AD552969	Ad552969 Hepatitis
306	15	53.6	18	6	AC61798	Ac61798 Sample pr	c 379	14.2	50.7	23	10	AD552920	Ad552920 Hepatitis
c 307	15	53.6	18	12	ADJ87103	AdJ87103 Probe use	c 380	14.2	50.7	23	10	AD552978	Ad552978 Hepatitis
308	15	53.6	18	12	ADK82247	AdK82247 Hepatitis	c 381	14.2	50.7	23	12	ADJ34749	AdJ34749 Mouse 2'
309	15	53.6	19	2	AAQ203674	Aaq203674 Hepatitis	c 382	14.2	50.7	26	2	AAQ06961	Aaq06961 Pestiviru
310	15	53.6	19	2	AAQ203674	Aaq203674 Hepatitis	c 383	14.2	50.7	26	2	AAQ06961	Aaq06961 Pestiviru
311	15	53.6	19	2	AAQ203674	Aaq203674 Hepatitis	c 384	14.2	50.7	26	2	AAV53190	Aav53190 Plasmid p
312	15	53.6	19	2	AAV20733	Aav20733 Hepatitis	c 385	14.2	50.7	30	2	AAV18340	Aav18340 Saccharom
313	15	53.6	19	2	AAV22783	Aav22783 Antisense	c 386	14.2	50.7	30	2	AAZ05337	Aaz05337 S. cerevi

387	14	50.0	30	2	AAX76357	PCR prime	460	13.4	47.9	45	12	ADM90618	Human DNA
388	14	50.0	33	6	ABL50363	Human rib	461	13.4	47.9	48	12	ADM91036	Human DNA
389	14	50.0	38	11	ADL52289	Human NOG	C 462	13.2	47.1	20	2	AAX21954	Human B-r
390	14	50.0	38	11	ADL52192	Human NOG	C 463	13.2	47.1	20	2	AAX21953	Human B-r
391	14	50.0	43	3	AA37285	Human PRO	C 464	13.2	47.1	20	6	AAX244817	Human B-r
392	14	50.0	43	4	AA37285	Human PRO	C 465	13.2	47.1	20	6	AAX244818	Human B-r
393	14	50.0	43	4	AA37285	Human PRO	C 466	13.2	47.1	20	6	AAX244819	Human B-r
394	14	50.0	43	9	ACD68468	Novel hum	C 467	13.2	47.1	20	10	ADF09811	Human b-r
395	14	50.0	43	9	ACD68468	Novel hum	C 468	13.2	47.1	20	10	ADF09812	Human b-r
396	14	50.0	43	10	ADL18189	Human PRO	C 469	13.2	47.1	20	10	ACD42200	Antisense
397	14	50.0	43	10	ADD70835	Human sec	C 470	13.2	47.1	25	5	AAI61993	Soybean 2
398	14	50.0	43	10	ADD39912	Human sec	C 471	13.2	47.1	25	5	AAI61993	Soybean 2
399	14	50.0	43	10	ADD70358	Human sec	C 472	13.2	47.1	25	5	AAI61993	Soybean 2
400	14	50.0	43	10	ADD38479	Human sec	C 473	13.2	47.1	25	9	AAK35695	Human mic
401	14	50.0	43	10	ADD38479	Human sec	C 474	13.2	47.1	27	3	AAZ61905	Hammerhea
402	14	50.0	43	10	ADD39435	Human sec	C 475	13.2	47.1	29	2	AAAT64949	Primer N1
403	14	50.0	43	10	ADD38958	Human sec	C 476	13.2	47.1	29	2	AAAT64949	Primer N1
404	14	50.0	43	10	ADD40389	Human sec	C 477	13.2	47.1	29	2	AAAT64949	Primer N1
405	14	50.0	43	10	ADE50610	Human sec	C 478	13.2	47.1	29	6	ABQ82432	Human NOV
406	14	50.0	43	10	ADE20222	Human sec	C 479	13.2	47.1	29	12	ADH42764	Novel hum
407	14	50.0	43	10	ADE50133	Human sec	C 480	13.2	47.1	30	2	AAH44313	Primer KT
408	14	50.0	43	10	ADE21691	Human sec	C 481	13.2	47.1	30	2	AAH44313	Primer KT
409	14	50.0	43	10	ADP30116	Human sec	C 482	13.2	47.1	31	3	AAAF60291	Human CD4
410	14	50.0	43	10	ADP56009	Human sec	C 483	13.2	47.1	31	3	AAAF60291	Human CD4
411	14	50.0	43	12	ADH99513	Human sec	C 484	13.2	47.1	31	3	AAAF60291	Human CD4
412	14	50.0	43	12	ADP26004	Human sec	C 485	13.2	47.1	31	3	AAAF60291	Human CD4
413	14	50.0	43	12	ADP24903	Human sec	C 486	13.2	47.1	31	3	AAAF60291	Human CD4
414	14	50.0	43	12	ADP29639	Human sec	C 487	13.2	47.1	31	3	AAAF60291	Human CD4
415	14	50.0	43	12	ADH03208	Human sec	C 488	13.2	47.1	31	3	AAAF60291	Human CD4
416	14	50.0	43	12	ADH04162	Human sec	C 489	13.2	47.1	31	3	AAAF60291	Human CD4
417	14	50.0	43	12	ADH03685	Human sec	C 490	13.2	47.1	31	3	AAAF60291	Human CD4
418	14	50.0	43	12	ADH04639	Human sec	C 491	13.2	47.1	31	3	AAAF60291	Human CD4
419	14	50.0	43	12	ADH04639	Human sec	C 492	13.2	47.1	31	3	AAAF60291	Human CD4
420	14	50.0	43	12	ADH04639	Human sec	C 493	13.2	47.1	31	3	AAAF60291	Human CD4

C 533	13	46.4	25	9	AC124149	Human mic	606	12.8	45.7	50	10	AAD54783	Aad54783 Human cys
C 534	13	46.4	25	9	ACH59841	DNA targe	607	12.8	45.7	50	10	AAD54782	Aad54782 Human cys
C 535	13	46.4	25	9	ACH59864	DNA targe	608	12.8	45.7	50	10	AAD54784	Aad54784 Human cys
C 536	13	46.4	27	8	ACD17040	Sample pr	609	12.6	45.0	19	12	ADK40294	Adk40294 Human HNP
C 537	13	46.4	27	8	ACD17035	Sample pr	610	12.6	45.0	19	12	ADQ61659	Adq61659 Anti-rp73
C 538	13	46.4	27	8	ACD17028	Sample pr	611	12.6	45.0	20	12	ADP11180	Adp11180 Set 1 rig
C 539	13	46.4	30	10	ADG95711	Human NOV	C 612	12.6	45.0	22	12	ADJ51105	Adj51105 Human NOV
C 540	13	46.4	31	8	ACD43614	Human gen	613	12.6	45.0	24	2	AAT73251	Aat73251 Detection
C 541	13	46.4	33	6	ABL50390	Human tra	C 614	12.6	45.0	24	6	ABQ03505	Abq03505 Oligonucle
C 542	13	46.4	33	6	ABL50390	Human tra	C 615	12.6	45.0	25	5	AAF60073	Aaf60073 Primer fo
C 543	13	46.4	35	2	AAE71246	Basic fib	C 616	12.6	45.0	25	9	ACI29642	Act29642 Human mic
C 544	13	46.4	35	4	AAE727342	SIV 5, LT	617	12.6	45.0	25	9	ACH52715	Act52715 DNA targe
C 545	13	46.4	35	10	ABX11696	Primer #2	618	12.6	45.0	25	9	ACI29643	Act29643 Human mic
C 546	13	46.4	36	2	AAT71249	Basic fib	619	12.6	45.0	29	2	AAE76034	Aae76034 TK-(teto)
C 547	13	46.4	37	3	AAZ64925	RPI motif	620	12.6	45.0	30	4	AAF60292	Aaf60292 Human CD4
C 548	13	46.4	37	6	ABX03347	Ribozyne	C 621	12.6	45.0	30	6	ABX67519	Abx67519 Novel Hel
C 549	13	46.4	38	6	ACN27267	WNV minus	622	12.6	45.0	31	2	AAV60718	Aav60718 Primer #1
C 550	13	46.4	38	6	ACN28766	WNV minus	623	12.6	45.0	31	2	AAV60718	Aav60718 Primer #1
C 551	13	46.4	38	6	ACN17677	Inozy	C 624	12.6	45.0	32	10	ADD25850	Add25850 Binding d
C 552	13	46.4	38	6	ACN15558	WNV Hamme	625	12.6	45.0	32	10	AAE56958	Aae56958 Human hyp
C 553	13	46.4	38	11	ADL52118	Human NOG	C 626	12.6	45.0	35	4	AAH25064	Aah25064 PCR prime
C 554	13	46.4	39	8	ABZ68718	PCR prime	C 627	12.6	45.0	35	10	ADG84263	Adg84263 Human TMD
C 555	13	46.4	40	6	ABZ46736	Human ATP	628	12.6	45.0	36	2	AAT70249	Aat70249 KPI(1-55)
C 556	13	46.4	40	6	ABZ46736	Human ATP	629	12.6	45.0	36	3	AAZ57501	Aaz57501 Kunitz pr
C 557	13	46.4	41	5	AAH46151	DNA ligas	630	12.6	45.0	36	4	AAH25064	Aah25064 PCR prime
C 558	13	46.4	41	6	ABL50387	Human tra	631	12.6	45.0	38	2	AAQ51681	Aaq51681 Primer to
C 559	13	46.4	41	6	ABL50386	Human tra	632	12.6	45.0	38	4	AAH96521	Aah96521 Human Chk
C 560	13	46.4	41	6	ABZ70159	Beta lact	633	12.6	45.0	38	4	ABK05063	Abk05063 Human NOG
C 561	13	46.4	41	6	AAH16266	DNA probe	634	12.6	45.0	38	6	ACN29302	Actn29302 WNV minus
C 562	13	46.4	41	6	AAH16265	DNA probe	C 635	12.6	45.0	39	4	AAH20281	Aah20281 Gol9 link
C 563	13	46.4	45	2	AAH88771	SV40 olig	C 636	12.6	45.0	40	2	AAZ22072	Aaz22072 Probe ana
C 564	13	46.4	45	2	AAH88771	SV40 olig	637	12.6	45.0	41	6	ABZ46298	Abz46298 Human ald
C 565	13	46.4	45	4	AAH46035	SV40 orig	638	12.6	45.0	41	6	ABZ46298	Abz46298 Human ald
C 566	13	46.4	45	4	AAH46035	SV40 orig	639	12.6	45.0	42	2	AAH62133	Aah62133 Granule b
C 567	12.8	45.7	17	8	ACC68190	Murine ol	C 640	12.6	45.0	45	3	AAH53222	Aah53222 Human Gp
C 568	12.8	45.7	18	2	AAH53222	GRK4 allele	C 641	12.6	45.0	45	8	ABX12052	Abx12052 Human NFI
C 569	12.8	45.7	19	2	AAH53222	GRK4 allele	C 642	12.6	45.0	45	10	ADE78398	Ad78398 DNA encod
C 570	12.8	45.7	21	6	ABN80440	Factor XI	C 643	12.6	45.0	46	12	ADM88037	Adm88037 Gene expr
C 571	12.8	45.7	21	6	ABN80440	DNA-RNA h	C 644	12.6	45.0	49	2	AAT80501	Aat80501 Hepatoma
C 572	12.8	45.7	23	12	ADN30310	Recombina	645	12.6	45.0	49	6	ABN71825	Abn71825 Streptoco
C 573	12.8	45.7	24	12	ADH51112	Human can	C 646	12.6	45.0	50	4	AAH29647	Aah29647 Human SNP
C 574	12.8	45.7	25	9	ACI65495	Human mic	C 647	12.6	45.0	50	4	AAH29647	Aah29647 Human SNP
C 575	12.8	45.7	25	9	ACI22729	Human mic	C 648	12.6	45.0	50	6	AAH29647	Aah29647 Human SNP
C 576	12.8	45.7	25	9	ACK27780	Human mic	C 649	12.6	45.0	50	6	AAH29647	Aah29647 Human SNP
C 577	12.8	45.7	25	9	ACK27881	Human mic	C 650	12.6	45.0	50	6	AAH29647	Aah29647 Human SNP
C 578	12.8	45.7	25	9	ADA14319	Human Skp	C 651	12.6	45.0	50	6	AAH29647	Aah29647 Human SNP
C 579	12.8	45.7	26	2	AAH19708	Pichia pa	C 652	12.6	45.0	50	6	AAH29647	Aah29647 Human SNP
C 580	12.8	45.7	26	2	AAH19710	Pichia pa	C 653	12.6	45.0	50	6	AAH29647	Aah29647 Human SNP
C 581	12.8	45.7	29	3	AAH19710	Pichia pa	654	12.6	45.0	50	6	AAH29647	Aah29647 Human SNP
C 582	12.8	45.7	31	4	AAH19710	Pichia pa	C 655	12.6	45.0	50	6	AAH29647	Aah29647 Human SNP
C 583	12.8	45.7	31	4	AAH19710	Pichia pa	C 656	12.6	45.0	50	6	AAH29647	Aah29647 Human SNP
C 584	12.8	45.7	31	4	AAH19710	Pichia pa	C 657	12.6	45.0	50	6	AAH29647	Aah29647 Human SNP
C 585	12.8	45.7	34	10	ABZ233645	N. gonorr	C 658	12.6	45.0	50	6	AAH29647	Aah29647 Human SNP
C 586	12.8	45.7	35	10	ADG40192	Human ade	C 659	12.6	45.0	50	6	AAH29647	Aah29647 Human SNP
C 587	12.8	45.7	37	11	ADO70335	PCR prime	C 660	12.6	45.0	50	6	AAH29647	Aah29647 Human SNP
C 588	12.8	45.7	41	6	AAH29647	Human mic	C 661	12.6	45.0	50	6	AAH29647	Aah29647 Human SNP
C 589	12.8	45.7	41	6	AAH29647	Human mic	C 662	12.6	45.0	50	6	AAH29647	Aah29647 Human SNP
C 590	12.8	45.7	41	6	AAH29647	Human mic	C 663	12.6	45.0	50	6	AAH29647	Aah29647 Human SNP
C 591	12.8	45.7	44	3	AAH288571	PCR prime	C 664	12.6	45.0	50	6	AAH29647	Aah29647 Human SNP
C 592	12.8	45.7	47	3	AAH288571	PCR prime	C 665	12.6	45.0	50	6	AAH29647	Aah29647 Human SNP
C 593	12.8	45.7	47	3	AAH288571	PCR prime	C 666	12.6	45.0	50	6	AAH29647	Aah29647 Human SNP
C 594	12.8	45.7	47	3	AAH288571	PCR prime	C 667	12.6	45.0	50	6	AAH29647	Aah29647 Human SNP
C 595	12.8	45.7	47	3	AAH288571	PCR prime	C 668	12.6	45.0	50	6	AAH29647	Aah29647 Human SNP
C 596	12.8	45.7	47	3	AAH288571	PCR prime	C 669	12.6	45.0	50	6	AAH29647	Aah29647 Human SNP
C 597	12.8	45.7	47	3	AAH288571	PCR prime	C 670	12.6	45.0	50	6	AAH29647	Aah29647 Human SNP
C 598	12.8	45.7	47	3	AAH288571	PCR prime	C 671	12.6	45.0	50	6	AAH29647	Aah29647 Human SNP
C 599	12.8	45.7	47	3	AAH288571	PCR prime	C 672	12.6	45.0	50	6	AAH29647	Aah29647 Human SNP
C 600	12.8	45.7	47	3	AAH288571	PCR prime	C 673	12.6	45.0	50	6	AAH29647	Aah29647 Human SNP
C 601	12.8	45.7	47	3	AAH288571	PCR prime	C 674	12.6	45.0	50	6	AAH29647	Aah29647 Human SNP
C 602	12.8	45.7	47	3	AAH288571	PCR prime	C 675	12.6	45.0	50	6	AAH29647	Aah29647 Human SNP
C 603	12.8	45.7	47	3	AAH288571	PCR prime	C 676	12.6	45.0	50	6	AAH29647	Aah29647 Human SNP
C 604	12.8	45.7	47	3	AAH288571	PCR prime	C 677	12.6	45.0	50	6	AAH29647	Aah29647 Human SNP
C 605	12.8	45.7	47	3	AAH288571	PCR prime	C 678	12.6	45.0	50	6	AAH29647	Aah29647 Human SNP

C 679	12.4	44.3	38	6	ACN26411	ACN26411 WNV minus	752	12.2	43.6	45	2	AAV99361	Aav99361 3' PCR pr
C 680	12.4	44.3	38	6	ACN29778	ACN29778 WNV minus	C 753	12.2	43.6	47	3	AAZ66791	Aaz66791 Human map
C 681	12.4	44.3	38	6	ACN17697	ACN17697 WNV Inozy	C 754	12.2	43.6	47	3	Az68983	Az68983 Human map
C 682	12.4	44.3	38	6	ACN29626	ACN29626 WNV minus	C 755	12.2	43.6	48	6	ABK22020	Abk22020 Human ERG
C 683	12.4	44.3	38	8	ACD50492	ACD50492 HBV hamme	756	12.2	43.6	48	11	ADL76321	Adl76321 Human PTG
C 684	12.4	44.3	38	11	ADM54985	ADM54985 NCH riboz	757	12.2	43.6	49	6	ABN72010	Abn72010 Streptoco
C 685	12.4	44.3	38	11	ADM54951	ADM54951 NCH riboz	758	12.2	43.6	50	2	AAQ76358	Aaq76358 Antisense
C 686	12.4	44.3	38	12	ADM60468	ADM60468 Hepatitis	C 759	12.2	43.6	50	2	AAQ76359	Aaq76359 Antisense
C 687	12.4	44.3	39	2	AAT51498	Aat51498 Fragment	C 760	12.2	43.6	50	2	AAQ76353	Aaq76353 Antisense
C 688	12.4	44.3	39	2	AAV30871	AAV30871 Human p53	C 761	12.2	43.6	50	4	AAQ76353	Aaq76353 Antisense
C 689	12.4	44.3	39	12	ADL64610	ADL64610 Human sin	C 762	12.2	43.6	50	4	AAQ76353	Aaq76353 Antisense
C 690	12.4	44.3	41	2	AAQ52872	AAQ52872 Cytochrome	C 763	12.2	43.6	50	6	ABZ05101	Abz05101 Human SNP
C 691	12.4	44.3	41	2	AAV50904	AAV50904 Maize pol	C 764	12.2	43.6	50	6	ABZ06100	Abz06100 Human leu
C 692	12.4	44.3	41	6	ABZ46709	ABZ46709 Human ATP	C 765	12.2	43.6	50	6	ADG33517	Adg33517 Human DNA
C 693	12.4	44.3	41	6	ABZ46710	ABZ46710 Human ATP	C 766	12.2	43.6	50	10	ADP13010	Adp13010 50-mer ol
C 694	12.4	44.3	41	6	ABZ44361	ABZ44361 Human ATP	C 767	12.2	43.6	50	12	ACD66038	AcD66038 Anti-HCV
C 695	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 768	12.2	43.6	50	8	ACD66054	AcD66054 Anti-HCV
C 696	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 769	12.2	43.6	50	8	ADL87698	AdL87698 Anti-HCV
C 697	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 770	12.2	43.6	50	12	ADL87588	AdL87588 Anti-HCV
C 698	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 771	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 699	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 772	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 700	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 773	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 701	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 774	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 702	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 775	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 703	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 776	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 704	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 777	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 705	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 778	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 706	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 779	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 707	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 780	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 708	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 781	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 709	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 782	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 710	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 783	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 711	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 784	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 712	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 785	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 713	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 786	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 714	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 787	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 715	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 788	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 716	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 789	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 717	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 790	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 718	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 791	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 719	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 792	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 720	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 793	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 721	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 794	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 722	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 795	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 723	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 796	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 724	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 797	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 725	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 798	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 726	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 799	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 727	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 800	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 728	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 801	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 729	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 802	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 730	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 803	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 731	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 804	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 732	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 805	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 733	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 806	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 734	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 807	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 735	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 808	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 736	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 809	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 737	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 810	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 738	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 811	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 739	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 812	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 740	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 813	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 741	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 814	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 742	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 815	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 743	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 816	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 744	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 817	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 745	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 818	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 746	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 819	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 747	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 820	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 748	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 821	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 749	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 822	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 750	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 823	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV
C 751	12.4	44.3	41	6	ABZ44362	ABZ44362 Human ATP	C 824	12.2	43.6	50	12	ADL87572	AdL87572 Anti-HCV



C 825	12	42.9	30	10	ADB79282	Adb79282 E-tag med	898	12	42.9	46	3	AAC68509	Aac68509 Periplaki
826	12	42.9	30	10	ADC22680	Adc22680 Human G p	C 899	12	42.9	46	12	ADG46560	Adg46560 pUC18 mod
827	12	42.9	30	10	ADH14153	Adh14153 Human GPC	C 900	12	42.9	47	3	AAC65934	Aac65934 Human map
828	12	42.9	30	10	ACF03426	Acf03426 Vector pG	901	12	42.9	47	3	AAZ67464	Aaz67464 Human map
829	12	42.9	30	11	ADM39449	Adm39449 Maize Zmf	C 902	12	42.9	49	6	ABL88614	Ab188614 Fungal ce
C 830	12	42.9	30	12	ADM18536	Adm18536 Human sub	C 903	12	42.9	49	10	ADC18795	Adc18795 Cell wall
831	12	42.9	30	12	ADO12772	Ado12772 Single mu	C 904	12	42.9	50	1	AAK90885	Aan90885 3'-5' pro
C 832	12	42.9	30	12	ADO12782	Ado12782 Single mu	905	12	42.9	50	3	AAC65183	Aaz65183 Probe spe
833	12	42.9	31	2	AAK39012	Aak39012 Human gen	906	12	42.9	50	3	AAC58254	Aac58254 Human PRO
834	12	42.9	32	3	AAA08336	Aaa08336 Spinach c	907	12	42.9	50	5	AAF44340	Aaf44340 Human PRO
835	12	42.9	33	2	AAO6297	Aao6297 Phage R1-	C 908	12	42.9	50	6	ABZ00735	Abz00735 Human leu
C 836	12	42.9	33	2	AAO6297	Aao6297 Phage R1-	C 909	12	42.9	50	6	ABZ00735	Abz00735 Human leu
837	12	42.9	33	4	AAI71682	Aai71682 Forward p	910	12	42.9	50	6	ABZ06083	Abz06083 Human leu
838	12	42.9	33	5	AB197614	Ab197614 Endogenou	911	12	42.9	50	6	ACA64331	Ac64331 Secreted
C 839	12	42.9	33	6	ABN85225	Abn85225 Human tra	912	12	42.9	50	8	ACA64331	Ac64331 Secreted
C 840	12	42.9	33	8	ADA14822	Ada14822 Anti-idio	913	12	42.9	50	8	ACD44299	Ac44299 Human PRO
841	12	42.9	33	10	ADC35351	Adc35351 Monoclonal	914	12	42.9	50	8	ACD44299	Ac44299 Human PRO
C 842	12	42.9	34	6	ABK14686	Abk14686 Human IRI	915	12	42.9	50	8	ABX79470	Abx79470 Human sec
843	12	42.9	36	2	AAAT97138	Aat97138 PCR prime	916	12	42.9	50	8	ACA93491	Ac93491 Novel hum
844	12	42.9	36	3	AAA94046	Aaa94046 Human hDC	917	12	42.9	50	8	ABX81173	Abx81173 Novel hum
845	12	42.9	36	6	ABX02606	Abx02606 HCV hamme	918	12	42.9	50	8	ACA92989	Ac92989 Novel hum
846	12	42.9	36	6	ABX02010	Abx02010 HCV hamme	919	12	42.9	50	8	ABX17073	Abx17073 Human PRO
847	12	42.9	36	6	ABX02092	Abx02092 HCV hamme	920	12	42.9	50	9	ACA67928	Ac67928 Novel hum
C 848	12	42.9	36	8	AD53388	Ad53388 PCR prime	921	12	42.9	50	9	ACA88377	Ac88377 Human sec
C 849	12	42.9	37	2	AAZ12403	Aaz12403 PCR prime	922	12	42.9	50	9	ACD81884	Ac81884 Human PRO
850	12	42.9	37	3	AAZ48307	Aaz48307 B. subtil	923	12	42.9	50	9	ADA37762	Ada37762 Human sec
851	12	42.9	38	4	ABK04095	Abk04095 Human NOG	924	12	42.9	50	9	ADA21448	Ada21448 Human sec
852	12	42.9	38	4	ABK03869	Abk03869 Human NOG	925	12	42.9	50	9	ADA10235	Ada10235 Human PRO
853	12	42.9	38	4	ABK05032	Abk05032 Human NOG	926	12	42.9	50	9	ADA17779	Ada17779 Human PRO
854	12	42.9	38	4	ABK08253	Abk08253 Human CD2	927	12	42.9	50	9	ADA27887	Ada27887 Human sec
855	12	42.9	38	6	ABK58046	Abk58046 Human CLC	928	12	42.9	50	9	ADA94467	Ada94467 Human sec
856	12	42.9	38	6	ACN26647	Acn26647 WNV minus	929	12	42.9	50	9	ADA38692	Ada38692 Human sec
857	12	42.9	38	6	ACN28513	Acn28513 WNV minus	930	12	42.9	50	9	ADA92813	Ada92813 Human sec
858	12	42.9	38	6	ACN18595	Acn18595 WNV Inozy	931	12	42.9	50	9	ACH65445	Ac65445 Human sec
859	12	42.9	38	6	ACN17480	Acn17480 WNV Inozy	932	12	42.9	50	9	ADA22374	Ada22374 Human sec
860	12	42.9	38	6	ACN16052	Acn16052 WNV Hamme	933	12	42.9	50	9	ADC339435	Adc339435 Human sec
C 861	12	42.9	38	6	ACN18103	Acn18103 WNV Inozy	934	12	42.9	50	9	ADA06540	Ada06540 Human sec
862	12	42.9	38	6	ACN27006	Acn27006 WNV minus	935	12	42.9	50	9	ADA39233	Ada39233 Human sec
863	12	42.9	38	6	ACN15327	Acn15327 WNV Hamme	936	12	42.9	50	9	ADB96259	Adb96259 Human PRO
864	12	42.9	38	6	ACN26671	Acn26671 WNV minus	937	12	42.9	50	10	ADC57731	Adc57731 Human PRO
865	12	42.9	38	6	ACN27305	Acn27305 WNV minus	938	12	42.9	50	10	ADC55095	Adc55095 Human PRO
866	12	42.9	38	6	ACN15673	Acn15673 WNV Hamme	939	12	42.9	50	10	ADC11962	Adc11962 Human sec
867	12	42.9	38	6	ACN15690	Acn15690 WNV Hamme	940	12	42.9	50	10	ADC56384	Adc56384 Human PRO
868	12	42.9	38	6	ACN15418	Acn15418 WNV Hamme	941	12	42.9	50	10	ADC07439	Adc07439 Human sec
869	12	42.9	38	6	ACN17502	Acn17502 WNV Inozy	942	12	42.9	50	10	ADC11429	Adc11429 Human sec
870	12	42.9	38	6	ACN15308	Acn15308 WNV Hamme	943	12	42.9	50	10	ADC114551	Adc114551 Novel hum
871	12	42.9	38	6	ACN26296	Acn26296 WNV minus	944	12	42.9	50	10	ADD08083	Add08083 Human sec
872	12	42.9	38	6	ACN17013	Acn17013 WNV Inozy	945	12	42.9	50	10	ADD08083	Add08083 Human sec
873	12	42.9	38	6	ACN18550	Acn18550 WNV Inozy	946	12	42.9	50	10	ADD07550	Add07550 Human sec
874	12	42.9	38	6	ACN16757	Acn16757 WNV Inozy	947	12	42.9	50	10	ADC82441	Adc82441 Human PRO
875	12	42.9	38	6	ACN27599	Acn27599 WNV minus	948	12	42.9	50	10	ADD08621	Add08621 Human sec
876	12	42.9	38	6	ACN15695	Acn15695 WNV Hamme	949	12	42.9	50	10	ADD06870	Add06870 Human sec
877	12	42.9	38	8	ACN07110	Acn07110 Necrosis	950	12	42.9	50	10	ADC83117	Adc83117 Human PRO
878	12	42.9	38	8	ACN07302	Acn07302 Necrosis	951	12	42.9	50	10	ADC83117	Adc83117 Human PRO
879	12	42.9	38	12	ADM61595	Adm61595 Hepatitis	C 952	12	42.9	50	10	ADD31890	Add31890 Human ret
C 880	12	42.9	39	6	AAK96515	Aak96515 Primer #3	953	12	42.9	50	10	ADD52224	Add52224 Buterfly
C 881	12	42.9	40	2	AAK22073	Aak22073 Probe ana	954	12	42.9	50	10	ADD56182	Ad56182 Human PRO
882	12	42.9	40	6	ABT12187	Abt12187 E coli ex	955	12	42.9	50	10	ADD54620	Ad54620 Human PRO
883	12	42.9	41	2	AAV25473	Aav25473 T7 promot	956	12	42.9	50	10	ADE26774	Ade26774 Novel hum
884	12	42.9	41	2	ABA02955	Ab02955 Human nuc	957	12	42.9	50	10	ADE26241	Ade26241 Novel hum
885	12	42.9	41	6	ABZ48822	Abz48822 Human ald	958	12	42.9	50	10	ADG67178	Adg67178 Human CDN
886	12	42.9	41	6	ABA02956	Ab02956 Human nuc	959	12	42.9	50	10	ADG33646	Adg33646 Human DNA
C 887	12	42.9	41	6	ABZ70160	Abz70160 Beta lact	960	12	42.9	50	10	ADG33646	Adg33646 Human DNA
888	12	42.9	41	6	ABA01830	Ab01830 Human reg	961	12	42.9	50	10	ADH99924	Adh99924 Novel hum
C 889	12	42.9	41	6	ABZ48091	Abz48091 Human ATP	962	12	42.9	50	10	ABX77874	Abx77874 Human PRO
890	12	42.9	41	6	ABZ46311	Abz46311 Human ald	963	12	42.9	50	10	ABX80286	Abx80286 Novel hum
891	12	42.9	41	6	ABZ48822	Abz48822 Human ald	964	12	42.9	50	10	ACA69192	Ac69192 Human sec
892	12	42.9	41	6	ABA97884	Ab97884 Human NAD	965	12	42.9	50	10	ABX90263	Abx90263 Human sec
C 893	12	42.9	42	8	AD53413	Ad53413 Alpha-gal	966	12	42.9	50	10	ABX64109	Abx64109 Human PRO
894	12	42.9	42	10	ADG87147	Adg87147 CAR genom	967	12	42.9	50	12	ADF35377	Adf35377 Human PRO
895	12	42.9	45	2	AAQ81186	Aaq81186 CTLA4 ext	968	12	42.9	50	12	ADG11627	Adg11627 Human PRO
C 896	12	42.9	45	10	ADG44362	Adg44362 Anti-path	969	12	42.9	50	12	ADH19497	Adh19497 Human sec
897	12	42.9	45	10	ADG44361	Adg44361 Anti-path	970	12	42.9	50	12	ADH20990	Adh20990 Human sec

971	12	42..9	50	12	ADH20030
972	11..8	42..1	15	4	AAF51089
973	11..8	42..1	17	2	AAX04635
974	11..8	42..1	17	8	ACC65098
975	11..8	42..1	18	2	AAT87814
976	11..8	42..1	18	2	AAX27644
977	11..8	42..1	18	6	AAD241177
978	11..8	42..1	18	6	AAL46928
979	11..8	42..1	18	10	ADI24999
980	11..8	42..1	18	11	ADM06741
981	11..8	42..1	18	11	ADM06515
982	11..8	42..1	19	11	ADM29450
983	11..8	42..1	20	2	AZ02396
984	11..8	42..1	20	3	AAH97621
985	11..8	42..1	20	4	AAH46338
986	11..8	42..1	20	10	ADO01033
987	11..8	42..1	20	10	ADH62993
988	11..8	42..1	20	10	ADH57148
989	11..8	42..1	20	12	ADK43228
990	11..8	42..1	20	12	ADK43351
991	11..8	42..1	20	12	ADO60079
992	11..8	42..1	20	12	ADO44584
993	11..8	42..1	21	11	ADM65618
994	11..8	42..1	21	12	ADK98392
995	11..8	42..1	22	6	AAD43483
996	11..8	42..1	22	6	AAK43460
997	11..8	42..1	22	6	ABK89951
998	11..8	42..1	23	6	ABS63490
999	11..8	42..1	23	8	ADA00131
1000	11..8	42..1	24	6	ABL41902

ALIGNMENTS

RESULT 1	
D	AAT67194 standard; DNA; 28 BP.
C	X
X	AAT67194;
T	X
T	13-FEB-1998 (first entry)
E	Hepatitis C virus (HCV) RNA amplification primer ST778AA.
X	Hepatitis C virus; HCV; ST778AA; reverse transcription PCR; RT-PCR;
W	detection; PCR primer; ss.
W	Synthetic.
WS	.
N	EP776981-A2.
N	X
KX	04-JUN-1997.
DK	21-NOV-1996; 96EP-00118704.
FF	29-NOV-1995; 95US-0007739P.
PR	(HOFF ) HOFFMANN LA ROCHE & CO AG F.
GA	Teang SY;
PI	WPI; 1997-291296/27.
KX	Oligonucleotide primers for hepatitis C virus RNA amplification - by
DR	polymerase chain reaction.
KX	Claim 1; Page 12; 16pp; English.
XX	This downstream primer ST778AA is used in the amplification of the
CC	Hepatitis C virus (HCV) RNA by reverse transcription PCR. This is used to
CC	amplify a 250 base pair product from the 5' untranslated region of the
CC	coding sequence which has been shown to increase the efficiency of the

```
SQ Sequence 28 BP; 10 A; 10 C; 5 G; 3 T; 0 U; 0 Other;
Query Match      100.0%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCTTATCAGGAGTACCAAA 28
   |||||
Db 1 GCAAGCACCTTATCAGGAGTACCAAA 28
   |||||

RESULT 3
AAH25414
ID AAH25414 standard; DNA; 28 BP.
XX
AC
XX
AC AAH25414;
XX
DT 22-AUG-2001 (first entry)
XX
DE Reverse PCR primer used to amplify a HCV DNA fragment.
XX
KW Magnetic glass particle; nucleic acid purification; PCR primer; ss.
XX
OS Hepatitis C virus.
XX
FH Key Location/Qualifiers
FT modified_base 28
FT FT /*tag= a
FT FT /note= "derivatisation with a p-(t-butyl)benzyl-residue"
XX
XX WO200137291-A1.
XX
FN
XX
PD 25-MAY-2001.
XX
XX
PF 17-NOV-2000; 2000WO-EP011459.
XX
PR 17-NOV-1999; 9SEP-00122853.
PR 12-MAY-2000; 2000EP-00110165.
XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX
PI Weindel K, Riedling M, Geiger A;
XX
DR WPI; 2001-381247/40.
XX
XX Novel composition of magnetic glass particles for purification of DNA or
PT RNA in automated processes.
XX
PS Example 7; Page 98; 105pp; English.
XX
XX The specification describes a composition of magnetic glass particles,
CC which contain at least one magnetic object with a mean diameter between 5
CC -500 nm. The composition is useful for the purification of nucleic acids.
CC The composition can be used to process large quantities of nucleic acid
CC samples, because it does not involve the particles being centrifuged or
CC the fluids being drawn through glass fiber filters. PCR primers AAH25413-
CC 14 were used to amplify HCV DNA fragments. The amplified fragment can be
CC purified using the method of the invention
XX
SQ Sequence 28 BP; 10 A; 10 C; 5 G; 3 T; 0 U; 0 Other;
Query Match      100.0%; Score 28; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCTTATCAGGAGTACCAAA 28
   |||||
Db 1 GCAAGCACCTTATCAGGAGTACCAAA 28
   |||||

RESULT 4
ADC84693
ID ADC84693 standard; DNA; 28 BP.
```

```
XX AC ADC84693;
XX DT 01-JAN-2004 (first entry)
XX DE PCR primer, #2, used to amplify HCV 5' UTR cDNA.
XX KW RNA purification; undegraded RNA; RNA binding solution;
XX KW RNA complexing salt; chaotropic substance; non-silica solid support;
XX KW RNA lysing solution; amphiphilic reagent; PCR; ss; primer; 5' UTR;
XX KW untranslated region.
XX OS Hepatitis C virus.
XX FN US2003073830-A1.
XX PD 17-APR-2003.
XX PF 12-OCT-2001; 2001US-00974798.
XX PR 12-OCT-2001; 2001US-00974798.
XX PA (HEAT/) HEATH E M.
XX PA (WAGE/) WAGES J M.
XX FI Heath EM, Wages JM;
XX DR WPI; 2003-786889/74.
XX PT Purifying substantially pure and undegraded RNA from biological material
PT involves use of high pH- and strong chaotropic substance-free RNA binding
PT solution that allows RNA to preferentially bind to a solid support.
XX PS Example 10; Page 11; 14pp; English.
XX CC The invention discloses a method for purifying substantially pure and
XX CC undegraded RNA from biological material (B). The method comprises mixing
XX CC (B) with RNA binding solution (I) that has RNA-complexing salt and is
XX CC free of strong chaotropic substance, to form a mixture which is contacted
XX CC with to a non-silica solid support (SS) such that nucleic acids
XX CC comprising substantially undegraded RNA in mixture preferentially bind to
XX CC SS, washing SS and eluting bound substantially undegraded RNA from SS.
XX CC The method may also comprise mixing (B), with an RNA lysing solution (II)
XX CC buffered at a pH of greater than about 7, and comprising an amphiphilic
XX CC reagent, and RNA-complexing salt, and is free of a strong chaotropic
XX CC substance, lysing (B) with (II) to form a lysate comprising nucleic acids
XX CC comprising substantially undegraded RNA and non-nucleic acid biological
XX CC matter, contacting the lysate to an immobilised non-silica SS such that
XX CC the nucleic acids comprising substantially undegraded RNA in the lysate
XX CC preferentially bind to SS, washing SS and eluting bound substantially
XX CC undegraded RNA. The methods are useful for purifying substantially pure
XX CC RNA, or its combinations) from biological material containing RNA. The
XX CC method is useful for purifying RNA from crude and partially purified
XX CC mixtures of nucleic acids, from (B) such as eukaryotic, prokaryotic,
XX CC microbial, bacterial or plant cells, mycoplasma, protozoa, bacteria,
XX CC fungi, viruses, yeasts, rickettsia or their homogenates. The method is
XX CC also useful for purifying RNA from (B) such as whole blood, bone marrow,
XX CC blood spots, blood serum, blood plasma, buffy coat preparations, saliva,
XX CC cerebrospinal fluid, solid animal tissues, faeces, urine, tears, sweat or
XX CC from environmental samples taken from air, water sediment or soil. The
XX CC purified RNA is useful in analytical and diagnostic methods such as
XX CC reverse transcriptase-PCR and micro array analyses. The method purifies
XX CC RNA from a variety of biological materials without the use of hazardous
XX CC substances such as phenol and chloroform or hazardous chaotropic
XX CC substances such as guanidinium salts, urea, etc. The method allows the
XX CC elution of RNA in low salt reagents thus eliminating tedious desalting
XX CC steps. The method is versatile and effective. The sequence presented is a
XX CC PCR primer which was used to amplify Hepatitis C virus (HCV) 5'
XX CC untranslated region (UTR) to demonstrate the integrity of the purified
XX CC mRNA.
XX SQ Sequence 28 BP; 10 A; 10 C; 5 G; 3 T; 0 U; 0 Other;
```

Db	1	GCAAGCACCCCTATCAGGCAGTACCACAA	28											
RESULT 5														
AD43288	AAD43288 standard; DNA; 29 BP.													
XX	AC													
XX	AD43288;													
DT	14-NOV-2002	(first entry)												
DE	HCV DNA amplifying PCR primer, ST778.													
XX	Amplification; target nucleic acid; PCR; primer; ss.													
OS	Hepatitis C virus.													
PH	Key	Location/Qualifiers												
FT	stem_loop	9..17	/*tag= a											
FT	misc_binding	9..11	/*tag= b											
FT	misc_binding	15..17	/bound_moiety= "Nucleotides 17-15"											
FT	misc_binding	15..17	/*tag= c											
FT	misc_binding	15..17	/bound_moiety= "Nucleotides 11-9"											
XX	EP1236805-A1..													
XX	04-SEP-2002.													
XX	27-FEB-2002;	2002EP-00004483.												
XX	02-MAR-2001;	2001EP-00105172.												
XX	(HOFF ) ROCHE DIAGNOSTICS GMBH.													
XX	(HOFF ) HOFFMANN LA ROCHE & CO AG F.													
XX	Jaeger S;													
XX	WPI; 2002-610695/66.													
XX	Amplification of a target nucleic acid region using a specific control sequence.													
XX	Example 2; Fig 3; 28pp; English.													
XX	The invention relates to a method for amplification of a target nucleic acid region in a sample using a specific control sequence. The invention is also directed to a method of determination of a target nucleic acid using a special control nucleic acid. Nucleic acids of the invention are used as a control in a reaction for amplifying target nucleic acids and as a control in a hybridisation reaction for determination of target nucleic acids. The present sequence is HCV (Hepatitis C virus) type I DNA amplifying PCR primer. This primer is used to illustrate the methods of the invention. Note: This sequence is stated to be same as that shown as SEQ ID NO:7 in sequence listing. However this sequence has additional A at its 3' end													
XX	Sequence 29 BP; 11 A; 10 C; 5 G; 3 T; 0 U; 0 Other;													
XX	Query Match	100.0%;	Score 28;			DB 6;	Length 29;							
XX	Best Local Similarity	100.0%;	Pred. No. 0.0061;											
XX	Matches	28;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;									
QY	1	GCAAGCACCCCTATCAGGCAGTACCACAA	28											

Db	1	GCAAGCACCCCTATCAGGCAGTACCACAA	28											
RESULT 6														
AD43740	AAD43740 standard; DNA; 29 BP.													
XX	AC													
XX	AD43740;													
DT	07-AUG-2003	(revised)												
DT	14-NOV-2002	(first entry)												
XX	HCV DNA amplifying PCR primer, ST778.													
XX	Amplification; target nucleic acid; control nucleic acid; PCR; primer; ss.													
OS	Hepatitis C virus.													
XX	Key	Location/Qualifiers												
FT	stem_loop	9..17	/*tag= a											
FT	misc_binding	9..11	/*tag= b											
FT	misc_binding	15..17	/bound_moiety= "Nucleotides 17-15"											
FT	misc_binding	15..17	/*tag= c											
FT	misc_binding	15..17	/bound_moiety= "Nucleotides 11-9"											
XX	EP1236804-A1.													
XX	04-SEP-2002.													
XX	02-MAR-2001;	2001EP-00105172.												
XX	02-MAR-2001;	2001EP-00105172.												
XX	(HOFF ) ROCHE DIAGNOSTICS GMBH.													
XX	(HOFF ) HOFFMANN LA ROCHE & CO AG F.													
XX	Jaeger S;													
XX	WPI; 2002-610694/66.													
XX	Amplification of a target nucleic acid region using control sequences.													
XX	Example 2; Fig 3; 29pp; English.													
XX	The invention relates to a method for amplification of a target nucleic acid region. The method is useful for amplification of a nucleic acid molecule using control nucleic acid sequences. The control nucleic acid sequences are at least in part parallel-complementary to the sequence of the target nucleic acid. The present sequence is HCV DNA amplifying PCR primer. Note: This sequence is stated to be same as that shown as SEQ ID NO:7 in sequence listing. However this sequence has additional A at its 3' end. (Updated on 07-AUG-2003 to correct OS field.)													
XX	Sequence 29 BP; 11 A; 10 C; 5 G; 3 T; 0 U; 0 Other;													
XX	Query Match	100.0%;	Score 28;			DB 6;	Length 29;							
XX	Best Local Similarity	100.0%;	Pred. No. 0.0061;											
XX	Matches	28;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;									
QY	1	GCAAGCACCCCTATCAGGCAGTACCACAA	28											
DB	1	GCAAGCACCCCTATCAGGCAGTACCACAA	28											
RESULT 7														
AA767195	AAT67195 standard; DNA; 27 BP.													
XX														

```

AC AA767195;
XX
DT 13-FEB-1998 (first entry)
XX
DE Hepatitis C virus (HCV) RNA amplification primer ST678A.
XX
KW Hepatitis C virus; HCV; ST678A; reverse transcription PCR; RT-PCR;
XX PCR primer; ss.
XX
OS Synthetic.
XX
PN EP776981-A2.
XX
PD 04-JUN-1997.
XX
PF 21-NOV-1996; 96EP-00118704.
XX
PR 29-NOV-1995; 95US-0007739P.
XX
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI Tsang SY;
XX
DR WPI; 1997-291296/27.
XX
PT Oligonucleotide primers for hepatitis C virus RNA amplification - by
PT polymerase chain reaction.
XX
PS Claim 1; Page 12; 16pp; English.
XX
CC This downstream primer ST678A is used in the amplification of the
CC Hepatitis C virus (HCV) RNA by reverse transcription PCR. This is used to
CC amplify a 250 base pair product from the 5' untranslated region of the
CC HCV genome. This can be used to detect HCV in a sample with increased
CC sensitivity. Amplification of HCV nucleic acid using this primer is up to
CC 100 times more efficient than amplification with prior art primers
XX
SQ Sequence 27 BP; 9 A; 10 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 96.4%; Score 27; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCGAGTACCACA 27
Db 1 GCAAGCACCTATCAGGCGAGTACCACA 27

RESULT 8
AAA74623
ID AAA74623 standard; DNA; 27 BP.
AC
AC AAA74623;
XX
DT 08-JAN-2001 (first entry)
XX
DE HCV-specific amplification primer C282R27.
XX
KW Hepatitis C virus; HCV; HCV detection; amplification primer; ss.
XX
OS Hepatitis C virus.
XX
PN EP1026262-A2.
XX
PD 09-AUG-2000.
XX
PF 01-FEB-2000; 2000EP-00300763.
XX
PR 03-FEB-1999; 99US-0118497P.
XX
PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
XX
PI Linnen JM, Gorman KM;

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XX WPI; 2000-507254/46.
XX
PT Detecting hepatitis C virus in biological sample involves amplifying
PT reverse transcribed products of virus RNA using amplification primers
PT whose sequences correspond to 5' or 3' non-coding region of the virus
XX RNA.
XX
PS Claim 30; Page 27; 28pp; English.
XX
CC The present sequence is an amplification primer used in a method for
CC detecting hepatitis C virus (HCV) RNA in biological samples. The HCV RNA
CC is reverse transcribed to generate cDNA. This is then amplified using
CC primers, including the present sequence, corresponding to the 5' or 3'
CC non-coding region of HCV. The method is useful for the diagnosis of HCV
CC infection in patients, in testing the efficacy of anti-HCV therapeutic
CC regimes, and in screening blood for HCV-infected samples. The method
CC provides an improved single-round, reverse transcription/amplification
CC assay which detects low copy levels of HCV RNA. The primers and assay
CC system are designed to allow the co-amplification of multiple regions of
CC the HCV genome, multiple viral species, and an internal positive control
CC (IPC) RNA (or DNA). Simultaneous amplification/detection of multiple
CC regions of the HCV genome increases assay sensitivity and the co-
CC amplification of an IPC decreases the likelihood of false negative
CC results because of PCR inhibition.
XX
SQ Sequence 27 BP; 9 A; 10 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 96.4%; Score 27; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCGAGTACCACA 27
Db 1 GCAAGCACCTATCAGGCGAGTACCACA 27

RESULT 9
ADC54073/C
ID ADC54073 standard; DNA; 29 BP.
XX
AC ADC54073;
XX
DT 18-DEC-2003 (first entry)
XX
DE HCV 5'UTR signal amplification probe, SEQ ID NO:24.
XX
KW HCV; hepatitis C virus; classification; interferon therapy; 5'UTR;
KW signal amplification; probe; ss.
XX
OS Hepatitis C virus.
XX
PN JP2002345467-A.
XX
PD 03-DEC-2002.
XX
PF 17-APR-2001; 2001JP-00118810.
XX
PR 23-OCT-2000; 2000JP-00322567.
XX
PA (SRLS-) SRL KK.
XX
DR WPI; 2003-460879/44.
XX
PT Probe and method for classification of hepatitis C virus (HCV) types used
PT for forecast of therapeutic effect of interferon administration.
XX
PS Disclosure; SEQ ID NO 24; 15pp; Japanese.
XX
CC The invention relates to a nucleic acid probe for the classification of
CC hepatitis C virus (HCV) into 3 genotypes. The 3 HCV genotypes are MH1ami
CC (type 1), MH2ami (type 2) and MHG3C+MHG3C' (type 3). The probe can be
CC used to classify HCV type to enable prediction of the success or

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CC otherwise of interferon therapy in a patient. Sequences ADC54068-ADC54073  
CC represent HCV 5'UTR signal amplification probes. Note: The present  
CC sequence is given in the sequence listing, but is not further referred to  
CC in the specification.

XX  
SQ Sequence 29 BP; 3 A; 6 C; 10 G; 10 T; 0 U; 0 Other;  
Query Match 96.4%; Score 27; DB 10; Length 29;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAAGCACCCCTATCAGGCAGTACCA 28  
DB 29 CAAGCACCCCTATCAGGCAGTACCA 3

RESULT 10  
AAV54436  
ID AAV54436 standard; DNA; 40 BP.  
XX  
AC AAV54436;  
XX  
DT 21-DEC-1998 (first entry)  
XX  
DE Nucleotide sequence of HCV PCR primer 3.  
XX  
KW Hepatitis C virus; HCV; PCR; primer; amplification; ss.  
XX  
OS Synthetic.  
XX  
PN JP10248579-A.  
XX  
PD 22-SEP-1998.  
XX  
PF 05-MAR-1997; 97JP-00067321.  
XX  
PR 05-MAR-1997; 97JP-00067321.  
XX  
PA (TOKR-) ZH TOKYO TO RINSHO IGAKU SOGO KENKYUSHO.  
XX  
PA (SRLS-) SRL KK.  
XX  
DR WPI; 1998-560731/48.  
XX  
PT Determination of hepatitis C virus (HCV) gene - with real time detective  
PT PCR and primer and probe used for determination.  
XX  
PS Claim 3; Page 6; 7pp; Japanese.  
XX  
CC This is the nucleotide sequence of a Hepatitis C virus (HCV) PCR primer  
CC used for amplification in the method of the invention. This is a useful  
CC for the detection of the HCV gene  
XX  
SQ Sequence 40 BP; 9 A; 17 C; 9 G; 5 T; 0 U; 0 Other;  
Query Match 89.3%; Score 25; DB 2; Length 40;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGCACCCCTATCAGGCAGTACCA 25  
DB 16 GCAGCACCCCTATCAGGCAGTACCA 40

RESULT 11  
AB281791/c  
ID AB281791 standard; RNA; 47 BP.  
XX  
AC AB281791;  
XX  
DT 11-JUN-2003 (first entry)  
XX  
XX HCV 5' UTR molecular interaction site 7 polynucleotide 2.  
XX  
XX

KW HCV; 5' untranslated region; 5' UTR; molecular interaction;  
KW secondary structure; combinatorial library; screening; virucide; ss.  
XX  
OS Hepatitis C virus.  
XX  
FH Key Location/Qualifiers  
FT misc\_binding 1..4  
FT /\*tag= a  
FT /bound\_moiety= "Polynucleotide 1"  
FT /note= "forms double-stranded region with bases 14-17 of  
FT sequence in AB281790"  
FT misc\_structure 5  
FT /\*tag= b  
FT /note= "forms internal loop with base 13 of sequence in  
FT AB281790"  
FT misc\_binding 6..7  
FT /\*tag= c  
FT /bound\_moiety= "Polynucleotide 1"  
FT /note= "forms double-stranded region with bases 11-12 of  
FT sequence in AB281790"  
FT stem\_loop 8..19  
FT /\*tag= d  
FT misc\_binding 20..21  
FT /\*tag= e  
FT /bound\_moiety= "Bases 30-31"  
FT /note= "forms double-stranded stem region with bases 30-  
FT 31"  
FT misc\_structure 22..29  
FT /\*tag= f  
FT /note= "internal loop"  
FT misc\_binding 23..28  
FT /\*tag= g  
FT /bound\_moiety= "Bases 42-47"  
FT /note= "forms double-stranded dangling structure"  
FT misc\_binding 30..31  
FT /\*tag= h  
FT /bound\_moiety= "Bases 20-21"  
FT /note= "forms double-stranded stem region with bases 20-  
FT 21"  
FT misc\_binding 32..40  
FT /\*tag= i  
FT /bound\_moiety= "Polynucleotide 1"  
FT /note= "forms double-stranded region with bases 2-10 of  
FT sequence in AB281790"  
FT misc\_binding 42..47  
FT /\*tag= g  
FT /bound\_moiety= "Bases 23-28"  
FT /note= "forms double-stranded dangling structure"  
FT  
XX WO2003018747-A2.  
XX 06-MAR-2003.  
XX 19-AUG-2002; 2002WO-US026219.  
XX 22-AUG-2001; 2001US-0314236P.  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Ecker DJ;  
XX WPI; 2003-300721/29.  
XX  
XX Polynucleotides useful for screening combinatorial libraries of compounds  
PT that inhibit or stimulate viral replication, comprise molecular  
PT interaction sites of hepatitis C virus RNA having a defined secondary  
PT structure.  
XX  
PS Claim 26; Page 38; 63pp; English.  
XX  
CC The present sequence is that of the second polynucleotide of a molecular  
CC interaction site (number 7) that has been identified in the 5',  
CC untranslated region (5' UTR) of hepatitis C virus (HCV) RNA (see  
CC

CC AB281793). The first polynucleotide forming site 7 is given in AB281790.  
 CC The 2 polynucleotides together form a double-stranded RNA including  
 CC internal and terminal loops and 2 dangling structures. The 8 molecular  
 CC interaction sites identified in the HCV 5' UTR each have a secondary  
 CC structure capable of interacting with cellular components, such as  
 CC factors and proteins required for translation and other cellular  
 CC processes. Nucleic acid molecules, polynucleotides or oligonucleotides  
 CC comprising the molecular interaction sites can be used to screen,  
 CC virtually or actually, combinatorial libraries of compounds that bind to  
 CC them. Such compounds can be used to modulate the activity of HCV RNA and  
 CC hence to modulate (inhibit or stimulate) viral replication. Thus, novel  
 CC drugs, and agricultural and industrial chemicals, that operate through  
 CC the modulation of HCV RNA can be identified

XX SQ Sequence 47 BP; 6 A; 11 C; 18 G; 0 T; 12 U; 0 Other;

Query Match 89.3%; Score 25; DB 8; Length 47;  
 Best Local Similarity 100.0%; Pred. No. 0.15;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCAGTACCA 25  
 Db 25 GCAAGCACCTATCAGGCAGTACCA 1

RESULT 12  
 AAT05222  
 ID AAT05222 standard; DNA; 28 BP.

AC AAT05222;

XX 13-JUN-1996 (first entry)

DE Hepatitis C virus antisense oligonucleotide A312.

XX Inhibition; expression; hepatitis C virus; HCV; non-A; non-B; RNA;  
 KW translation; in vivo; ex vivo; in vitro; treatment; prevention;  
 KW infection; antisense; non coding; region; NCR; core region; ss.  
 XX Synthetic.

XX WO9530746-A1.

XX 16-NOV-1995.

XX 08-MAY-1995; 95WO-US005812.

XX 10-MAY-1994; 94US-00240382.

XX (GEHO) GEN HOSPITAL CORP.

XX Wakita T, Wands JR;

XX WPI; 1995-404113/51.

XX New anti-sense hepatitis C virus oligo:nucleotide(s) - used for  
 PT inhibiting HCV RNA translation, for the treatment or prevention of HCV  
 PT infection.

XX Claim 1; Page 29; 50pp; English.

XX The present oligonucleotide (ON) inhibits the expression of hepatitis C  
 CC virus (HCV) RNA, specifically HCV type II and type III protein synthesis  
 CC is inhibited by 45% and 18%, respectively. The ONs of the invention  
 CC inhibit translation of HCV types I-V RNA in vivo, ex vivo or in vitro,  
 CC and can therefore be used to treat or prevent HCV infection. The  
 CC antisense ONs comprise 10-28 nucleotides complementary to the entire HCV  
 CC 5'-non-coding and part of the core region. The A or S in the ONs name  
 CC denotes antisense or sense, and the no. indicates the position of the 5'-  
 CC end of the ON. The ON was tested at 10 fold molar excess to HCV RNA

XX Sequence 28 BP; 8 A; 11 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 85.7%; Score 24; DB 2; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 0.39;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCAGTACC 24  
 Db 5 GCAAGCACCTATCAGGCAGTACC 28

RESULT 13  
 AA257757  
 ID AA257757 standard; DNA; 28 BP.

XX AA257757;

XX 05-APR-2000 (first entry)

XX Hepatitis C virus antisense inhibitor oligonucleotide A312.

XX Hepatitis C virus; HCV; antisense oligonucleotide; hepatotropic; ss;  
 KW anti-inflammatory; translation inhibition; HCV infection; virucide.

XX Hepatitis C virus.

XX US6001990-A.

XX 14-DEC-1999.

XX 07-JUN-1995; 95US-00474700.

XX 10-MAY-1994; 94US-00240382.

XX (GEHO) GEN HOSPITAL CORP.

XX Moradpour D, Wands JR, Wakita T;

XX WPI; 2000-104900/09.

XX Antisense oligonucleotide to Hepatitis C virus RNA, useful for treating  
 PT Hepatitis C virus infections.

XX Claim 1; Col 23; 31pp; English.

XX This sequence is an antisense oligonucleotide that hybridises to  
 CC Hepatitis C virus (HCV) RNA, under physiological conditions. The  
 CC invention relates to HCV antisense oligonucleotides, and also for a  
 CC vector comprising a nucleotide sequence which is transcribed in an animal  
 CC cell to generate an antisense oligonucleotide. The oligonucleotides have  
 CC virucide, hepatotropic and anti-inflammatory activity, and are useful for  
 CC treating HCV infection by inhibiting translation of type I-V HCV RNA.  
 CC Hepatitis C virus is a positive strand RNA virus, and is the major  
 CC causative agent of post-transfusion hepatitis. Persistent HCV infection  
 CC can lead to chronic hepatitis, cirrhosis, and hepatocellular carcinoma

XX SQ Sequence 28 BP; 8 A; 11 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 85.7%; Score 24; DB 3; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 0.39;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCAGTACC 24  
 Db 5 GCAAGCACCTATCAGGCAGTACC 28

RESULT 14  
 AAQ55728  
 ID AAQ55728 standard; DNA; 30 BP.

XX AAQ55728;

XX 13-OCT-1994 (first entry)

DE Hepatitis C detection primer 2.  
XX Key.  
XX Synthetic.  
OS JP06014800-A.  
XX PN  
XX PD  
XX 25-JAN-1994.  
XX PF 02-JUL-1992; 92JP-00197407.  
XX PR 02-JUL-1992; 92JP-00197407.  
XX PA (TOXJ ) TOSOH CORP.  
XX DR WPI; 1994-061488/08.  
XX PT Detection of human hepatitis C virus - using primer contg. at least 15  
XX continuous bases.  
XX PS Claim 1; Page 1; 5pp; Japanese.  
XX CC The primers (AAQ55727-728) are used to detect hepatitis C virus. The  
XX method can amplify and detect specifically the nucleic acid sequence  
XX originated from a trace amount of HCV contained in a sample  
XX SQ Sequence 30 BP; 8 A; 12 C; 6 G; 4 T; 0 U; 0 Other;  
Query Match 85.7%; Score 24; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 0.4;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCAAGCACCCCTATCAGGCAGTACC 24  
DB 7 GCAAGCACCCCTATCAGGCAGTACC 30  
RESULT 15  
AAQ31158  
ID AAQ31158 standard; DNA; 33 BP.  
XX AC AAQ31158;  
XX DT 25-MAR-2003 (revised)  
XX DT 24-MAR-1993 (first entry)  
XX DE Probe 127 for genotyping analysis of HCV-1.  
XX KW Hepatitis C virus; non-A, non-B hepatitis; polymerase chain reaction;  
XX KW amplified solution phase nucleic acid sandwich assay;  
XX KW genotyping analysis; capture probe; detection probe; ss.  
XX OS Synthetic.  
XX PN WO9219743-A2.  
XX PD 12-NOV-1992.  
XX PF 08-MAY-1992; 92WO-US004036.  
XX PR 08-MAY-1991; 91US-00697326.  
XX PA (CHIR ) CHIRON CORP.  
XX PI Cha T, Beall E, Irvine B, Kolberg J, Urdea MS;  
XX DR WPI; 1992-398869/48.  
XX CC Compan. comprising a non-hepatitis C virus-1 nucleotide sequence -  
XX PT related to HCV-1, useful for treating and detecting HCV-1 infections and  
XX PT as a vaccine.  
XX

PS Claim 63; Page 140; 186pp; English.  
XX A sandwich hybridisation assay can be used for HCV-1 genotyping analysis.  
XX One example uses nucleotide sequences which correspond to sequences in  
XX the C gene and the 5' UT region of HCV isolates as either capture or  
XX detection probes. Probe 127 is preferably used as a capture probe.  
XX (Updated on 25-MAR-2003 to correct PN field.)  
XX SQ Sequence 33 BP; 8 A; 12 C; 9 G; 4 T; 0 U; 0 Other;  
Query Match 85.7%; Score 24; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.4;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCAAGCACCCCTATCAGGCAGTACC 24  
DB 10 GCAAGCACCCCTATCAGGCAGTACC 33  
RESULT 16  
AAQ45464  
ID AAQ45464 standard; DNA; 33 BP.  
XX AC AAQ45464;  
XX DT 25-MAR-2003 (revised)  
XX DT 13-DEC-1993 (first entry)  
XX DE Hepatitis C virus RNA assay capture probe HCV.33.9.  
XX KW Detection; HCV; reduced background signal; improved reproducibility;  
XX KW hybridisation; 5'-untranslated region; C gene; ss.  
XX OS Synthetic.  
XX PN WO9313224-A1.  
XX PD 08-JUL-1993.  
XX PF 22-DEC-1992; 92WO-US011343.  
XX PR 23-DEC-1991; 91US-00813338.  
XX PA (CHIR ) CHIRON CORP.  
XX PI Sheridan P, Chang C, Running J;  
XX DR WPI; 1993-227338/28.  
XX KW Immobilising nucleic acid probe on styreneI, useful for HCV sequence  
XX PT detection - by using intermediate passively adsorbed polymer having  
XX PT functional gps. for covalently bonding to probe via its base-stable  
XX PT linkages.  
XX PS Example; Fig 3.1; 34pp; English.  
XX CC The sequence is that of a synthetic capture probe which is complementary  
XX to nucleotide sequences in the hepatitis C virus C gene and the 5'-  
XX untranslated region. It may be used in an assay for the detection of HCV  
XX RNA. (Updated on 25-MAR-2003 to correct PN field.)  
XX SQ Sequence 33 BP; 8 A; 12 C; 9 G; 4 T; 0 U; 0 Other;  
Query Match 85.7%; Score 24; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.4;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCAAGCACCCCTATCAGGCAGTACC 24  
DB 10 GCAAGCACCCCTATCAGGCAGTACC 33  
RESULT 17



AAV07838  
ID AAV07838 standard; DNA; 33 BP.  
XX AC AAV07838;

XX 27-AUG-2003 (revised)  
DT 25-MAR-2003 (revised)  
DT 10-DEC-1998 (first entry)  
XX XX

DE HCV.33.9 amplifier probe.  
XX XX

XX Comb-type branched polynucleotide; amplification multimer; analyte;  
KW hybridisation assay; hepatitis C virus; HCV; amplifier probe; ss.  
XX XX

OS Synthetic.  
OS Hepatitis C virus.

PN US5710264-A.

XX 20-JAN-1998.  
XX XX

XX 07-JUN-1995; 95US-00478085.  
XX XX

XX 27-JUL-1990; 90US-00558897.  
PR 23-DEC-1991; 91US-00813588.  
XX XX

XX (CHIR ) CHIRON CORP.  
XX XX

PI Chang C, Fultz TJ, Warner B, Urdea MS, Horn T;  
XX WPI; 1998-109872/10.

DR New large comb-type branched polynucleotides - useful as amplification  
XX multimers in nucleic acid hybridisation assays.

XX Example 6; Col 25; 33pp; English.  
XX XX

CC The invention relates to a large comb-type branched polynucleotide of  
CC formula: 3'-A-S-(S'-X'm-S''-5'; where X' is a branched site joined to -  
CC (R)n-S''-E-L; A = an oligonucleotide complementary to an analyte nucleic  
CC acid sequence; S = a first spacer segment of 1-50 linked monomers where  
CC each monomer is selected from nucleotides and a cleavable linker R; S' =  
CC a branching site spacer segment of 0-15 linked monomers where each of the  
CC monomers is selected from nucleotides and cleavable linker R; X' = a  
CC multifunctional nucleotide that provides a branch site; m = 1-100; S'' =  
CC a second spacer segment of 0-10 linked monomers where each of the  
CC monomers is selected from nucleotides and cleavable linker R; R = a  
CC cleavable linker molecule; n = 0 or 1; S''' = a third spacer segment of 0  
CC -10 linked monomers where each of the monomers is selected from  
CC nucleotides and cleavable linker R; E = an oligonucleotide segment of 5-  
CC 10 nucleotides; L = an oligonucleotide containing 2-10 iterations of a  
CC nucleotide sequence complementary to a labelled nucleic acid probe. The  
CC invention also relates to a branched nucleic acid polymer. The poly-  
CC nucleotides are useful as amplification multimers in nucleic acid  
CC hybridisation assays used for genetic research, biomedical research and  
CC clinical diagnostics. Since the polynucleotide multimers include a large  
CC number (at least 20) iterations of a sequence that are available for  
CC specific hybridisation, they permit a greater degree of amplification and  
CC decrease the threshold level of a detectable analyte. The present  
CC sequence represents a hepatitis C virus (HCV) amplifier probe. (Updated  
CC on 25-MAR-2003 to correct PF field.) (Updated on 27-AUG-2003 to correct  
CC OS field.)  
XX XX

SQ Sequence 33 BP; 8 A; 12 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 85.7%; Score 24; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.4;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCAAGCACCTATCAGGCAGTACC 24  
DB 10 GCAAGCACCTATCAGGCAGTACC 33

RESULT 18-  
AAV83066

ID AAV83066 standard; DNA; 33 BP.  
XX XX

XX 24-FEB-1999 (first entry)  
DT 24-FEB-1999 (first entry)  
XX XX

DE Amplifier probe HCV.33.9.  
XX XX

XX Comb-type branched polynucleotide; amplifier probe;  
KW multifunctional nucleotide; pendant polynucleotide sidechain;  
KW hybridisation assay; amplification multimer; sandwich assay; ss.  
XX XX

OS Synthetic.  
OS Hepatitis C virus.

PN US5849481-A.  
XX 15-DEC-1998.  
XX XX

XX 05-JUN-1995; 95US-00470124.  
XX XX

XX 27-JUL-1990; 90US-00558897.  
PR 23-DEC-1991; 91US-00813588.  
XX XX

XX (CHIR ) CHIRON CORP.  
XX XX

PI Warner B, Horn T, Fultz TJ, Urdea MS, Chang C;  
XX WPI; 1999-069715/06.

DR Improved nucleic acid hybridisation assays - using large comb-type  
XX polypeptide(s).

XX Example 6; Col 24; 31pp; English.  
XX XX

CC Oligonucleotides AAV83063-80 represent amplifier probes, used in a  
CC sandwich hybridisation assay for Hepatitis C virus (HCV) DNA. The  
CC sandwich hybridisation assay utilises the comb-type branched  
CC polynucleotide amplification multimer of the invention. This large comb-  
CC type branched polynucleotide comprises a polynucleotide backbone having  
CC at least 15 multifunctional nucleotides each defining a sidechain site  
CC and pendant polynucleotide sidechains extending from the multifunctional  
CC nucleotides, each comprising iterations of an single stranded  
CC oligonucleotide unit capable of binding specifically to a second single-  
CC stranded polynucleotide sequence. The total number of iterations in all  
CC sidechains is at least 20. The first single-stranded polynucleotide  
CC sequence is a labelled polynucleotide, directly or indirectly linked to a  
CC nucleic acid analyte. In the nucleic acid hybridisation assay of the  
CC invention, the labelled nucleic acid probe is hybridised to the branched  
CC polymeric nucleotide via the second single-stranded oligonucleotide unit.  
CC The comb-type branched polynucleotides are used as amplification  
CC multimers in nucleic acid hybridisation assays and other assays such as  
CC direct, indirect and sandwich assays  
XX XX

SQ Sequence 33 BP; 8 A; 12 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 85.7%; Score 24; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.4;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCAAGCACCTATCAGGCAGTACC 24  
DB 10 GCAAGCACCTATCAGGCAGTACC 33

RESULT 19  
ADF52816/c  
ID ADF52816 standard; RNA; 23 BP.  
XX XX  
AC ADF52816;

XX DT 12-FEB-2004 (first entry)  
XX DE Hepatitis C virus siNA target sequence SeqID1406.  
XX short interfering nucleic acid; siNA; virus replication inhibition;  
KW Hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;  
KW hepatocellular cancer; cirrhosis; ss.  
XX OS Hepatitis C virus.  
XX PN WO2003070750-A2.  
XX PD 28-AUG-2003.  
XX PF 20-FEB-2003; 2003WO-US005043.  
XX PR 20-FEB-2002; 2002US-0358580P.  
XX PR 11-MAR-2002; 2002US-0363124P.  
XX PR 26-MAR-2002; 2002WO-US009187.  
XX PR 06-JUN-2002; 2002US-0386782P.  
XX PR 05-AUG-2002; 2002US-0401104P.  
XX PR 29-AUG-2002; 2002US-0406784P.  
XX PR 05-SEP-2002; 2002US-0408378P.  
XX PR 09-SEP-2002; 2002US-0409293P.  
XX PR 15-JAN-2003; 2003US-0440129P.  
XX PA (SIRN-) SIRNA THERAPEUTICS INC.  
XX PI Mcswiggen J, Beigelman L, Macejak D, Morrissey D;  
XX PI WPI; 2003-689778/65.  
XX DR New double-stranded short interfering nucleic acid comprises sugar-  
PT modified pyrimidine bases useful for treating infection with hepatitis C  
PT virus.  
XX Example 3; SEQ ID NO 1406; 183pp; English.  
XX PS This invention relates to novel double-stranded short interfering nucleic  
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where  
CC one strand is an antisense strand (ASS) that is complementary to (part  
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
CC modification. The invention may allow development of compounds with  
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by  
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
CC interference. The siNA's of the invention may be used to inhibit  
CC replication of HCV, in cells, tissue explants or organisms, for treating  
CC HCV infection and its consequences (liver failure; hepatocellular cancer  
CC and cirrhosis), and also for drug screening, diagnosis, target  
CC identification and validation, genetic engineering, pharmacogenomics,  
CC studying gene function and gene mapping (for example of single-nucleotide  
CC polymorphisms). The chemical modification improves stability, activity,  
CC cellular uptake and/or binding affinity. The siNA can be directed to  
CC conserved regions of HCV genes, so are active against many different  
CC strains.  
XX SQ Sequence 23 BP; 3 A; 4 C; 8 G; 0 T; 8 U; 0 Other;  
Query Match 82.1%; Score 23; DB 10; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 AGCACCCCTATCAGGCAGTACCA 25  
DB 23 AAGCACCCCTATCAGGCAGTACCA 1  
RESULT 20  
ADFS2808/c  
.ID ADFS2808 standard; RNA; 23 BP.

XX AC ADFS2808;  
XX DT 12-FEB-2004 (first entry)  
XX DE Hepatitis C virus siNA target sequence SeqID1398.  
XX short interfering nucleic acid; siNA; virus replication inhibition;  
KW Hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;  
KW hepatocellular cancer; cirrhosis; ss.  
XX OS Hepatitis C virus.  
XX PN WO2003070750-A2.  
XX PD 28-AUG-2003.  
XX PF 20-FEB-2003; 2003WO-US005043.  
XX PR 20-FEB-2002; 2002US-0358580P.  
XX PR 11-MAR-2002; 2002US-0363124P.  
XX PR 26-MAR-2002; 2002WO-US009187.  
XX PR 06-JUN-2002; 2002US-0386782P.  
XX PR 05-AUG-2002; 2002US-0401104P.  
XX PR 29-AUG-2002; 2002US-0406784P.  
XX PR 05-SEP-2002; 2002US-0408378P.  
XX PR 09-SEP-2002; 2002US-0409293P.  
XX PR 15-JAN-2003; 2003US-0440129P.  
XX PA (SIRN-) SIRNA THERAPEUTICS INC.  
XX PI Mcswiggen J, Beigelman L, Macejak D, Morrissey D;  
XX PI WPI; 2003-689778/65.  
XX DR New double-stranded short interfering nucleic acid comprises sugar-  
PT modified pyrimidine bases useful for treating infection with hepatitis C  
PT virus.  
XX Example 3; SEQ ID NO 1398; 183pp; English.  
XX PS This invention relates to novel double-stranded short interfering nucleic  
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where  
CC one strand is an antisense strand (ASS) that is complementary to (part  
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
CC modification. The invention may allow development of compounds with  
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by  
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
CC interference. The siNA's of the invention may be used to inhibit  
CC replication of HCV, in cells, tissue explants or organisms, for treating  
CC HCV infection and its consequences (liver failure; hepatocellular cancer  
CC and cirrhosis), and also for drug screening, diagnosis, target  
CC identification and validation, genetic engineering, pharmacogenomics,  
CC studying gene function and gene mapping (for example of single-nucleotide  
CC polymorphisms). The chemical modification improves stability, activity,  
CC cellular uptake and/or binding affinity. The siNA can be directed to  
CC conserved regions of HCV genes, so are active against many different  
CC strains.  
XX SQ Sequence 23 BP; 3 A; 3 C; 9 G; 0 T; 8 U; 0 Other;  
Query Match 82.1%; Score 23; DB 10; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CACCCCTATCAGGCAGTACCA 28  
DB 23 CACCCCTATCAGGCAGTACCA 1  
RESULT 21

ADFS2814/c  
ID ADF52814 standard; RNA; 23 BP.  
AC ADF52814;  
XX  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Hepatitis C virus siRNA target sequence SeqID1404.  
XX  
KW short interfering nucleic acid; siRNA; virus replication inhibition;  
KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;  
KW hepatocellular cancer; cirrhosis; ss.  
XX  
OS Hepatitis C virus.  
XX  
XX WO2003070750-A2.  
XX  
XX 28-AUG-2003.  
XX  
XX 20-FEB-2003; 2003WO-US005043.  
XX  
XX 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 26-MAR-2002; 2002WO-US009187.  
PR 06-JUN-2002; 2002US-0386782P.  
PR 05-AUG-2002; 2002US-0401104P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX  
XX (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;  
XX  
XX WPI; 2003-689778/65.  
XX  
XX New double-stranded short interfering nucleic acid comprises sugar-  
XX modified pyrimidine bases useful for treating infection with hepatitis C  
XX virus.  
XX  
XX Example 3; SEQ ID NO 1404; 183pp; English.  
XX  
XX This invention relates to novel double-stranded short interfering nucleic  
XX acids (siRNA) that inhibits replication of hepatitis C virus (HCV), where  
XX one strand is an antisense strand (ASS) that is complementary to (part  
XX of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
XX ASS, and where most of the pyrimidine nucleotides comprise a sugar  
XX modification. The invention may allow development of compounds with  
XX virucide, antiinflammatory, hepatotropic or cytostatic activities by  
XX modulation (inhibition) of expression or activity of HCV RNA, by RNA  
XX interference. The siRNA's of the invention may be used to inhibit  
XX replication of HCV, in cells, tissue explants or organisms, for treating  
XX HCV infection and its consequences (liver failure; hepatocellular cancer  
XX and cirrhosis), and also for drug screening, diagnosis, target  
XX identification and validation, genetic engineering, pharmacogenomics,  
XX studying gene function and gene mapping (for example of single-nucleotide  
XX polymorphisms). The chemical modification improves stability, activity,  
XX cellular uptake and/or binding affinity. The siRNA can be directed to  
XX conserved regions of HCV genes, so are active against many different  
XX strains.  
XX  
XX Sequence 23 BP; 3 A; 4 C; 9 G; 0 T; 7 U; 0 Other;  
XX  
XX Query Match 82.1%; Score 23; DB 10; Length 23;  
XX Best Local Similarity 100.0%; Pred. No. 1.1;  
XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 5 GCACCCCTATCAGGCAGTACCACA 27  
XX  
XX 23 GCACCCCTATCAGGCAGTACCACA 1

RESULT 22  
ADFS2817/c  
ID ADF52817 standard; RNA; 23 BP.  
XX  
XX  
AC ADF52817;  
XX  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Hepatitis C virus siRNA target sequence SeqID1407.  
XX  
KW short interfering nucleic acid; siRNA; virus replication inhibition;  
KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;  
KW hepatocellular cancer; cirrhosis; ss.  
XX  
OS Hepatitis C virus.  
XX  
XX WO2003070750-A2.  
XX  
XX 28-AUG-2003.  
XX  
XX 20-FEB-2003; 2003WO-US005043.  
XX  
XX 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 26-MAR-2002; 2002WO-US009187.  
PR 06-JUN-2002; 2002US-0386782P.  
PR 05-AUG-2002; 2002US-0401104P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX  
XX (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;  
XX  
XX WPI; 2003-689778/65.  
XX  
XX New double-stranded short interfering nucleic acid comprises sugar-  
XX modified pyrimidine bases useful for treating infection with hepatitis C  
XX virus.  
XX  
XX Example 3; SEQ ID NO 1407; 183pp; English.  
XX  
XX This invention relates to novel double-stranded short interfering nucleic  
XX acids (siRNA) that inhibits replication of hepatitis C virus (HCV), where  
XX one strand is an antisense strand (ASS) that is complementary to (part  
XX of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
XX ASS, and where most of the pyrimidine nucleotides comprise a sugar  
XX modification. The invention may allow development of compounds with  
XX virucide, antiinflammatory, hepatotropic or cytostatic activities by  
XX modulation (inhibition) of expression or activity of HCV RNA, by RNA  
XX interference. The siRNA's of the invention may be used to inhibit  
XX replication of HCV, in cells, tissue explants or organisms, for treating  
XX HCV infection and its consequences (liver failure; hepatocellular cancer  
XX and cirrhosis), and also for drug screening, diagnosis, target  
XX identification and validation, genetic engineering, pharmacogenomics,  
XX studying gene function and gene mapping (for example of single-nucleotide  
XX polymorphisms). The chemical modification improves stability, activity,  
XX cellular uptake and/or binding affinity. The siRNA can be directed to  
XX conserved regions of HCV genes, so are active against many different  
XX strains.  
XX  
XX Sequence 23 BP; 3 A; 4 C; 9 G; 0 T; 7 U; 0 Other;  
XX  
XX Query Match 82.1%; Score 23; DB 10; Length 23;  
XX Best Local Similarity 100.0%; Pred. No. 1.1;  
XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 2 CAAGCACCCCTATCAGGCAGTACC 24  
XX  
XX |||||

Db 23 CAAGCACCTATCAGGCGAGTACC 1

RESULT 23  
ADF52815/c  
ID ADF52815 standard; RNA; 23 BP.

XX ADF52815;  
AC  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Hepatitis C virus siRNA target sequence SeqID1405.  
XX short interfering nucleic acid; siRNA; virus replication inhibition;  
KW hepatitis C virus; HCV; sugar modification; virucide; anti-inflammatory;  
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;  
KW hepatocellular cancer; cirrhosis; ss.

XX Hepatitis C virus.  
OS  
XX  
PN WO2003070750-A2.  
XX  
PD 28-AUG-2003.  
XX  
PF 20-FEB-2003; 2003WO-US005043.  
XX  
PR 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 26-MAR-2002; 2002WO-US009187.  
PR 06-JUN-2002; 2002US-0386782P.  
PR 05-AUG-2002; 2002US-0401104P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX  
PA (SIRN-) SIRNA THERAPEUTICS INC.

XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;  
XX WPI; 2003-689778/65.  
XX  
DR New double-stranded short interfering nucleic acid comprises sugar-  
PT modified pyrimidine bases useful for treating infection with hepatitis C  
PT virus.

XX Example 3; SEQ ID NO 1405; 183pp; English.  
XX  
XX This invention relates to novel double-stranded short interfering nucleic  
CC acids (siRNA) that inhibits replication of hepatitis C virus (HCV), where  
CC one strand is an antisense strand (ASS) that is complementary to (part  
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
CC modification. The invention may allow development of compounds with  
CC virucide, anti-inflammatory, hepatotropic or cytostatic activities by  
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
CC interference. The siRNA's of the invention may be used to inhibit  
CC replication of HCV, in cells, tissue explants or organisms, for treating  
CC HCV infection and its consequences (liver failure; hepatocellular cancer  
CC and cirrhosis), and also for drug screening, diagnosis, target  
CC identification and validation, genetic engineering, pharmacogenomics,  
CC studying gene function and gene mapping (for example of single-nucleotide  
CC polymorphisms). The chemical modification improves stability, activity,  
CC cellular uptake and/or binding affinity. The siRNA can be directed to  
CC conserved regions of HCV genes, so are active against many different  
CC strains.

XX Sequence 23 BP; 3 A; 4 C; 9 G; 0 T; 7 U; 0 Other;  
XX  
XX Query Match 82.1%; Score 23; DB 10; Length 23;  
XX Best Local Similarity 100.0%; Pred. No. 1.1;  
XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AGCACCTATCAGGCGAGTACC 26  
Db 23 AGCACCTATCAGGCGAGTACC 1

RESULT 24  
AAD19057  
ID AAD19057 standard; DNA; 24 BP.

XX AAD19057;  
AC  
XX  
DT 18-DEC-2001 (first entry)  
XX  
DE Hepatitis viral DNA amplifying reverse PCR primer #31.  
XX Hepatitis virus; bacterial infection; fungi; protozoa; PCR primer;  
KW amplification; blood-borne pathogen; sexually transmitted disease;  
KW respiratory disease; ss.

XX Hepatitis virus.  
OS  
XX  
PN WO200168921-A2.  
XX  
PD 20-SEP-2001.  
XX  
PF 14-MAR-2001; 2001WO-US008110.  
XX  
PR 14-MAR-2000; 2000US-0189344P.  
XX  
PA (INVE-) INVESTIGEN.  
XX  
PI Koshinsky H, Zwick MS, Mccue KP;  
XX WPI; 2001-611396/70.  
XX  
DR Simultaneous detection of biological entities such as bacteria, fungi and  
XX viruses by specific nucleic acid amplification.

XX Disclosure; Page 31; 55pp; English.

XX The invention relates to a method and apparatus for the simultaneous  
CC detection of multiple biological entities such as bacteria, fungi and  
CC viruses by specific nucleic acid amplification. The invention also  
CC relates to a kit for simultaneous detection of biological entities. The  
CC kit is employed for detecting blood-borne pathogens, associated with a  
CC variety of infectious diseases such as respiratory and sexually  
CC transmitted diseases. The methods and apparatus are used for the  
CC simultaneous detection of biological entities present in biological and  
CC environment samples. In particular, they are used for monitoring diseases  
CC caused by microorganisms associated with a respiratory or sexually  
CC transmitted disease such as a bacterium (Staphylococcus, Pneumococcus,  
CC Gonococcus, Haemophilus, Bacteroides, Escherichia or Salmonella), virus  
CC (DNA or RNA virus, such as adenovirus, adeno-associated virus, HAV, HCV,  
CC HDV, HEV, HGV or TTV), fungus (Aspergillus fumigatus, Blastomycosis,  
CC dermatitis, Candida albicans) or protozoa (Entamoeba histolytica). The  
CC present sequence is a PCR primer used for amplifying Hepatitis viral DNA

XX Sequence 24 BP; 7 A; 9 C; 5 G; 3 T; 0 U; 0 Other;

XX Query Match 82.1%; Score 23; DB 4; Length 24;  
XX Best Local Similarity 100.0%; Pred. No. 1.1;  
XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGCACCTATCAGGCGAGTACC 23  
Db 2 GCAAGCACCTATCAGGCGAGTACC 24

RESULT 25  
AAZ87367  
ID AAZ87367 standard; cDNA; 27 BP.

XX AAZ87367;  
AC

```

XX DT 22-MAY-2000 (first entry)
XX DE Hepatitis C virus 5'NCR RT-PCR primer NC4.
XX KW Hepatitis C virus; HCV; in vitro culture; primary mammalian hepatocyte;
XX KW culture medium; replication; drug screening; antibody testing; diagnosis;
XX KW vaccine development; 5'NCR; reverse transcriptase-PCR; RT-PCR primer; ss.
XX OS Hepatitis C virus.
XX PN WO9967362-A1.
XX PD 29-DEC-1999.
XX PF 23-JUN-1999; 99WO-EP004337.
XX PR 24-JUN-1998; 98EP-00401554.
XX PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX PI Rumin S, Inchauspe G, Trepo C, Gripon P;
XX DR WPI; 2000-160580/14.
XX PT Use of a culture medium comprising at least one mammalian plasma or sera
XX PT and antioxidants and/or corticoids, for in vitro replication of hepatitis
XX PT C virus in hepatocytes.
XX PS Example 3; Page 18; 39pp; English.
XX CC The invention relates to a novel process and cell culture medium for in
XX CC vitro replication of hepatitis C virus (HCV) in primary mammalian
XX CC hepatocytes. The culture medium comprising one or more mammalian plasma
XX CC or sera, a chemical or biological compound with an anti-oxidative
XX CC property and/or a differentiating property, such as dimethyl sulphoxide
XX CC (DMSO), retinoic acid, vitamin (e.g., vitamin E), or selenium, and/or at
XX CC least one corticoid. The culture medium may be used in an in vitro HCV
XX CC infection and culture system. This would allow the mechanisms of viral
XX CC replication to be studied, and could also be used for in vitro screening
XX CC of anti-HCV drugs; to test neutralising antibodies; for in vitro
XX CC diagnosis of HCV; and for the preparation of vaccines against HCV. The
XX CC HCV-infected hepatocytes survive for at least 4 months in the culture
XX CC medium. Previously, a reliable and robust in vitro HCV culture method has
XX CC not been available. Sequences AAZ87367-287375 represent reverse
XX CC transcriptase-PCR (RT-PCR) primers used in an exemplification of the
XX CC present invention
XX SQ Sequence 27 BP; 8 A; 10 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 82.1%; Score 23; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTTATCAGGCAGTAC 23
Db 5 GCAAGCACCTTATCAGGCAGTAC 27

RESULT 26
AAH78439
ID AAH78439 standard; DNA; 27 BP.
XX AC AAH78439;
XX DT 10-DEC-2001 (first entry)
XX DE PCR primer used to amplify HCV cDNA fragment.
XX KW Protein isolation; magnetic colloidal particle; polymer envelope;
XX KW vaccine; HCV; PCR primer; ss.
XX OS Hepatitis C virus.

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XX PN WO200152612-A2.
XX PD 26-JUL-2001.
XX PF 22-JAN-2001; 2001WO-FR000205.
XX PR 21-JAN-2000; 2000FR-00000862.
XX PA (INRM ) BIO MERIEUX.
XX PI Elaiseari A, Mandrand B, Delair T, Spencer D, Arkis A;
XX DR WPI; 2001-596423/67.
XX PT Isolation of protein and protein-nucleic acid complexes, useful e.g. for
XX PT subsequent analysis or transport, by binding to magnetic beads coated
XX PT with functionalized polymer.
XX PS Example 4; Page 13; 29pp; French.
XX CC The specification describes a method for the isolation of proteins and/or
XX CC their complexes with nucleic acid. The method comprises treating a sample
XX CC with magnetic colloidal particles that comprise a magnetic core and an
XX CC envelope of a polymer (P1) containing ionizable functional groups. The
XX CC mixture is incubated then the proteins or complexes are recovered by
XX CC application of a magnetic field. The core is covered by at least one
XX CC polymer (P2) containing functional groups, at least some of which have
XX CC reacted with groups in (P1). Functional groups in P1 and P2 are the same
XX CC or different, and are amino, hydroxy thiol, formyl, ester, anhydride,
XX CC acyl chloride, carbonate, carbamate and/or isothio) cyanate. The method
XX CC is used for extraction, identification, detection and/or quantification
XX CC of protein and their complexes. It is also used for establishing cell
XX CC cultures and biological samples. The complexes formed between magnetic
XX CC colloidal particles and the proteins are useful for transfer, transport
XX CC and/or storage of infectious agents (virus, bacterium or yeast) and for
XX CC preparation of vaccines. PCR primers AAH78438-39 were used to amplify a
XX CC fragment of HCV cDNA. The amplified fragment was used to demonstrate the
XX CC use of the method of the invention for capture of HCV particles by
XX CC magnetic latex
XX SQ Sequence 27 BP; 8 A; 10 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 82.1%; Score 23; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTTATCAGGCAGTAC 23
Db 5 GCAAGCACCTTATCAGGCAGTAC 27

RESULT 27
AAH78441
ID AAH78441 standard; DNA; 27 BP.
XX AC AAH78441;
XX DT 10-DEC-2001 (first entry)
XX DE PCR primer used to amplify HCV cDNA fragment.
XX KW Protein isolation; magnetic colloidal particle; polymer envelope;
XX KW vaccine; HCV; PCR primer; ss.
XX OS Hepatitis C virus.
XX PN WO200152612-A2.
XX PD 26-JUL-2001.
XX PR 22-JAN-2001; 2001WO-FR000205.
XX PS
XX

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PR 21-JAN-2000; 2000FR-00000862.
XX (INNR ) BIO MERIEUX.
PA Elaissari A, Mandrand B, Delair T, Spencer D, Arkis A;
XX WPI; 2001-596423/67.
DR
XX
XX Isolation of protein and protein-nucleic acid complexes, useful e.g. for
PT subsequent analysis or transport, by binding to magnetic beads coated
PT with functionalized polymer.
XX
XX Example 4; Page 13; 29pp; French.
XX
XX The specification describes a method for the isolation of proteins and/or
CC their complexes with nucleic acid. The method comprises treating a sample
CC with magnetic colloidal particles that comprise a magnetic core and an
CC envelope of a polymer (P1) containing ionizable functional groups. The
CC mixture is incubated then the proteins or complexes are recovered by
CC application of a magnetic field. The core is covered by at least one
CC polymer (P2) containing functional groups, at least some of which have
CC reacted with groups in (P1). Functional groups in P1 and P2 are the same
CC or different, and are amino, hydroxy thiol, formyl, ester, anhydride,
CC acyl chloride, carbonate, carbamate and/or isothiocyanate. The method
CC is used for extraction, identification, detection and/or quantification
CC of protein and their complexes. It is also used for establishing cell
CC cultures and biological samples. The complexes formed between magnetic
CC colloidal particles and the proteins are useful for transfer, transport
CC and/or storage of infectious agents (virus, bacterium or yeast) and for
CC preparation of vaccines. PCR primers AAH78440-41 were used to amplify a
CC fragment of HCV cDNA. The amplified fragment was used to demonstrate the
CC use of the method of the invention for capture of HCV particles by
CC magnetic latex
XX
XX Sequence 27 BP; 8 A; 10 C; 5 G; 4 T; 0 U; 0 Other;
SQ
Query Match 82.1%; Score 23; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCAGCACCCTATCAGGCAGTAC 23
DB 5 GCAAGCACCCTATCAGGCAGTAC 27
RESULT 28
ADFS2809/C
ID ADFS2809 standard; RNA; 23 BP.
XX
XX ADFS2809;
XX
XX 12-FEB-2004 (first entry)
XX
XX Hepatitis C virus siRNA target sequence SeqID1399.
XX
XX short interfering nucleic acid; siRNA; virus replication inhibition;
XX hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
XX hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
XX hepatocellular cancer; cirrhosis; ss.
XX
XX Hepatitis C virus.
OS
XX
XX WO2003070750-A2.
XX
XX 28-AUG-2003.
XX
XX 20-FEB-2003; 2003WO-US005043.
XX
XX 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 26-MAR-2002; 2002WO-US009187.
PR 05-JUN-2002; 2002US-0386782P.
PR 05-AUG-2002; 2002US-0401104P.
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PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX
XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX WPI; 2003-689778/65.
XX
XX New double-stranded short interfering nucleic acid comprises sugar-
PT modified pyrimidine bases useful for treating infection with hepatitis C
PT virus.
XX
XX Example 3; SEQ ID NO 1399; 183pp; English.
XX
XX This invention relates to novel double-stranded short interfering nucleic
CC acids (siRNA) that inhibits replication of hepatitis C virus (HCV), where
CC one strand is an antisense strand (ASS) that is complementary to (part
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
CC modification. The invention may allow development of compounds with
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
CC interference. The siRNA's of the invention may be used to inhibit
CC replication of HCV, in cells, tissue explants or organisms, for treating
CC HCV infection and its consequences (liver failure; hepatocellular cancer
CC and cirrhosis), and also for drug screening, diagnosis, target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function and gene mapping (for example of single-nucleotide
CC polymorphisms). The chemical modification improves stability, activity,
CC cellular uptake and/or binding affinity. The siRNA can be directed to
CC conserved regions of HCV genes, so are active against many different
CC strains.
XX
XX Sequence 23 BP; 3 A; 4 C; 8 G; 0 T; 8 U; 0 Other;
SQ
Query Match 78.6%; Score 22; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 ACCCTATCAGGCAGTACCACAA 28
DB 23 ACCCTATCAGGCAGTACCACAA 2
RESULT 29
ADFS2818/C
ID ADFS2818 standard; RNA; 23 BP.
XX
XX ADFS2818;
XX
XX 12-FEB-2004 (first entry)
XX
XX Hepatitis C virus siRNA target sequence SeqID1408.
XX
XX short interfering nucleic acid; siRNA; virus replication inhibition;
XX hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
XX hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
XX hepatocellular cancer; cirrhosis; ss.
XX
XX Hepatitis C virus.
OS
XX
XX WO2003070750-A2.
XX
XX 28-AUG-2003.
XX
XX 20-FEB-2003; 2003WO-US005043.
XX
XX 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 26-MAR-2002; 2002US-0386782P.
PR 05-AUG-2002; 2002US-0401104P.
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PR 06-JUN-2002; 2002US-0386782P.  
 PR 05-AUG-2002; 2002US-0401104P.  
 PR 05-SEP-2002; 2002US-0406784P.  
 PR 05-SEP-2002; 2002US-0408378P.  
 PR 09-SEP-2002; 2002US-0409293P.  
 PR 15-JAN-2003; 2003US-0440123P.  
 XX (SIRN-) SIRNA THERAPEUTICS INC.  
 XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;  
 PI WPI; 2003-689778/65.  
 DR  
 XX New double-stranded short interfering nucleic acid comprises sugar-  
 PT modified pyrimidine bases useful for treating infection with hepatitis C  
 PT virus.  
 XX  
 PS Example 3; SEQ ID NO 1408; 183pp; English.  
 XX  
 CC This invention relates to novel double-stranded short interfering nucleic  
 CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where  
 CC one strand is an antisense strand (ASS) that is complementary to (part  
 CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
 CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
 CC modification. The invention may allow development of compounds with  
 CC virucide, antiinflammatory, hepatotropic or cytostatic activities by  
 CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
 CC interference. The siNA's of the invention may be used to inhibit  
 CC replication of HCV, in cells, tissue explants or organisms, for treating  
 CC HCV infection and its consequences (liver failure; hepatocellular cancer  
 CC and cirrhosis), and also for drug screening, diagnosis, target  
 CC identification and validation, genetic engineering, pharmacogenomics,  
 CC studying gene function and gene mapping (for example of single-nucleotide  
 CC polymorphisms). The chemical modification improves stability, activity,  
 CC cellular uptake and/or binding affinity. The siNA can be directed to  
 CC conserved regions of HCV genes, so are active against many different  
 CC strains.  
 XX  
 SQ Sequence 23 BP; 3 A; 5 C; 8 G; 0 T; 7 U; 0 Other;  
 Query Match 78.6%; Score 22; DB 10; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 3.1;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 GCAAGCACCCCTATCAGGCAGTA 22  
 Db 22 GCAAGCACCCCTATCAGGCAGTA 1  
 RESULT 30  
 AAQ71839  
 ID AAQ71839 standard; DNA; 27 BP.  
 XX  
 AC AAQ71839;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 25-MAR-1995 (first entry)  
 XX  
 DE PCR primer for hepatitis G virus.  
 XX  
 KW DNA primer; sense; polymerase chain reaction; hepatitis G virus;  
 KW diagnostic; ss.  
 XX  
 OS Synthetic.  
 XX  
 FN WO9418217-A1.  
 XX  
 PD 18-AUG-1994.  
 XX  
 PF 03-FEB-1993; 93WO-US000928.  
 XX  
 PR 03-FEB-1993; 93WO-US000928.  
 XX  
 XX  
 PA (ABBO ) ABBOTT LAB.  
 XX Tassopoulos NC, Hatzakis AE, Troonen H, Kuhns MC;  
 XX WPI; 1994-279671/34.  
 XX Hepatitis G virus polypeptides, nucleic acids, antibodies and cell  
 PT cultures - used to detect the virus in a test sample and to screen  
 PT antiviral agents.  
 XX  
 PS Disclosure; Page 60; 67pp; English.  
 XX  
 CC The sense primer is used with an antisense primer (AAQ71840) in a reverse  
 CC transcription-polymerase chain reaction assay for hepatitis E virus. A  
 CC DNA probe (AAQ71841) is used to detect the PCR products generated by the  
 CC 2 primers. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 27 BP; 8 A; 10 C; 5 G; 4 T; 0 U; 0 Other;  
 Query Match 78.6%; Score 22; DB 2; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 3.1;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 GCAAGCACCCCTATCAGGCAGTA 22  
 Db 6 GCAAGCACCCCTATCAGGCAGTA 27  
 RESULT 31  
 AAA74624  
 ID AAA74624 standard; DNA; 27 BP.  
 XX  
 AC AAA74624;  
 XX  
 DT 08-JAN-2001 (first entry)  
 XX  
 DE HCV-specific amplification primer C287R27.  
 XX  
 KW Hepatitis C virus; HCV; HCV detection; amplification primer; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 FN EP1026262-A2.  
 XX  
 PD 09-AUG-2000.  
 XX  
 PF 01-FEB-2000; 2000EP-00300763.  
 XX  
 PR 03-FEB-1999; 99US-0118497P.  
 XX  
 PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.  
 XX  
 PI Linnen JM, Gorman KM;  
 XX  
 DR WPI; 2000-507254/46.  
 XX  
 PT Detecting hepatitis C virus in biological sample involves amplifying  
 PT reverse transcribed products of virus RNA using amplification primers  
 PT whose sequences correspond to 5' or 3' non-coding region of the virus  
 PT RNA.  
 XX  
 PS Claim 30; Page 27; 28pp; English.  
 XX  
 CC The present sequence is an amplification primer used in a method for  
 CC detecting hepatitis C virus (HCV) RNA in biological samples. The HCV RNA  
 CC is reverse transcribed to generate cDNA. This is then amplified using  
 CC primers, including the present sequence, corresponding to the 5' or 3'  
 CC non-coding region of HCV. The method is useful for the diagnosis of HCV  
 CC infection in patients, in testing the efficacy of anti-HCV therapeutic  
 CC regimes, and in screening blood for HCV-infected samples. The method  
 CC provides an improved single-round, reverse transcription/amplification  
 CC assay which detects low copy levels of HCV RNA. The primers and assay  
 CC system are designed to allow the co-amplification of multiple regions of



CC the HCV genome, multiple viral species, and an internal positive control  
CC (IPC) RNA (or DNA). Simultaneous amplification/detection of multiple  
CC regions of the HCV genome increases assay sensitivity and the co-  
CC amplification of an IPC decreases the likelihood of false negative  
CC results because of PCR inhibition  
XX  
SQ Sequence 27 BP; 8 A; 10 C; 5 G; 4 T; 0 U; 0 Other;  
  
Query Match 78.6%; Score 22; DB 3; Length 27;  
Best Local Similarity 100.0%; Pred. No. 3.1;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GCAAGCACCTTATCAGGACGTA 22  
Db 6 GCAAGCACCTTATCAGGACGTA 27  
  
RESULT 32  
ABK09262  
ID ABK09262 standard; RNA; 27 BP.  
XX  
AC ABK09262;  
XX  
DT 12-MAR-2002 (first entry)  
XX  
DE Enzymatic nucleic acid effector molecule sequence 1-2.3.  
XX  
KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;  
KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;  
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
KW DNazyme; inozyme; G-cleaver; amberszyme; zinzyme; lymphoma; leukaemia;  
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;  
KW inflammatory arthropathy; central nervous system injury;  
KW chemotherapeutic-induced neuropathy; CVA; Alzheimer's disease; multiple sclerosis;  
KW chemotherapeutic-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
KW Parkinson's disease; ataxia; Huntington's disease;  
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200159103-A2.  
XX  
PD 16-AUG-2001.  
XX  
PF 09-FEB-2001; 2001WO-US004273.  
XX  
XX

CC the HCV genome, multiple viral species, and an internal positive control  
CC (IPC) RNA (or DNA). Simultaneous amplification/detection of multiple  
CC regions of the HCV genome increases assay sensitivity and the co-  
CC amplification of an IPC decreases the likelihood of false negative  
CC results because of PCR inhibition  
XX  
SQ Sequence 27 BP; 8 A; 10 C; 5 G; 4 T; 0 U; 0 Other;  
  
Query Match 78.6%; Score 22; DB 3; Length 27;  
Best Local Similarity 100.0%; Pred. No. 3.1;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GCAAGCACCTTATCAGGACGTA 22  
Db 6 GCAAGCACCTTATCAGGACGTA 27  
  
RESULT 33  
ABK09264/c  
ID ABK09264 standard; RNA; 27 BP.  
XX  
AC ABK09264;  
XX  
DT 12-MAR-2002 (first entry)  
XX  
DE Enzymatic nucleic acid effector molecule sequence 1-2.5.  
XX  
KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;  
KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;  
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
KW DNazyme; inozyme; G-cleaver; amberszyme; zinzyme; lymphoma; leukaemia;  
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;  
KW inflammatory arthropathy; central nervous system injury;  
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
KW chemotherapeutic-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
KW Parkinson's disease; ataxia; Huntington's disease;  
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200159103-A2.  
XX  
PD 16-AUG-2001.  
XX  
PF 09-FEB-2001; 2001WO-US004273.  
XX  
XX

CC the invention relates to a nucleic acid molecule which down regulates  
CC expression of a CD20 gene and a nucleic acid molecule which down  
CC regulates expression of a neurite growth inhibitor gene (NOGO). The  
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
XX

CC DNazyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule  
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr  
CC an amberszyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA  
CC with a Ydr motif). The CD20-targeting nucleic acid is used to cleave RNA  
CC of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
CC the cell and treat a patient having a condition associated with the level  
CC of CD20. The treatment may further comprise the use of one or more  
CC therapies. In particular, the CD20 targeting nucleic acid may be used to  
CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-  
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-  
CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the  
CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
CC nucleic acid may be contacted with a cell to reduce NOGO activity of the  
CC cell and treat a patient having a condition associated with the level of  
CC NOGO. The treatment may further comprise the use of one or more  
CC therapies. In particular, the NOGO-targeting nucleic acid may be used to  
CC treat central nervous system (CNS) injury and cerebrovascular accident  
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
CC disease, muscular dystrophy, and/or other neurodegenerative disease  
CC states which respond to the modulation of NOGO expression. The present  
CC sequence is an enzymatic nucleic acid with trans-acting inhibitory  
CC sequences (S- are substrate sequences, RZ- are enzymatic nucleic acid and  
CC I- are inhibitory sequences)  
XX  
SQ Sequence 27 BP; 8 A; 10 C; 5 G; 0 T; 4 U; 0 Other;  
  
Query Match 78.6%; Score 22; DB 4; Length 27;  
Best Local Similarity 86.4%; Pred. No. 3.1;  
Matches 19; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GCAAGCACCTTATCAGGACGTA 22  
Db 6 GCAAGCACCTTATCAGGACGTA 27  
  
RESULT 33  
ABK09264/c  
ID ABK09264 standard; RNA; 27 BP.  
XX  
AC ABK09264;  
XX  
DT 12-MAR-2002 (first entry)  
XX  
DE Enzymatic nucleic acid effector molecule sequence 1-2.5.  
XX  
KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;  
KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;  
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
KW DNazyme; inozyme; G-cleaver; amberszyme; zinzyme; lymphoma; leukaemia;  
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;  
KW inflammatory arthropathy; central nervous system injury;  
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
KW chemotherapeutic-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
KW Parkinson's disease; ataxia; Huntington's disease;  
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200159103-A2.  
XX  
PD 16-AUG-2001.  
XX  
PF 09-FEB-2001; 2001WO-US004273.  
XX  
XX





XX OS Synthetic.  
 XX PN WO200166721-A2.  
 XX PD 13-SEP-2001.  
 XX PF 06-MAR-2001; 2001WO-US007163.  
 XX PR 06-MAR-2000; 2000US-0187128P.  
 XX PA (RIBO-) RIBOZYME PHARM INC.  
 XX PI Usman N, Mcswiggen JA, Zinnen S, Seiwert S, Haerberli P;  
 PI Chowrira B, Blatt L;  
 XX WIPI; 2001-616242/71.  
 XX DR New nucleic acid sensor molecule useful in diagnostic applications,  
 XX PT nucleic acid-based electronics and functional genomics, comprises an  
 XX PT enzymatic nucleic acid and one or more sensors.  
 XX PS Example 1; Page 69; 115pp; English.  
 XX CC The invention relates to a nucleic acid sensor molecule (I) comprising an  
 XX CC enzymatic nucleic acid component and one or more sensor components. (I)  
 XX CC is useful in diagnostic applications to identify the presence of genes  
 XX CC and/or gene products indicative of a particular genotype and/or  
 XX CC phenotype, e.g. a disease state or infection and for diagnosis of disease  
 XX CC states or physiological abnormalities related to the expression of viral,  
 XX CC bacterial or cellular RNA and DNA. (I) is useful in nucleic acid-based  
 XX CC electronics, for the detection of specific target signalling molecules,  
 XX CC in assays to assess the specificity, toxicity and effectiveness of  
 XX CC various small molecules, nucleoside analogues or non-nucleic acid drugs  
 XX CC or for detection of pathogens, biochemicals, organic or inorganic  
 XX CC compounds. The present sequence is that of a nucleic acid sensor molecule  
 XX CC of the invention  
 XX SQ Sequence 27 BP; 4 A; 5 C; 10 G; 0 T; 8 U; 0 Other;  
 Query Match 78.6%; Score 22; DB 4; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 3.1;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCAAGCACCCCTATCAGGCAGTA 22  
 DB 22 GCAAGCACCCCTATCAGGCAGTA 1  
 RESULT 36  
 AAF58265  
 ID AAF58265 standard; DNA; 46 BP.  
 AC AAF58265;  
 XX 24-APR-2001 (first entry)  
 XX Hepatitis C virus primer #1.  
 XX DE Hepatitis C virus.  
 XX PR primer; fluorescence polarization; detection; ss.  
 XX OS Hepatitis C virus.  
 XX PN JP2000333699-A.  
 XX PD 05-DEC-2000.  
 XX PF 31-MAY-1999; 99JP-00152109.  
 XX PR 31-MAY-1999; 99JP-00152109.  
 XX PA (KARO/) KAROBE M.  
 XX PA (TSUR/) TSURUOKA M.

PA (TOWA-) TOWA KAGAKU KK.  
 XX WIPI; 2001-172352/18.  
 XX DR Detecting ribonucleic acid (RNA) comprises transcription with RNA  
 XX PT polymerase, contacting with a fluorescently labelled probe and detecting  
 XX PT changes in fluorescent polarization.  
 XX PS Example 1; Page 4; 8pp; Japanese.  
 XX CC The present invention relates to detection of ribonucleic acid (RNA) with  
 XX CC fluorescence polarization. The method gives sensitive and specific  
 XX CC detection of RNA  
 XX SQ Sequence 46 BP; 16 A; 12 C; 8 G; 10 T; 0 U; 0 Other;  
 Query Match 78.6%; Score 22; DB 4; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 3.4;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCAAGCACCCCTATCAGGCAGTA'22  
 DB 25 GCAAGCACCCCTATCAGGCAGTA 46  
 RESULT 37  
 AAQ58380  
 ID AAQ58380 standard; DNA; 21 BP.  
 XX AC AAQ58380;  
 XX DT 25-MAR-2003 (revised)  
 XX DT 04-OCT-1994 (first entry)  
 XX DE Antisense oligonucleotide targetted to HCV 5'untranslated region.  
 XX KW Hepatitis C virus; HCV; non-A, non-B hepatitis virus; NANBHV;  
 XX KW antisense oligonucleotide; translation inhibition; therapy; ss.  
 XX OS Synthetic.  
 XX PN WO9405813-A1.  
 XX PD 17-MAR-1994.  
 XX PF 10-SEP-1993; 93WO-JP001293.  
 XX PR 10-SEP-1992; 92US-00945289.  
 XX PR 14-APR-1993; 93JP-00087195.  
 XX PA (MOCH ) MOCHIDA PHARM CO LTD.  
 XX PA (KAGA ) CEMO SERO THERAPEUTIC RES INST.  
 XX PA (ISIS-) ISIS PHARM INC.  
 XX PI Anderson KP, Hanecak RC, Hoshiko K, Nozaki C, Nishihara T;  
 PI Nakatake H, Hamada F, Eto T, Furukawa S;  
 XX WIPI; 1994-101217/12.  
 XX PT Anti:sense oligo:nucleotide(s) complementary to hepatitis C viral genome  
 XX PT - useful for inhibiting HCV replication, to treat related diseases.  
 XX PS Claim 5; Page 14; 91pp; English.  
 XX CC Oligonucleotides which are complementary to part of the hepatitis C virus  
 XX CC genomic or messenger RNA are claimed. Preferred antisense  
 XX CC oligonucleotides (see AAQ58364-Q58387) are complementary to RNA  
 XX CC comprising the 5'end hairpin loop, 5'end 6bp repeat, 5'end untranslated  
 XX CC region, polypeptide translation initiation codon, ORF3 translation R2  
 XX CC initiation codon, 3' untranslated region, 3'end palindromic region, R2  
 XX CC sequence or 3' end hairpin loop of HCV. (Updated on 25-MAR-2003 to  
 XX CC correct PN field.)

SQ Sequence 21 BP; 7 A; 8 C; 3 G; 3 T; 0 U; 0 Other;  
 Query Match 75.0%; Score 21; DB 2; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 8.6;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCTATCAGGCAGTACCACAA 28  
 DB 1 CCTATCAGGCAGTACCACAA 21

RESULT 38  
 AAQ75034  
 ID AAQ75034 standard; DNA; 21 BP.  
 XX  
 AC AAQ75034;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 04-AUG-1995 (first entry)  
 XX  
 DE PCR primer for the amplification of a peptide-streptavidin-oligo.  
 XX  
 KW Synthetic peptide; solid phase immunoassay; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_difference 1  
 FT /\*tag= a  
 FT /note= "linked to digoxigenin"  
 XX  
 PN WO9426932-A1.  
 XX  
 PD 24-NOV-1994.  
 XX  
 PF 13-MAY-1994; 94WO-US005407.  
 XX  
 PR 13-MAY-1993; 93US-00061694.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Fields HA, Khudyakov YE;  
 XX  
 DR WPI; 1995-006819/01.  
 XX  
 PT Solid phase immunoassay using oligo:nucleotide as label - also new  
 PT conjugates of oligo:nucleotide coupled to antigenic peptide, partic. for  
 PT diagnosing hepatitis C or E virus infection.  
 XX  
 PS Example; Page 19; 34pp; English.  
 CC  
 CC AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides.  
 CC They are used in a method for detecting an antigen in a subject. The  
 CC method involves binding the antigen to a solid support and then reacting  
 CC it with an immunoreactive ligand (L) bound to an oligo; removing any  
 CC unreacted L, and then detecting the presence of the oligo. A similar  
 CC method can be used to detect Abs, in which case the ligand is an oligo-  
 CC labelled Ag. The use of an amplifiable oligo as the label allows Ag or Ab  
 CC to be detected at very low levels. In the example, anti-human antibodies  
 CC are adsorbed on the surface of microcentrifuge tubes and used to capture  
 CC antibodies from human sera specimens. Then the tubes are incubated with a  
 CC peptide- streptavidin-oligo complex. After washing, PCR is performed,  
 CC using primers AAQ75034 and AAQ75035. AAQ75034 could be labelled with  
 CC another moiety, for example, biotin. (Updated on 25-MAR-2003 to correct  
 CC PN field.)  
 XX  
 SQ Sequence 21 BP; 7 A; 8 C; 3 G; 3 T; 0 U; 0 Other;  
 Query Match 75.0%; Score 21; DB 2; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 8.6;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCTATCAGGCAGTACCACAA 28

RESULT 39  
 AAQ85921  
 ID AAQ85921 standard; DNA; 21 BP.  
 XX  
 AC AAQ85921;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 02-NOV-1995 (first entry)  
 XX  
 DE Hepatitis C virus genome internal PCR primer YK-106B.  
 XX  
 KW Hepatitis C virus; HCV; non-A non-B; external PCR primer; YK-106B;  
 KW primer specific detection; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1  
 FT /\*tag= a  
 FT /label= biotinylated  
 XX  
 PN WO9506753-A1.  
 XX  
 PD 09-MAR-1995.  
 XX  
 PF 02-SEP-1994; 94WO-US009869.  
 XX  
 PR 03-SEP-1993; 93US-00116344.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Fields HA, Khudyakov YE;  
 XX  
 DR WPI; 1995-115465/15.  
 XX  
 PT New method and kit for primer-specific detection of nucleic acids - using  
 PT two primers having a known sequence and a marker, resp for solid-phase  
 PT detection of amplification prods.  
 XX  
 PS Example 1; Page 12; 20pp; English.  
 CC  
 CC AAQ85918/19 are external, and AAQ85820/21 are internal PCR primers for  
 CC the Hepatitis C virus (HCV) genome. They were used to demonstrate a new  
 CC method for the primer specific detection of nucleic acids. (Updated on 25  
 CC -MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 21 BP; 7 A; 8 C; 3 G; 3 T; 0 U; 0 Other;  
 Query Match 75.0%; Score 21; DB 2; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 8.6;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCTATCAGGCAGTACCACAA 28  
 DB 1 CCTATCAGGCAGTACCACAA 21

RESULT 40  
 AAQ25792  
 ID AAQ25792 standard; DNA; 21 BP.  
 XX  
 AC AAQ25792;  
 XX  
 DT 11-JAN-2000 (first entry)  
 XX  
 DE Hepatitis C virus PCR primer #4.  
 XX  
 KW Hepatitis C virus; HCV; PCR primer; ribavirin; interferon alpha;  
 KW antiviral; detection; infection; ss.

Search completed: November 23, 2004, 17:29:30  
Job time : 167.277 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:59:48 ; Search time 32.4045 Seconds  
(without alignments)  
614.177 Million cell updates/sec

Title: US-10-087-631B-7

Perfect score: 28  
Sequence: 1 gcaagccattatcaggcagtcaccacaa 28

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 905748

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Issued Patents NA.\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	28	2	US-08-738-928-2
2	28	100.0	28	3	US-09-039-866-4
c	3	28	100.0	47	US-09-547-757-1
	4	27	96.4	27	US-08-738-928-3
5	27	96.4	27	4	US-09-493-353-5
6	24	85.7	28	3	US-08-474-700B-12
7	24	85.7	28	5	PCT-US95-05812-12
8	24	85.7	33	1	US-08-438-639-51
9	24	85.7	33	1	US-07-813-338A-51
10	24	85.7	33	2	US-08-470-124-61
11	24	85.7	33	3	US-08-441-971-127
12	24	85.7	33	3	US-08-221-653-137
13	24	85.7	33	3	US-08-442-144A-127
14	24	85.7	33	3	US-08-441-970-127
15	22	78.6	27	4	US-09-493-353-6
16	22	78.6	27	5	PCT-US93-00928-1
17	21	75.0	21	3	US-09-078-290A-10
18	21	75.0	21	3	US-08-938-033-4
19	21	75.0	21	3	US-08-397-220B-17
20	21	75.0	21	3	US-08-650-093C-17
21	21	75.0	21	4	US-08-823-895A-17
22	21	75.0	21	4	US-09-311-487-4
23	21	75.0	21	5	PCT-US94-05407-13
24	21	75.0	23	1	US-08-356-287-25
25	21	75.0	23	5	PCT-US93-04863-25
26	21	75.0	24	1	US-08-240-547-18
27	21	75.0	24	1	US-08-449-050-16

28	21	75.0	24	1	US-08-332-616A-8	Sequence 8, Appli
29	21	75.0	24	1	US-08-317-220-8	Sequence 8, Appli
30	21	75.0	24	1	US-08-675-153-8	Sequence 8, Appli
31	21	75.0	24	1	US-08-244-116B-51	Sequence 51, Appli
32	21	75.0	24	2	US-08-738-928-5	Sequence 5, Appli
33	21	75.0	24	2	US-08-841-252-8	Sequence 8, Appli
34	21	75.0	24	2	US-08-881-571-8	Sequence 8, Appli
35	21	75.0	24	3	US-09-282-054-8	Sequence 8, Appli
36	21	75.0	24	3	US-09-665-638-8	Sequence 8, Appli
37	21	75.0	24	4	US-10-007-389-5	Sequence 5, Appli
38	21	75.0	26	1	US-08-240-547-19	Sequence 19, Appli
39	21	75.0	26	2	US-08-256-568B-4	Sequence 4, Appli
40	21	75.0	26	3	US-09-038-369B-4	Sequence 4, Appli
41	21	75.0	26	4	US-09-378-900A-4	Sequence 4, Appli
42	21	75.0	26	4	US-09-720-201A-23	Sequence 23, Appli
43	21	75.0	26	4	US-09-899-044-4	Sequence 4, Appli
44	21	75.0	29	1	US-08-240-547-20	Sequence 20, Appli
45	20	71.4	24	2	US-08-440-209-2	Sequence 2, Appli
46	20	71.4	24	3	US-08-439-996-2	Sequence 2, Appli
47	19.8	70.7	33	4	US-09-770-158-20	Sequence 20, Appli
48	19.8	70.7	33	4	US-09-770-158-21	Sequence 21, Appli
49	19	67.9	20	3	US-08-397-220B-64	Sequence 64, Appli
50	19	67.9	20	3	US-08-397-220B-65	Sequence 65, Appli
51	19	67.9	20	3	US-08-650-093C-64	Sequence 64, Appli
52	19	67.9	20	3	US-08-650-093C-65	Sequence 65, Appli
53	19	67.9	22	1	US-08-356-287-27	Sequence 27, Appli
54	19	67.9	22	5	PCT-US93-04863-27	Sequence 27, Appli
55	18.4	65.7	26	1	US-08-244-116B-23	Sequence 23, Appli
56	18	64.3	28	3	US-08-474-700B-11	Sequence 11, Appli
57	18	64.3	28	3	US-08-474-700B-34	Sequence 34, Appli
58	18	64.3	28	3	US-08-474-700B-35	Sequence 35, Appli
59	18	64.3	28	5	PCT-US95-05812-11	Sequence 11, Appli
60	18	64.3	28	5	PCT-US95-05812-34	Sequence 34, Appli
61	18	64.3	28	5	PCT-US95-05812-35	Sequence 35, Appli
62	17.4	62.1	34	4	US-09-770-158-22	Sequence 22, Appli
63	17.4	62.1	34	4	US-09-770-158-24	Sequence 24, Appli
64	17.4	62.1	35	4	US-09-770-158-26	Sequence 26, Appli
65	17	60.7	30	4	US-10-353-589-2	Sequence 2, Appli
66	17	60.7	30	4	US-10-029-907-18	Sequence 18, Appli
67	16.4	58.6	33	4	US-09-770-158-23	Sequence 23, Appli
68	16.4	58.6	34	4	US-09-770-158-25	Sequence 25, Appli
69	16	57.1	16	4	US-09-474-432B-34	Sequence 34, Appli
70	16	57.1	16	4	US-09-476-387-34	Sequence 34, Appli
71	15.4	55.0	22	4	US-09-706-649-4	Sequence 4, Appli
72	15	53.6	15	1	US-08-182-968A-13	Sequence 13, Appli
73	15	53.6	15	1	US-08-182-968A-14	Sequence 14, Appli
74	15	53.6	15	2	US-08-774-306A-13	Sequence 13, Appli
75	15	53.6	15	2	US-08-774-306A-14	Sequence 14, Appli
76	15	53.6	15	3	US-09-064-156A-13	Sequence 13, Appli
77	15	53.6	15	3	US-09-064-156A-14	Sequence 14, Appli
78	15	53.6	16	4	US-09-474-432B-18	Sequence 18, Appli
79	15	53.6	16	4	US-09-476-387-18	Sequence 18, Appli
80	15	53.6	18	3	US-09-034-205-24	Sequence 24, Appli
81	15	53.6	18	3	US-08-934-097A-24	Sequence 24, Appli
82	15	53.6	18	3	US-08-851-588-24	Sequence 24, Appli
83	15	53.6	18	3	US-09-677-192B-24	Sequence 24, Appli
84	15	53.6	18	3	US-09-677-192-24	Sequence 24, Appli
85	15	53.6	18	4	US-09-402-618B-24	Sequence 24, Appli
86	15	53.6	18	4	US-09-825-574-24	Sequence 24, Appli
87	15	53.6	18	4	US-09-676-768-24	Sequence 24, Appli
88	15	53.6	19	1	US-09-798-641-37	Sequence 37, Appli
89	15	53.6	19	2	US-08-690-495-37	Sequence 37, Appli
90	15	53.6	19	2	US-08-690-494-37	Sequence 37, Appli
91	15	53.6	19	3	US-09-220-848A-3	Sequence 3, Appli
92	15	53.6	19	4	US-09-702-758A-3	Sequence 3, Appli
93	15	53.6	19	4	US-09-299-217-37	Sequence 37, Appli
94	15	53.6	19	4	US-09-728-265-37	Sequence 37, Appli
95	15	53.6	20	3	US-09-214-471-2	Sequence 2, Appli
96	15	53.6	20	4	US-09-661-364-2	Sequence 2, Appli
97	15	53.6	21	3	US-09-012-573-4	Sequence 4, Appli
98	15	53.6	25	4	US-09-494-332A-2	Sequence 2, Appli
99	15	53.6	25	4	US-09-494-332A-11	Sequence 11, Appli
100	15	53.6	25	4	US-09-493-353-7	Sequence 7, Appli

101	14.6	52.1	30	2	US-08-859-998-151	Sequence 151, Appl	174	12.4	44.3	32	5	PCT-US96-07496-18	Sequence 18, Appl
102	14.6	52.1	30	3	US-09-225-928-151	Sequence 151, Appl	c 175	12.4	44.3	32	5	PCT-US96-07496-19	Sequence 19, Appl
103	14.6	52.1	30	4	US-09-225-201B-151	Sequence 151, Appl	c 176	12.4	44.3	38	4	US-09-371-772B-7206	Sequence 7206, Ap
c 104	14.4	51.4	31	4	US-09-417-197-32	Sequence 32, Appl	c 177	12.4	44.3	38	4	US-09-371-772B-8954	Sequence 8954, Ap
c 105	14	50.0	16	4	US-09-474-432B-19	Sequence 19, Appl	c 178	12.4	44.3	38	4	US-09-371-772B-11675	Sequence 11675, A
c 106	14	50.0	16	4	US-09-476-387-19	Sequence 19, Appl	c 179	12.4	44.3	39	1	US-08-399-696-42	Sequence 42, Appl
107	14	50.0	18	3	US-09-012-573-1	Sequence 1, Appl	180	12.4	44.3	45	3	US-09-199-737-53	Sequence 53, Appl
108	14	50.0	19	3	US-09-165-264-10	Sequence 10, Appl	181	12.4	44.3	45	3	US-09-058-333A-53	Sequence 53, Appl
c 109	14	50.0	30	1	US-08-468-557-24	Sequence 24, Appl	182	12.4	44.3	47	4	US-09-422-978-777	Sequence 777, Ap
c 110	14	50.0	30	1	US-08-451-715A-63	Sequence 63, Appl	c 183	12.4	44.3	47	4	US-09-422-978-3819	Sequence 3819, Ap
c 111	14	50.0	30	2	US-08-743-130A-35	Sequence 35, Appl	c 184	12.2	43.6	18	2	US-09-157-378-27	Sequence 27, Appl
c 112	14	50.0	30	2	US-08-742-026-15	Sequence 15, Appl	c 185	12.2	43.6	20	4	US-09-676-610B-97	Sequence 97, Appl
c 113	14	50.0	30	2	US-08-415-593-23	Sequence 23, Appl	c 186	12.2	43.6	22	4	US-08-822-445-27	Sequence 27, Appl
c 114	13.6	48.6	21	3	US-08-927-219-33	Sequence 33, Appl	c 187	12.2	43.6	22	3	US-09-396-540-37	Sequence 37, Appl
c 115	13.2	47.1	20	2	US-08-888-982A-40	Sequence 40, Appl	c 188	12.2	43.6	29	2	US-08-450-905B-31	Sequence 31, Appl
c 116	13.2	47.1	20	2	US-08-888-982A-41	Sequence 41, Appl	c 189	12.2	43.6	29	3	US-07-982-759F-31	Sequence 31, Appl
c 117	13.2	47.1	20	3	US-09-462-261-40	Sequence 40, Appl	c 190	12.2	43.6	32	2	US-08-450-905B-30	Sequence 30, Appl
c 118	13.2	47.1	20	3	US-09-462-261-41	Sequence 41, Appl	c 191	12.2	43.6	32	3	US-07-982-759F-30	Sequence 30, Appl
c 119	13.2	47.1	20	4	US-09-506-073-129	Sequence 129, Appl	c 192	12.2	43.6	36	2	US-08-868-162A-3	Sequence 3, Appl
c 120	13.2	47.1	20	4	US-09-506-073-130	Sequence 130, Appl	c 193	12.2	43.6	38	1	US-07-598-737C-14	Sequence 14, Appl
121	13.2	47.1	29	2	US-08-799-825-1	Sequence 1, Appl	194	12.2	43.6	38	1	US-08-084-718-27	Sequence 27, Appl
122	13.2	47.1	29	3	US-09-280-068-1	Sequence 1, Appl	195	12.2	43.6	38	1	US-08-443-976-27	Sequence 27, Appl
c 123	13.2	47.1	30	2	US-08-716-284-15	Sequence 15, Appl	c 196	12.2	43.6	38	1	US-08-443-977-27	Sequence 27, Appl
c 124	13.2	47.1	30	4	US-09-929-922-29	Sequence 29, Appl	c 197	12.2	43.6	38	1	US-08-373-124A-635	Sequence 635, App
c 125	13.2	47.1	43	2	US-08-850-049-107	Sequence 107, Appl	c 198	12.2	43.6	38	1	US-08-435-628-635	Sequence 635, App
126	13.2	47.1	43	2	US-08-050-478-107	Sequence 107, Appl	c 199	12.2	43.6	39	1	US-07-846-181-7	Sequence 7, Appl
127	13.2	47.1	43	3	US-09-414-117-107	Sequence 107, Appl	c 200	12.2	43.6	39	1	US-07-846-181-8	Sequence 8, Appl
128	13.2	47.1	43	4	US-09-678-437-107	Sequence 107, Appl	c 201	12.2	43.6	39	1	US-07-845-989-7	Sequence 7, Appl
c 129	13.2	47.1	43	4	US-09-943-722-107	Sequence 107, Appl	c 202	12.2	43.6	39	1	US-07-845-989-8	Sequence 8, Appl
c 130	13	46.4	19	3	US-08-745-310-4	Sequence 4, Appl	c 203	12.2	43.6	39	1	US-07-598-737C-13	Sequence 13, Appl
c 131	13	46.4	24	1	US-08-484-557C-16	Sequence 16, Appl	c 204	12.2	43.6	39	1	US-08-084-718-26	Sequence 26, Appl
c 132	13	46.4	24	1	US-08-487-426B-16	Sequence 16, Appl	c 205	12.2	43.6	39	1	US-08-443-976-26	Sequence 26, Appl
c 133	13	46.4	24	2	US-08-487-720A-16	Sequence 16, Appl	c 206	12.2	43.6	39	1	US-08-443-977-26	Sequence 26, Appl
c 134	13	46.4	38	4	US-09-371-772B-9976	Sequence 9976, Ap	c 207	12.2	43.6	41	3	US-08-813-507-109	Sequence 109, App
c 135	13	46.4	38	4	US-09-371-772B-11318	Sequence 11318, A	c 208	12.2	43.6	41	3	US-09-351-814-42	Sequence 42, Appl
c 136	13	46.4	45	2	US-08-882-756-2	Sequence 2, Appl	c 209	12.2	43.6	41	3	US-09-464-453-109	Sequence 109, App
c 137	13	46.4	45	2	US-08-882-756-5	Sequence 5, Appl	c 210	12.2	43.6	42	2	US-08-716-284-3	Sequence 3, Appl
c 138	13	46.4	45	2	US-08-882-756-5	Sequence 5, Appl	c 211	12	42.9	20	1	US-07-752-101A-31	Sequence 31, Appl
c 139	13	46.4	45	3	US-09-301-153-1	Sequence 1, Appl	c 212	12	42.9	20	1	US-07-752-101A-49	Sequence 49, Appl
c 140	13	46.4	45	3	US-09-301-153-2	Sequence 2, Appl	c 213	12	42.9	20	2	US-08-117-952-168	Sequence 168, App
c 141	12.8	45.7	18	4	US-09-614-748A-31	Sequence 31, Appl	c 214	12	42.9	20	3	US-09-418-641-67	Sequence 67, Appl
c 142	12.8	45.7	26	4	US-09-127-578-15	Sequence 15, Appl	c 215	12	42.9	25	4	US-09-647-563-30	Sequence 30, Appl
c 143	12.8	45.7	26	4	US-09-127-578-17	Sequence 17, Appl	c 216	12	42.9	27	3	US-08-513-974B-165	Sequence 165, App
c 144	12.8	45.7	31	4	US-09-648-667-2	Sequence 2, Appl	c 217	12	42.9	29	4	US-09-807-784B-13	Sequence 13, Appl
c 145	12.8	45.7	31	4	US-09-648-667-8	Sequence 8, Appl	c 218	12	42.9	30	3	US-09-338-907-170	Sequence 170, App
c 146	12.8	45.7	44	3	US-08-617-454-11	Sequence 11, Appl	c 219	12	42.9	30	3	US-09-218-207-170	Sequence 170, App
c 147	12.8	45.7	47	4	US-09-422-978-2844	Sequence 2844, Ap	c 220	12	42.9	30	4	US-09-170-496D-161	Sequence 161, App
c 148	12.8	45.7	50	4	US-09-613-263-12	Sequence 12, Appl	c 221	12	42.9	33	2	US-08-752-844-60	Sequence 60, Appl
c 149	12.8	45.7	50	4	US-09-613-263-13	Sequence 13, Appl	c 222	12	42.9	33	4	US-08-752-844-60	Sequence 60, Appl
c 150	12.6	45.0	24	4	US-08-952-899-10	Sequence 10, Appl	c 223	12	42.9	36	1	US-08-639-256-10	Sequence 10, Appl
c 151	12.6	45.0	25	4	US-09-615-095-1	Sequence 1, Appl	c 224	12	42.9	37	3	US-09-311-626B-53	Sequence 53, Appl
c 152	12.6	45.0	30	4	US-09-929-922-30	Sequence 30, Appl	c 225	12	42.9	38	4	US-09-371-772B-9487	Sequence 9487, Ap
c 153	12.6	45.0	31	3	US-08-951-923-19	Sequence 19, Appl	c 226	12	42.9	45	3	US-08-894-727-7	Sequence 7, Appl
c 154	12.6	45.0	35	4	US-09-736-116-56	Sequence 56, Appl	c 227	12	42.9	46	4	US-09-552-322-23	Sequence 23, Appl
c 155	12.6	45.0	36	2	US-08-829-876-60	Sequence 60, Appl	c 228	12	42.9	46	4	US-10-150-048-5	Sequence 5, Appl
c 156	12.6	45.0	36	3	US-09-234-874A-60	Sequence 60, Appl	c 229	12	42.9	47	4	US-09-422-978-281	Sequence 281, App
c 157	12.6	45.0	36	4	US-09-234-873A-60	Sequence 60, Appl	c 230	11.8	42.1	20	3	US-09-280-181B-2	Sequence 2, Appl
c 158	12.6	45.0	38	4	US-09-371-772B-7868	Sequence 7868, Ap	c 231	11.8	42.1	21	4	US-09-657-472-1069	Sequence 1069, Ap
c 159	12.6	45.0	38	4	US-09-371-772B-10726	Sequence 10726, A	c 232	11.8	42.1	22	4	US-09-989-002-26	Sequence 26, Appl
c 160	12.6	45.0	41	2	US-08-386-198A-8	Sequence 8, Appl	c 233	11.8	42.1	22	4	US-09-989-002-26	Sequence 26, Appl
c 161	12.6	45.0	42	3	US-08-679-645-7	Sequence 7, Appl	c 234	11.8	42.1	25	4	US-09-641-259B-35	Sequence 35, Appl
c 162	12.4	44.3	18	1	US-08-487-135B-15	Sequence 15, Appl	c 235	11.8	42.1	26	4	US-08-442-010-2	Sequence 2, Appl
c 163	12.4	44.3	18	2	US-08-443-342A-19	Sequence 19, Appl	c 236	11.8	42.1	27	2	US-08-123-761A-3	Sequence 3, Appl
c 164	12.4	44.3	18	2	US-08-915-972A-15	Sequence 15, Appl	c 237	11.8	42.1	28	3	US-09-006-636-19	Sequence 19, Appl
c 165	12.4	44.3	18	2	US-09-177-909-15	Sequence 15, Appl	c 238	11.8	42.1	28	3	US-09-006-632-19	Sequence 19, Appl
c 166	12.4	44.3	24	1	US-08-487-135B-4	Sequence 4, Appl	c 239	11.8	42.1	28	3	US-09-325-274-19	Sequence 19, Appl
c 167	12.4	44.3	24	2	US-08-915-972A-4	Sequence 4, Appl	c 240	11.8	42.1	30	1	US-08-219-012-31	Sequence 31, Appl
c 168	12.4	44.3	24	2	US-09-177-909-4	Sequence 4, Appl	c 241	11.8	42.1	30	3	US-08-687-421-219	Sequence 219, App
c 169	12.4	44.3	30	3	US-09-423-744A-8	Sequence 8, Appl	c 242	11.8	42.1	30	4	US-09-270-957-52	Sequence 52, Appl
c 170	12.4	44.3	32	2	US-08-454-028-18	Sequence 18, Appl	c 243	11.8	42.1	31	3	US-08-679-645-355	Sequence 355, App
c 171	12.4	44.3	32	2	US-08-454-028-19	Sequence 19, Appl	c 244	11.8	42.1	32	2	US-08-811-492-54	Sequence 54, Appl
c 172	12.4	44.3	32	5	PCT-US94-05388-18	Sequence 18, Appl	c 245	11.8	42.1	32	2	US-08-859-998-1208	Sequence 1208, Ap
c 173	12.4	44.3	32	5	PCT-US94-05388-19	Sequence 19, Appl	c 246	11.8	42.1	32	2		



393	11.6	41.4	48	1	US-08-466-344-12	Sequence 12, Appl	c 466	11.4	40.7	38	4	US-09-371-772B-8869	Sequence 8869, A
c 394	11.6	41.4	48	3	US-09-091-814-12	Sequence 12, Appl	c 467	11.4	40.7	38	4	US-09-371-772B-9046	Sequence 9046, Ap
395	11.6	41.4	48	4	US-09-119-507B-92	Sequence 92, Appl	c 468	11.4	40.7	38	4	US-09-371-772B-9198	Sequence 9198, Ap
396	11.6	41.4	48	4	US-08-897-556A-92	Sequence 92, Appl	c 469	11.4	40.7	38	4	US-09-371-772B-9287	Sequence 9287, Ap
397	11.6	41.4	48	4	US-09-547-693-92	Sequence 92, Appl	c 470	11.4	40.7	38	4	US-09-371-772B-9540	Sequence 9540, Ap
398	11.6	41.4	49	3	US-09-091-814-58	Sequence 58, Appl	c 471	11.4	40.7	38	4	US-09-371-772B-9847	Sequence 9847, Ap
c 399	11.6	41.4	49	3	US-08-687-580B-20	Sequence 20, Appl	c 472	11.4	40.7	38	4	US-09-371-772B-9907	Sequence 9907, Ap
c 400	11.6	41.4	50	1	US-08-146-422-19	Sequence 19, Appl	c 473	11.4	40.7	38	4	US-09-371-772B-10741	Sequence 10741, A
c 401	11.6	41.4	50	1	US-08-146-424-21	Sequence 21, Appl	c 474	11.4	40.7	38	4	US-09-371-772B-11014	Sequence 11014, A
c 402	11.6	41.4	50	1	US-08-047-413-16	Sequence 16, Appl	c 475	11.4	40.7	38	4	US-09-371-772B-11269	Sequence 11269, A
c 403	11.6	41.4	50	1	US-08-047-413-17	Sequence 17, Appl	c 476	11.4	40.7	38	4	US-09-371-772B-11645	Sequence 11645, A
c 404	11.6	41.4	50	1	US-08-626-554-1	Sequence 1, Appli	c 477	11.4	40.7	38	4	US-09-371-772B-11841	Sequence 11841, A
c 405	11.6	41.4	50	1	US-08-633-709-3	Sequence 3, Appli	c 478	11.4	40.7	38	4	US-09-371-772B-11930	Sequence 11930, A
c 406	11.6	41.4	50	2	US-08-253-877C-42	Sequence 42, Appl	c 479	11.4	40.7	38	4	US-09-371-772B-12015	Sequence 12015, A
c 407	11.6	41.4	50	2	US-08-452-164A-42	Sequence 42, Appl	c 480	11.4	40.7	38	4	US-09-371-772B-12293	Sequence 12293, A
c 408	11.6	41.4	50	3	US-08-229-050-16	Sequence 16, Appl	c 481	11.4	40.7	38	4	US-09-371-772B-13902	Sequence 13902, A
c 409	11.6	41.4	50	3	US-08-229-050-17	Sequence 17, Appl	c 482	11.4	40.7	39	1	US-07-834-539A-47	Sequence 47, Appl
c 410	11.6	41.4	50	3	US-08-801-563-16	Sequence 16, Appl	c 483	11.4	40.7	39	1	US-08-053-131-59	Sequence 59, Appl
c 411	11.6	41.4	50	3	US-08-801-563-17	Sequence 17, Appl	c 484	11.4	40.7	39	1	US-08-645-641-59	Sequence 59, Appl
c 412	11.6	41.4	50	3	US-08-569-147-23	Sequence 23, Appl	c 485	11.4	40.7	39	1	US-07-853-408B-59	Sequence 59, Appl
c 413	11.6	41.4	50	3	US-08-976-183A-18	Sequence 18, Appl	c 486	11.4	40.7	39	2	US-08-096-762-59	Sequence 47, Appl
c 414	11.6	41.4	50	3	US-09-270-767-264A5	Sequence 18, Appl	c 487	11.4	40.7	39	2	US-08-800-353-47	Sequence 47, Appl
c 415	11.4	40.7	15	4	US-09-935-194-15	Sequence 15, Appl	c 488	11.4	40.7	39	2	US-08-308-865-59	Sequence 59, Appl
c 416	11.4	40.7	15	4	US-09-409-096-13	Sequence 13, Appl	c 489	11.4	40.7	39	2	US-08-807-332B-24	Sequence 24, Appl
c 417	11.4	40.7	25	4	US-09-206-942-75	Sequence 75, Appl	c 490	11.4	40.7	39	2	US-08-807-332B-25	Sequence 25, Appl
c 418	11.4	40.7	25	4	US-09-437-568A-31	Sequence 31, Appl	c 491	11.4	40.7	39	3	US-09-338-876-24	Sequence 24, Appl
c 419	11.4	40.7	25	4	US-09-980-777-21	Sequence 21, Appl	c 492	11.4	40.7	39	3	US-09-338-876-25	Sequence 25, Appl
c 420	11.4	40.7	26	3	US-09-814-134A-10	Sequence 10, Appl	c 493	11.4	40.7	39	3	US-09-042-353-222	Sequence 22, Appl
c 421	11.4	40.7	26	4	US-09-789-556A-17	Sequence 17, Appl	c 494	11.4	40.7	39	3	US-08-758-417A-70	Sequence 70, Appl
c 422	11.4	40.7	27	2	US-08-330-394A-24	Sequence 24, Appl	c 495	11.4	40.7	39	5	PCT-US92-0618B-47	Sequence 47, Appl
c 423	11.4	40.7	27	2	US-08-330-394A-31	Sequence 31, Appl	c 496	11.4	40.7	39	5	PCT-US92-0618B-47	Sequence 47, Appl
c 424	11.4	40.7	27	3	US-08-985-162-1123	Sequence 1123, Ap	c 497	11.4	40.7	41	3	US-08-813-507-69	Sequence 69, Appl
c 425	11.4	40.7	27	3	US-08-584-040-98	Sequence 88, Appl	c 498	11.4	40.7	41	3	US-09-464-453-69	Sequence 69, Appl
c 426	11.4	40.7	27	3	US-08-584-040-385	Sequence 385, Ap	c 499	11.4	40.7	41	3	US-08-962-281-34	Sequence 34, Appl
c 427	11.4	40.7	28	4	US-09-401-063-1123	Sequence 7, Appli	c 501	11.4	40.7	45	2	US-08-367-890-2	Sequence 2, Appli
c 428	11.4	40.7	28	4	US-09-878-756-7	Sequence 7, Appli	c 502	11.4	40.7	45	2	US-08-157-185-8	Sequence 8, Appli
c 429	11.4	40.7	29	4	US-09-599-220-2	Sequence 2, Appli	c 503	11.4	40.7	45	3	US-08-281-526B-8	Sequence 8, Appli
c 430	11.4	40.7	30	4	US-08-388-852B-5	Sequence 5, Appli	c 504	11.4	40.7	45	3	US-09-450-790A-8	Sequence 8, Appli
c 431	11.4	40.7	32	1	US-08-591-070A-31	Sequence 31, Appl	c 505	11.4	40.7	45	4	US-09-332-837-8	Sequence 8, Appli
c 432	11.4	40.7	32	2	US-08-927-855-31	Sequence 31, Appl	c 506	11.4	40.7	45	4	US-09-592-480-14	Sequence 14, Appl
c 433	11.4	40.7	33	1	US-08-068-945A-46	Sequence 46, Appl	c 507	11.4	40.7	46	3	US-09-453-702B-221	Sequence 221, App
c 434	11.4	40.7	33	1	US-08-442-806-46	Sequence 46, Appl	c 508	11.4	40.7	46	3	US-09-338-907-188	Sequence 188, App
c 435	11.4	40.7	33	2	US-08-394-177-9	Sequence 9, Appli	c 509	11.4	40.7	47	3	US-09-338-907-265	Sequence 265, App
c 436	11.4	40.7	33	4	US-09-333-636-9	Sequence 9, Appli	c 510	11.4	40.7	47	3	US-09-218-207-188	Sequence 188, App
c 437	11.4	40.7	34	3	US-09-079-812E-27	Sequence 27, Appl	c 511	11.4	40.7	47	3	US-09-218-207-265	Sequence 265, App
c 438	11.4	40.7	35	3	US-08-433-263B-7	Sequence 7, Appli	c 512	11.4	40.7	47	4	US-09-641-638-750	Sequence 750, App
c 439	11.4	40.7	36	1	US-07-834-539A-10	Sequence 10, Appl	c 513	11.4	40.7	47	4	US-09-641-638-1090	Sequence 1090, Ap
c 440	11.4	40.7	36	1	US-08-053-131-18	Sequence 18, Appl	c 514	11.4	40.7	47	4	US-09-641-638-1206	Sequence 1206, Ap
c 441	11.4	40.7	36	1	US-08-334-847-183	Sequence 183, App	c 515	11.4	40.7	47	4	US-09-422-378-2836	Sequence 2836, Ap
c 442	11.4	40.7	36	1	US-08-334-847-185	Sequence 185, App	c 516	11.4	40.7	47	4	US-10-170-097-750	Sequence 750, App
c 443	11.4	40.7	36	1	US-08-645-641-18	Sequence 18, Appl	c 517	11.4	40.7	47	4	US-10-170-097-1090	Sequence 1090, Ap
c 444	11.4	40.7	36	1	US-07-853-408B-18	Sequence 18, Appl	c 518	11.4	40.7	47	4	US-10-170-097-1206	Sequence 1206, Ap
c 445	11.4	40.7	36	1	US-08-311-486C-803	Sequence 803, App	c 519	11.4	40.7	49	2	US-08-299-074A-13	Sequence 13, Appl
c 446	11.4	40.7	36	1	US-08-096-762-18	Sequence 18, Appl	c 520	11.4	40.7	49	2	US-09-399-773-13	Sequence 13, Appl
c 447	11.4	40.7	36	2	US-08-800-353-10	Sequence 10, Appl	c 521	11.4	40.7	50	3	US-08-849-567A-61	Sequence 61, Appl
c 448	11.4	40.7	36	2	US-08-585-684B-1568	Sequence 1568, Ap	c 522	11.2	40.0	18	2	US-08-585-684B-2636	Sequence 2636, Ap
c 449	11.4	40.7	36	2	US-08-585-684B-2450	Sequence 2450, Ap	c 523	11.2	40.0	18	3	US-09-161-443-44	Sequence 44, Appl
c 450	11.4	40.7	36	3	US-08-308-865-18	Sequence 18, Appl	c 524	11.2	40.0	18	3	US-09-339-964-15	Sequence 15, Appl
c 451	11.4	40.7	36	3	US-09-038-073-1568	Sequence 1568, Ap	c 525	11.2	40.0	18	3	US-09-038-073-2636	Sequence 2636, Ap
c 452	11.4	40.7	36	3	US-09-042-353-186	Sequence 186, App	c 526	11.2	40.0	18	4	US-09-614-748A-32	Sequence 32, Appl
c 453	11.4	40.7	36	3	US-09-042-353-186	Sequence 186, App	c 527	11.2	40.0	19	3	US-09-050-159-28	Sequence 28, Appl
c 454	11.4	40.7	36	3	US-08-758-417A-34	Sequence 34, Appl	c 528	11.2	40.0	19	4	US-09-656-791A-3380	Sequence 3380, App
c 455	11.4	40.7	36	5	PCT-US92-0618B-10	Sequence 10, Appl	c 529	11.2	40.0	19	4	US-10-071-411A-54	Sequence 54, Appl
c 456	11.4	40.7	36	5	PCT-US92-0618B-10	Sequence 10, Appl	c 530	11.2	40.0	20	3	US-09-338-907-90	Sequence 90, Appl
c 457	11.4	40.7	38	1	US-08-435-350-117	Sequence 117, App	c 531	11.2	40.0	20	3	US-09-428-583-45	Sequence 45, Appl
c 458	11.4	40.7	38	1	US-08-373-124A-259	Sequence 259, App	c 532	11.2	40.0	20	3	US-09-218-207-90	Sequence 90, Appl
c 459	11.4	40.7	38	1	US-08-373-124A-2292	Sequence 2292, Ap	c 533	11.2	40.0	20	3	US-09-659-791A-41	Sequence 41, Appl
c 460	11.4	40.7	38	1	US-08-373-124A-2476	Sequence 2476, Ap	c 534	11.2	40.0	20	3	US-09-659-791A-41	Sequence 41, Appl
c 461	11.4	40.7	38	1	US-08-435-628-259	Sequence 259, App	c 535	11.2	40.0	20	3	US-09-428-583-45	Sequence 45, Appl
c 462	11.4	40.7	38	1	US-08-435-628-2292	Sequence 2292, Ap	c 536	11.2	40.0	20	4	US-09-198-452A-1493	Sequence 1493, Ap
c 463	11.4	40.7	38	1	US-08-435-628-2476	Sequence 2476, Ap	c 537	11.2	40.0	20	4	US-09-198-452A-6209	Sequence 6209, Ap
c 464	11.4	40.7	38	4	US-09-371-772B-7682	Sequence 7682, Ap	c 538	11.2	40.0	21	2	US-09-068-821-8	Sequence 8, Appli
c 465	11.4	40.7	38	4	US-09-371-772B-7733	Sequence 7733, Ap	c 539	11.2	40.0	21	2	US-08-793-107-1	Sequence 3, Appli



c 539	11.2	40.0	21	3	US-08-793-110-3	Sequence 3, Appli	612	11.2	40.0	44	1	US-07-931-473B-232	Sequence 232, App
540	11.2	40.0	23	1	US-08-227-689-4	Sequence 4, Appli	613	11.2	40.0	44	1	US-07-714-131C-232	Sequence 232, App
541	11.2	40.0	23	3	US-09-368-169-4	Sequence 4, Appli	614	11.2	40.0	44	1	US-08-412-110-232	Sequence 232, App
542	11.2	40.0	24	3	US-08-995-369-11	Sequence 11, Appl	615	11.2	40.0	44	1	US-08-409-442A-232	Sequence 232, App
543	11.2	40.0	24	5	PCT-US95-10075-11	Sequence 11, Appl	616	11.2	40.0	44	2	US-08-469-609A-232	Sequence 232, App
c 544	11.2	40.0	25	4	US-09-289-180-7	Sequence 7, Appli	617	11.2	40.0	44	3	US-08-143-190-232	Sequence 232, App
545	11.2	40.0	26	1	US-08-608-881A-5	Sequence 5, Appli	618	11.2	40.0	44	3	US-09-502-344-232	Sequence 232, App
c 546	11.2	40.0	26	1	US-08-608-881A-6	Sequence 6, Appli	c 619	11.2	40.0	47	4	US-09-641-638-232	Sequence 232, App
c 547	11.2	40.0	26	3	US-08-089-974B-24	Sequence 24, Appl	c 620	11.2	40.0	47	4	US-08-641-638-1197	Sequence 1197, Ap
548	11.2	40.0	26	3	US-08-804-439A-98	Sequence 98, Appl	c 621	11.2	40.0	47	4	US-08-585-593A-7	Sequence 7, Appli
549	11.2	40.0	26	3	US-08-720-229-98	Sequence 98, Appl	622	11.2	40.0	47	4	US-09-422-978-1779	Sequence 1779, Ap
c 550	11.2	40.0	26	4	US-09-390-134B-6	Sequence 6, Appli	623	11.2	40.0	47	4	US-09-422-978-2165	Sequence 2165, Ap
551	11.2	40.0	26	4	US-09-727-758-2	Sequence 2, Appli	c 624	11.2	40.0	47	4	US-09-422-978-3007	Sequence 3007, Ap
552	11.2	40.0	27	3	US-09-253-396A-55	Sequence 55, Appl	c 625	11.2	40.0	47	4	US-09-422-978-3508	Sequence 3508, Ap
553	11.2	40.0	28	2	US-08-995-998-622	Sequence 622, App	c 626	11.2	40.0	47	4	US-10-170-097-933	Sequence 933, App
554	11.2	40.0	28	3	US-09-225-928-622	Sequence 622, App	c 627	11.2	40.0	47	4	US-10-170-097-933	Sequence 933, App
555	11.2	40.0	28	4	US-09-225-201B-622	Sequence 622, App	c 628	11.2	40.0	47	4	US-10-170-097-1197	Sequence 1197, Ap
c 556	11.2	40.0	29	4	US-09-304-232-408	Sequence 408, App	c 629	11.2	40.0	48	2	US-08-479-275D-14	Sequence 14, Appl
557	11.2	40.0	30	3	US-09-593-012-25	Sequence 25, Appl	c 630	11.2	40.0	48	2	US-08-488-271B-14	Sequence 14, Appl
c 558	11.2	40.0	30	3	US-09-318-786-13	Sequence 13, Appl	c 631	11.2	40.0	48	3	US-08-488-551B-802	Sequence 802, App
c 559	11.2	40.0	31	1	US-08-350-884-46	Sequence 46, Appl	632	11.2	40.0	48	4	US-10-007-073-5	Sequence 5, Appli
c 560	11.2	40.0	31	1	US-08-440-548-46	Sequence 46, Appl	c 633	11.2	40.0	49	4	US-09-935-916B-66	Sequence 66, Appl
c 561	11.2	40.0	31	1	US-08-709-173-46	Sequence 46, Appl	c 634	11.2	40.0	50	1	US-08-374-641-27	Sequence 27, Appl
c 562	11.2	40.0	31	1	US-08-191-866D-87	Sequence 87, Appl	c 635	11	39.3	16	4	US-09-474-432B-20	Sequence 20, Appl
c 563	11.2	40.0	31	2	US-08-185-949B-95	Sequence 95, Appl	c 636	11	39.3	16	4	US-09-476-387-20	Sequence 20, Appl
c 564	11.2	40.0	31	2	US-08-709-177-46	Sequence 46, Appl	c 637	11	39.3	18	4	US-08-363-240A-1081	Sequence 1081, Ap
c 565	11.2	40.0	31	3	US-08-480-640A-137	Sequence 137, App	c 638	11	39.3	19	3	US-09-338-907-363	Sequence 363, App
c 566	11.2	40.0	31	3	US-08-295-802-137	Sequence 137, App	c 639	11	39.3	19	3	US-09-218-207-363	Sequence 363, App
c 567	11.2	40.0	31	3	US-08-444-818-194	Sequence 194, App	c 640	11	39.3	19	4	US-09-422-978-6231	Sequence 6231, Ap
c 568	11.2	40.0	31	3	US-08-686-968C-64	Sequence 64, Appl	c 641	11	39.3	20	3	US-09-468-872-77	Sequence 77, Appl
c 569	11.2	40.0	31	3	US-08-488-237A-137	Sequence 137, App	c 642	11	39.3	20	4	US-09-198-452A-6236	Sequence 6236, Ap
c 570	11.2	40.0	31	3	US-08-375-992A-137	Sequence 137, App	c 643	11	39.3	20	4	US-09-198-452A-6502	Sequence 6502, Ap
c 571	11.2	40.0	31	4	US-09-545-481-2	Sequence 2, Appli	c 644	11	39.3	21	4	US-08-368-870-7	Sequence 7, Appli
c 572	11.2	40.0	31	4	US-08-472-679H-137	Sequence 137, App	c 645	11	39.3	21	4	US-09-657-472-763	Sequence 763, App
c 573	11.2	40.0	32	1	US-08-410-739-4	Sequence 4, Appli	c 646	11	39.3	21	4	US-09-657-472-1153	Sequence 1153, Ap
574	11.2	40.0	32	2	US-08-997-080-67	Sequence 67, Appl	c 647	11	39.3	21	4	US-09-657-472-2525	Sequence 2525, Ap
575	11.2	40.0	32	2	US-08-997-362-67	Sequence 67, Appl	c 648	11	39.3	22	3	PCT-US96-001082-7	Sequence 7, Appli
576	11.2	40.0	32	3	US-08-873-970-67	Sequence 67, Appl	c 649	11	39.3	22	3	US-08-765-332-191	Sequence 191, App
577	11.2	40.0	32	3	US-09-095-855-67	Sequence 67, Appl	c 650	11	39.3	22	3	US-09-047-347-3	Sequence 3, Appli
578	11.2	40.0	32	3	US-09-324-542-67	Sequence 67, Appl	c 651	11	39.3	23	1	US-09-448-894-191	Sequence 191, App
579	11.2	40.0	32	4	US-09-205-436-67	Sequence 67, Appl	c 652	11	39.3	23	2	US-08-297-299B-86	Sequence 86, Appl
580	11.2	40.0	33	2	US-08-417-435-10	Sequence 10, Appl	c 653	11	39.3	23	2	US-08-858-083-86	Sequence 86, Appl
581	11.2	40.0	33	2	US-08-284-391B-10	Sequence 10, Appl	c 654	11	39.3	23	5	PCT-US95-11029-86	Sequence 86, Appl
582	11.2	40.0	33	2	US-08-394-177-4	Sequence 4, Appli	c 655	11	39.3	24	3	US-08-868-373-17	Sequence 17, Appl
583	11.2	40.0	33	3	US-08-394-912A-4	Sequence 4, Appli	c 656	11	39.3	25	1	US-08-466-033-9	Sequence 9, Appli
584	11.2	40.0	33	3	US-09-218-950-10	Sequence 10, Appl	c 657	11	39.3	25	1	US-08-444-733-9	Sequence 9, Appli
585	11.2	40.0	33	4	US-09-333-636-4	Sequence 4, Appli	c 658	11	39.3	25	2	US-08-464-134-9	Sequence 9, Appli
586	11.2	40.0	33	4	US-08-394-388A-10	Sequence 10, Appl	c 659	11	39.3	25	2	US-08-461-361-9	Sequence 9, Appli
587	11.2	40.0	33	4	PCT-US92-01785-10	Sequence 9, Appli	c 660	11	39.3	25	5	US-08-485-910-9	Sequence 9, Appli
588	11.2	40.0	33	5	PCT-US95-00454-10	Sequence 10, Appl	c 661	11	39.3	27	1	PCT-US95-06266-9	Sequence 8, Appli
589	11.2	40.0	35	3	US-08-715-628B-8	Sequence 8, Appli	c 662	11	39.3	27	3	US-08-886-886-4	Sequence 4, Appli
c 590	11.2	40.0	36	1	US-08-291-932A-478	Sequence 478, App	c 663	11	39.3	27	3	US-09-253-396A-169	Sequence 169, App
c 591	11.2	40.0	36	1	US-08-291-932A-667	Sequence 667, App	c 664	11	39.3	28	2	US-08-859-998-724	Sequence 724, App
c 592	11.2	40.0	36	1	US-08-363-240A-505	Sequence 505, App	c 665	11	39.3	28	2	US-08-859-998-1075	Sequence 1075, Ap
c 593	11.2	40.0	36	2	US-08-868-162A-7	Sequence 7, Appli	c 666	11	39.3	28	3	US-09-225-928-724	Sequence 724, App
c 594	11.2	40.0	37	1	US-07-977-696C-22	Sequence 22, Appl	c 667	11	39.3	28	3	US-09-225-928-1075	Sequence 1075, Ap
c 595	11.2	40.0	37	1	US-08-129-930B-22	Sequence 22, Appl	c 668	11	39.3	28	3	US-09-368-770-6	Sequence 6, Appli
c 596	11.2	40.0	37	3	US-08-134-346A-9	Sequence 9, Appli	c 669	11	39.3	28	4	US-09-225-201B-724	Sequence 724, App
c 597	11.2	40.0	37	3	US-08-976-288A-22	Sequence 22, Appl	c 670	11	39.3	28	4	US-09-225-201B-1075	Sequence 1075, Ap
c 598	11.2	40.0	38	4	US-09-757-207-9	Sequence 9, Appli	c 671	11	39.3	29	4	US-09-304-232-402	Sequence 402, App
c 599	11.2	40.0	39	1	US-08-682-218-24	Sequence 24, Appl	c 672	11	39.3	29	4	US-09-304-232-878	Sequence 878, App
c 600	11.2	40.0	39	4	US-09-219-797-9	Sequence 9, Appli	c 673	11	39.3	30	3	US-07-661-370-2	Sequence 2, Appli
c 601	11.2	40.0	41	3	US-08-813-507-111	Sequence 111, App	c 674	11	39.3	31	1	US-08-390-850-151	Sequence 151, App
c 602	11.2	40.0	41	3	US-09-464-453-111	Sequence 111, App	c 675	11	39.3	31	1	US-08-390-850-152	Sequence 152, App
c 603	11.2	40.0	42	1	US-08-271-880A-52	Sequence 52, Appl	c 676	11	39.3	31	1	US-08-435-634-151	Sequence 151, App
c 604	11.2	40.0	42	2	US-08-910-408-52	Sequence 52, Appl	c 677	11	39.3	31	1	US-08-435-634-152	Sequence 152, App
c 605	11.2	40.0	42	3	US-09-249-215-52	Sequence 52, Appl	c 678	11	39.3	33	1	US-08-639-256-13	Sequence 13, App
c 606	11.2	40.0	43	2	US-08-850-049-108	Sequence 108, App	c 679	11	39.3	33	4	US-08-677-970-5	Sequence 5, Appli
607	11.2	40.0	43	2	US-08-050-478-108	Sequence 108, App	c 680	11	39.3	33	4	US-08-675-499A-22	Sequence 22, Appl
608	11.2	40.0	43	2	US-08-050-478-108	Sequence 108, App	c 681	11	39.3	33	4	US-08-812-008-22	Sequence 22, Appl
609	11.2	40.0	43	3	US-09-414-117-108	Sequence 108, App	c 682	11	39.3	33	4	US-08-933-821-11	Sequence 11, Appl
610	11.2	40.0	43	4	US-09-678-437-108	Sequence 108, App	c 683	11	39.3	34	2	US-08-960-507-11	Sequence 11, Appl
611	11.2	40.0	43	4	US-09-943-722-108	Sequence 108, App	c 684	11	39.3	34	3		

c 685	11	39.3	34	3	US-08-966-341-8	Sequence 8, Appli	758	11	39.3	50	1	US-08-171-389-229	Sequence 229, App
c 686	11	39.3	34	3	US-08-966-341-9	Sequence 9, Appli	759	11	39.3	50	1	US-08-530-492-55	Sequence 55, Appl
c 687	11	39.3	34	3	US-09-064-411A-30	Sequence 30, Appl	760	11	39.3	50	1	US-08-123-936-229	Sequence 229, App
c 688	11	39.3	34	3	US-09-136-828-11	Sequence 11, Appl	761	11	39.3	50	2	US-08-475-288A-229	Sequence 229, App
c 689	11	39.3	34	3	US-09-332-928A-11	Sequence 11, Appl	762	11	39.3	50	3	US-08-482-080A-229	Sequence 229, App
c 690	11	39.3	34	3	US-09-136-801-11	Sequence 11, Appl	763	11	39.3	50	3	US-08-906-517-55	Sequence 55, Appl
c 691	11	39.3	34	4	US-09-332-923-11	Sequence 11, Appl	764	11	39.3	50	3	US-09-354-947-229	Sequence 229, App
c 692	11	39.3	34	4	US-09-333-075-11	Sequence 11, Appl	765	11	39.3	50	5	PCT-US93-12388-229	Sequence 32, Appl
c 693	11	39.3	34	4	US-09-202-088A-11	Sequence 11, Appl	766	10.8	38.6	16	4	US-09-649-747A-32	Sequence 5349, Ap
c 694	11	39.3	34	4	US-09-333-077-11	Sequence 11, Appl	767	10.8	38.6	17	3	US-08-584-040-5349	Sequence 5350, Ap
c 695	11	39.3	35	4	US-09-284-100A-43	Sequence 43, Appl	c 768	10.8	38.6	17	3	US-08-584-040-8021	Sequence 8021, Ap
c 696	11	39.3	35	4	US-09-284-100A-47	Sequence 47, Appl	769	10.8	38.6	17	3	US-08-584-040-8021	Sequence 8021, Ap
c 697	11	39.3	35	4	US-09-284-100A-49	Sequence 49, Appl	c 770	10.8	38.6	17	4	US-09-371-772B-2252	Sequence 2252, Ap
c 698	11	39.3	35	4	US-09-284-100A-51	Sequence 51, Appl	c 771	10.8	38.6	17	4	US-09-371-772B-3804	Sequence 3804, Ap
c 699	11	39.3	36	1	US-08-363-240A-320	Sequence 920, App	772	10.8	38.6	17	4	US-08-487-135B-12	Sequence 12, Appl
c 700	11	39.3	36	1	US-08-363-240A-321	Sequence 921, App	773	10.8	38.6	18	2	US-08-915-972A-12	Sequence 12, Appl
c 701	11	39.3	36	2	US-08-585-684B-1002	Sequence 1002, Ap	774	10.8	38.6	18	2	US-09-177-909-12	Sequence 4, Appli
c 702	11	39.3	36	3	US-09-038-073-1002	Sequence 34, Appl	775	10.8	38.6	18	4	US-09-824-629-4	Sequence 11, Appl
c 703	11	39.3	36	4	US-09-897-425-34	Sequence 2320, Ap	c 776	10.8	38.6	20	1	US-08-564-002-12	Sequence 143, App
c 704	11	39.3	38	2	US-08-876-078-1	Sequence 1, Appli	c 777	10.8	38.6	20	3	US-09-166-186-143	Sequence 26, Appl
c 705	11	39.3	38	3	US-09-071-845-2320	Sequence 2320, Ap	c 778	10.8	38.6	20	3	US-09-166-186-143	Sequence 143, App
c 706	11	39.3	38	3	US-08-831-823-1	Sequence 1, Appli	c 779	10.8	38.6	20	3	US-09-313-932-143	Sequence 20, Appl
c 707	11	39.3	38	4	US-09-371-772B-7262	Sequence 7262, Ap	780	10.8	38.6	20	3	US-09-313-930-20	Sequence 53, Appl
c 708	11	39.3	38	4	US-09-371-772B-7679	Sequence 7679, Ap	781	10.8	38.6	20	3	US-09-467-842-53	Sequence 8, Appli
c 709	11	39.3	38	4	US-09-371-772B-7721	Sequence 7721, Ap	782	10.8	38.6	20	3	US-09-556-031-8	Sequence 91, Appl
c 710	11	39.3	38	4	US-09-371-772B-7860	Sequence 7860, Ap	c 783	10.8	38.6	20	4	US-09-780-175-91	Sequence 3426, Ap
c 711	11	39.3	38	4	US-09-371-772B-8356	Sequence 8356, Ap	784	10.8	38.6	20	4	US-09-198-452A-3426	Sequence 56, Appl
c 712	11	39.3	38	4	US-09-371-772B-8653	Sequence 8653, Ap	c 785	10.8	38.6	20	4	US-09-780-045-56	Sequence 1, Appli
c 713	11	39.3	38	4	US-09-371-772B-8708	Sequence 8708, Ap	c 786	10.8	38.6	20	4	US-07-702-163B-1	Sequence 1, Appli
c 714	11	39.3	38	4	US-09-371-772B-9047	Sequence 9047, Ap	c 787	10.8	38.6	21	1	US-08-060-884-1	Sequence 1, Appli
c 715	11	39.3	38	4	US-09-371-772B-10685	Sequence 10685, A	c 788	10.8	38.6	21	1	US-08-783-742-1	Sequence 1, Appli
c 716	11	39.3	38	4	US-09-371-772B-11069	Sequence 11069, A	c 789	10.8	38.6	21	1	US-08-783-660B-17	Sequence 4, Appli
c 717	11	39.3	38	4	US-09-371-772B-11319	Sequence 11319, A	c 790	10.8	38.6	21	3	US-08-793-109-4	Sequence 8249, Ap
c 718	11	39.3	38	4	US-09-371-772B-11468	Sequence 11468, A	c 791	10.8	38.6	21	3	US-09-422-978-8249	Sequence 71, Appl
c 719	11	39.3	38	4	US-09-371-772B-12425	Sequence 12425, A	c 792	10.8	38.6	21	4	US-08-934-386-63	Sequence 7, Appli
c 720	11	39.3	38	4	US-09-371-772B-12582	Sequence 12582, A	c 793	10.8	38.6	22	3	US-09-177-650-64	Sequence 64, Appl
c 721	11	39.3	38	4	US-09-155-989A-10	Sequence 10, Appl	c 794	10.8	38.6	24	4	US-09-177-650-64	Sequence 351, App
c 722	11	39.3	39	4	US-08-447-169A-227	Sequence 227, App	c 795	10.8	38.6	24	4	US-09-286-682A-10	Sequence 10, Appl
c 723	11	39.3	40	1	US-09-091-814-83	Sequence 83, Appl	c 796	10.8	38.6	24	4	US-09-866-108A-11047	Sequence 11047, A
c 724	11	39.3	40	3	US-09-672-609-45	Sequence 45, Appl	c 797	10.8	38.6	24	4	US-09-866-108A-11048	Sequence 11048, A
c 725	11	39.3	40	3	US-08-956-653A-29	Sequence 29, Appl	c 798	10.8	38.6	25	3	US-09-866-108A-11049	Sequence 11049, A
c 726	11	39.3	40	3	US-09-025-403A-45	Sequence 45, Appl	c 799	10.8	38.6	25	3	US-09-866-108A-11050	Sequence 21, Appl
c 727	11	39.3	40	4	US-09-789-556A-33	Sequence 33, Appl	c 800	10.8	38.6	25	3	US-08-584-040-5193	Sequence 5193, Ap
c 728	11	39.3	40	4	US-09-860-474-227	Sequence 227, App	c 801	10.8	38.6	25	4	US-08-584-040-5193	Sequence 5193, Ap
c 729	11	39.3	40	4	US-08-813-507-159	Sequence 159, App	c 802	10.8	38.6	25	4	US-08-584-040-5193	Sequence 5193, Ap
c 730	11	39.3	41	3	US-09-464-453-159	Sequence 159, App	c 803	10.8	38.6	25	4	US-08-584-040-5193	Sequence 5193, Ap
c 731	11	39.3	41	3	US-08-679-645-6	Sequence 6, Appli	c 804	10.8	38.6	26	4	US-09-116-676-21	Sequence 21, Appl
c 732	11	39.3	42	3	US-08-353-372A-5	Sequence 5, Appli	c 805	10.8	38.6	26	4	US-08-758-306-648	Sequence 648, App
c 733	11	39.3	44	2	US-08-629-039-8	Sequence 8, Appli	c 806	10.8	38.6	27	1	US-08-584-040-5193	Sequence 3502, Ap
c 734	11	39.3	45	2	US-08-283-067-55	Sequence 55, Appl	c 807	10.8	38.6	27	3	US-08-584-040-5193	Sequence 4921, Ap
c 735	11	39.3	46	1	US-08-271-880A-98	Sequence 98, Appl	c 808	10.8	38.6	27	3	US-08-584-040-5193	Sequence 5193, Ap
c 736	11	39.3	46	2	US-08-910-408-98	Sequence 98, Appl	c 809	10.8	38.6	27	3	US-08-584-040-5193	Sequence 5193, Ap
c 737	11	39.3	46	3	US-09-249-215-98	Sequence 16, Appl	c 810	10.8	38.6	27	3	US-08-584-040-5193	Sequence 5193, Ap
c 738	11	39.3	46	3	US-09-486-241-16	Sequence 23, Appl	c 811	10.8	38.6	27	4	US-08-639-763-20	Sequence 20, Appl
c 739	11	39.3	46	4	US-07-972-032-23	Sequence 56, Appl	c 812	10.8	38.6	28	1	US-09-171-755B-20	Sequence 20, Appl
c 740	11	39.3	47	1	US-08-175-155-56	Sequence 91, Appl	c 813	10.8	38.6	28	4	US-09-509-871-4	Sequence 4, Appli
c 741	11	39.3	47	1	US-08-477-509B-91	Sequence 37, Appl	c 814	10.8	38.6	28	4	US-08-048-164A-5	Sequence 6, Appli
c 742	11	39.3	47	1	US-08-642-255-37	Sequence 63, Appl	c 815	10.8	38.6	29	1	US-08-048-164A-7	Sequence 7, Appli
c 743	11	39.3	47	2	US-08-707-237A-63	Sequence 91, Appl	c 816	10.8	38.6	29	1	US-08-460-462-6	Sequence 6, Appli
c 744	11	39.3	47	3	US-09-444-731A-91	Sequence 91, Appl	c 817	10.8	38.6	29	1	US-08-460-462-6	Sequence 7, Appli
c 745	11	39.3	47	4	US-09-422-978-765	Sequence 765, App	c 818	10.8	38.6	29	1	US-08-460-457-6	Sequence 6, Appli
c 746	11	39.3	47	4	US-09-422-978-897	Sequence 897, App	c 819	10.8	38.6	29	1	US-08-460-457-6	Sequence 7, Appli
c 747	11	39.3	47	4	US-09-422-978-1339	Sequence 1339, Ap	c 820	10.8	38.6	29	1	US-08-460-457-6	Sequence 6, Appli
c 748	11	39.3	47	4	US-09-422-978-1876	Sequence 1876, Ap	c 821	10.8	38.6	29	1	US-08-460-457-6	Sequence 7, Appli
c 749	11	39.3	47	4	US-09-422-978-2358	Sequence 2358, Ap	c 822	10.8	38.6	29	2	US-08-460-455-6	Sequence 6, Appli
c 750	11	39.3	47	4	US-09-422-978-2756	Sequence 2756, Ap	c 823	10.8	38.6	29	2	US-08-460-455-6	Sequence 7, Appli
c 751	11	39.3	47	4	US-09-422-978-2787	Sequence 2787, Ap	c 824	10.8	38.6	29	2	US-08-330-394A-6	Sequence 6, Appli
c 752	11	39.3	47	4	US-09-422-978-3349	Sequence 3349, Ap	c 825	10.8	38.6	29	2	US-08-330-394A-7	Sequence 7, Appli
c 753	11	39.3	47	4	US-09-422-978-3547	Sequence 3547, Ap	c 826	10.8	38.6	29	4	US-09-291-874-12	Sequence 12, Appl
c 754	11	39.3	48	4	US-09-306-417-7	Sequence 7, Appli	c 827	10.8	38.6	29	4	US-09-344-783C-29	Sequence 29, Appl
c 755	11	39.3	48	2	US-09-438-954-7	Sequence 92, Appli	c 828	10.8	38.6	30	1	US-07-764-466-4	Sequence 4, Appli
c 756	11	39.3	49	2	US-08-417-210A-92	Sequence 92, Appl	c 829	10.8	38.6	30	1	US-09-608-706-2	Sequence 2, Appli
c 757	11	39.3	49	4	US-09-136-159A-92	Sequence 92, Appl	c 830	10.8	38.6	30	3		

C 831	10.8	31	1	US-08-073-384C-18	Sequence 18, Appl	904	10.8	38.6	40	4	US-09-636-595-19	Sequence 19, Appl
C 832	10.8	31	1	US-08-390-850-153	Sequence 153, App	905	10.8	38.6	40	4	US-09-694-862-3	Sequence 19, Appl
C 833	10.8	31	1	US-08-254-359A-18	Sequence 18, Appl	906	10.8	38.6	42	1	US-08-416-873-3	Sequence 3, Appl
C 834	10.8	31	1	US-08-373-124A-44	Sequence 44, Appl	907	10.8	38.6	42	2	US-09-035-241-3	Sequence 3, Appl
C 835	10.8	31	1	US-08-483-043-18	Sequence 18, Appl	c 908	10.8	38.6	42	3	US-08-952-973-19	Sequence 19, Appl
C 836	10.8	31	1	US-08-435-624-153	Sequence 153, App	909	10.8	38.6	42	3	US-08-990-140-7	Sequence 7, Appl
C 837	10.8	31	1	US-08-481-238-18	Sequence 18, Appl	910	10.8	38.6	42	3	US-09-546-238-7	Sequence 7, Appl
C 838	10.8	31	1	US-08-435-628-44	Sequence 44, Appl	c 911	10.8	38.6	42	4	US-09-578-634A-58	Sequence 58, Appl
C 839	10.8	31	2	US-08-471-066B-18	Sequence 18, Appl	912	10.8	38.6	42	5	PCT-US94-06197-3	Sequence 3, Appl
C 840	10.8	31	2	US-08-484-956-18	Sequence 18, Appl	913	10.8	38.6	44	3	US-08-864-473-67	Sequence 67, Appl
C 841	10.8	31	2	US-08-757-653-18	Sequence 18, Appl	914	10.8	38.6	44	3	US-09-440-523-67	Sequence 67, Appl
C 842	10.8	31	2	US-08-599-431-18	Sequence 18, Appl	915	10.8	38.6	44	4	US-09-360-376-41	Sequence 41, Appl
C 843	10.8	31	2	US-08-956-047-3	Sequence 3, Appl	916	10.8	38.6	44	4	US-09-918-156-67	Sequence 67, Appl
C 844	10.8	31	2	US-08-956-047-37	Sequence 37, Appl	c 917	10.8	38.6	45	4	US-09-518-914-13	Sequence 13, Appl
C 845	10.8	31	2	US-08-756-386-18	Sequence 18, Appl	918	10.8	38.6	45	4	US-09-478-189-160	Sequence 160, App
C 846	10.8	31	2	US-08-823-516-18	Sequence 18, Appl	919	10.8	38.6	45	4	US-09-636-215-790	Sequence 790, App
C 847	10.8	31	3	US-08-682-853A-18	Sequence 18, Appl	c 920	10.8	38.6	45	4	US-09-685-166A-790	Sequence 790, App
C 848	10.8	31	3	US-08-759-038-18	Sequence 18, Appl	c 921	10.8	38.6	45	4	US-09-679-426-790	Sequence 790, App
C 849	10.8	31	3	US-08-758-344-18	Sequence 18, Appl	922	10.8	38.6	46	1	US-08-271-880A-91	Sequence 91, Appl
C 850	10.8	31	3	US-09-350-309-18	Sequence 18, Appl	923	10.8	38.6	46	1	US-08-271-880A-93	Sequence 93, Appl
C 851	10.8	31	3	US-08-520-946-18	Sequence 18, Appl	924	10.8	38.6	46	1	US-08-271-880A-114	Sequence 114, App
C 852	10.8	31	4	US-08-684-938-18	Sequence 18, Appl	925	10.8	38.6	46	1	US-08-271-880A-116	Sequence 116, App
C 853	10.8	31	4	US-09-308-825A-18	Sequence 18, Appl	926	10.8	38.6	46	2	US-08-910-408-91	Sequence 91, Appl
C 854	10.8	31	4	US-09-097-055B-80	Sequence 80, Appl	927	10.8	38.6	46	2	US-08-910-408-93	Sequence 93, Appl
C 855	10.8	31	4	US-09-655-378A-18	Sequence 18, Appl	928	10.8	38.6	46	2	US-08-910-408-114	Sequence 114, App
C 856	10.8	31	4	US-09-940-244-18	Sequence 18, Appl	929	10.8	38.6	46	2	US-08-910-408-116	Sequence 116, App
C 857	10.8	31	4	US-09-333-145-18	Sequence 18, Appl	930	10.8	38.6	46	3	US-09-249-215-91	Sequence 91, Appl
C 858	10.8	31	4	US-08-246-704-4	Sequence 4, Appl	931	10.8	38.6	46	3	US-09-249-215-114	Sequence 93, Appl
C 859	10.8	32	3	US-09-014-416-21	Sequence 21, Appl	932	10.8	38.6	46	3	US-09-249-215-116	Sequence 114, App
C 860	10.8	32	4	US-09-206-551-3	Sequence 3, Appl	933	10.8	38.6	46	3	US-09-199-737-40	Sequence 116, App
C 861	10.8	33	1	US-08-073-807A-13	Sequence 13, Appl	c 934	10.8	38.6	46	3	US-09-302-620B-72	Sequence 40, Appl
C 862	10.8	34	3	US-09-038-909-8	Sequence 8, Appl	935	10.8	38.6	46	3	US-09-474-432B-72	Sequence 40, Appl
C 863	10.8	34	4	US-09-762-428A-8	Sequence 8, Appl	936	10.8	38.6	46	3	US-09-474-432B-72	Sequence 72, Appl
C 864	10.8	34	4	US-09-543-141-8	Sequence 8, Appl	937	10.8	38.6	47	4	US-09-422-978-1137	Sequence 1137, Ap
C 865	10.8	34	4	US-09-254-180C-12	Sequence 12, Appl	938	10.8	38.6	47	4	US-09-422-978-1216	Sequence 1216, Ap
C 866	10.8	36	1	US-08-095-726-40	Sequence 40, Appl	939	10.8	38.6	47	4	US-09-422-978-1582	Sequence 1582, Ap
C 867	10.8	36	1	US-08-096-043-37	Sequence 37, Appl	c 940	10.8	38.6	47	4	US-09-422-978-1622	Sequence 1622, Ap
C 868	10.8	36	1	US-08-093-577-33	Sequence 33, Appl	c 941	10.8	38.6	47	4	US-09-422-978-1701	Sequence 1701, Ap
C 869	10.8	36	1	US-08-331-004A-7	Sequence 7, Appl	c 942	10.8	38.6	47	4	US-09-422-978-1701	Sequence 1701, Ap
C 870	10.8	36	1	US-08-411-796-364	Sequence 364, App	c 943	10.8	38.6	47	4	US-09-422-978-1961	Sequence 1961, Ap
C 871	10.8	36	1	US-08-096-623A-45	Sequence 45, Appl	c 944	10.8	38.6	47	4	US-09-422-978-3440	Sequence 3440, Ap
C 872	10.8	36	3	US-08-471-039-364	Sequence 364, App	c 945	10.8	38.6	47	4	US-09-422-978-3573	Sequence 3573, Ap
C 873	10.8	36	4	US-08-593-390-364	Sequence 364, App	c 946	10.8	38.6	47	4	US-09-422-978-3772	Sequence 3772, Ap
C 874	10.8	36	5	PCT-US93-11198-364	Sequence 364, App	c 947	10.8	38.6	47	4	US-09-422-978-3785	Sequence 3785, Ap
C 875	10.8	36	5	PCT-US95-13937A-7	Sequence 7, Appl	c 948	10.8	38.6	48	3	US-09-453-702B-216	Sequence 216, App
C 876	10.8	37	3	US-08-995-156A-14	Sequence 14, Appl	949	10.8	38.6	48	4	US-09-301-511A-34	Sequence 34, Appl
C 877	10.8	37	3	US-09-419-281-14	Sequence 14, Appl	950	10.8	38.6	48	4	US-09-476-387-72	Sequence 72, Appl
C 878	10.8	37	6	5310667-23	Patent No. 5310667	951	10.8	38.6	48	2	US-09-002-177-21	Sequence 21, Appl
C 879	10.8	38	1	US-08-373-124A-221	Sequence 221, App	952	10.8	38.6	49	3	US-09-374-584-21	Sequence 21, Appl
C 880	10.8	38	1	US-08-373-124A-1354	Sequence 1354, Ap	953	10.8	38.6	49	4	US-09-538-709-1085	Sequence 1085, Ap
C 881	10.8	38	1	US-08-591-070A-18	Sequence 18, Appl	c 954	10.8	38.6	50	2	US-08-556-424-5	Sequence 5, Appl
C 882	10.8	38	1	US-08-435-628-221	Sequence 221, App	c 955	10.8	38.6	50	3	US-09-263-914-5	Sequence 5, Appl
C 883	10.8	38	1	US-08-435-628-1354	Sequence 1354, App	956	10.8	38.6	50	4	US-09-613-263-5	Sequence 5, Appl
C 884	10.8	38	2	US-08-927-855-18	Sequence 18, Appl	957	10.8	38.6	50	4	US-09-613-263-6	Sequence 6, Appl
C 885	10.8	38	4	US-09-371-772B-9234	Sequence 9234, Ap	958	10.8	38.6	50	4	US-09-613-263-9	Sequence 9, Appl
C 886	10.8	38	4	US-09-371-772B-9947	Sequence 9947, Ap	959	10.8	38.6	50	4	US-09-613-263-10	Sequence 10, Appl
C 887	10.8	38	4	US-09-371-772B-10643	Sequence 10643, A	960	10.8	38.6	50	4	US-09-554-929-8	Sequence 8, Appl
C 888	10.8	38	4	US-09-371-772B-10896	Sequence 10896, A	c 961	10.8	38.6	50	4	US-09-554-929-187	Sequence 187, App
C 889	10.8	38	4	US-09-371-772B-11647	Sequence 11647, A	962	10.8	38.6	50	4	US-08-956-171E-1789	Sequence 1789, Ap
C 890	10.8	38	4	US-09-371-772B-11914	Sequence 11914, A	963	10.8	38.6	50	4	US-09-909-496-5	Sequence 5, Appl
C 891	10.8	38	4	US-09-371-772B-12046	Sequence 12046, A	964	10.8	38.6	50	4	US-09-909-496-6	Sequence 6, Appl
C 892	10.8	38	4	US-09-371-772B-12221	Sequence 12221, A	965	10.8	38.6	50	4	US-09-909-496-7	Sequence 7, Appl
C 893	10.8	38	4	US-09-371-772B-12417	Sequence 12417, A	966	10.8	38.6	50	4	US-09-909-496-11	Sequence 11, Appl
C 894	10.8	38	4	US-09-371-772B-12754	Sequence 12754, A	967	10.8	38.6	50	4	US-09-270-767-35222	Sequence 25222, A
C 895	10.8	38	4	US-09-371-772B-13756	Sequence 13756, A	968	10.8	38.6	50	4	US-08-781-986A-1789	Sequence 1789, Ap
C 896	10.8	38	4	US-09-968-255-15	Sequence 15, Appl	969	10.8	38.6	50	4	US-08-513-999C-15243	Sequence 15243, A
C 897	10.8	39	2	US-08-570-155-10	Sequence 10, Appl	970	10.6	37.9	17	1	US-08-373-124A-558	Sequence 558, App
C 898	10.8	39	5	PCT-US95-02861-10	Sequence 10, Appl	971	10.6	37.9	17	1	US-08-435-628-558	Sequence 558, App
C 899	10.8	40	3	US-09-626-929-19	Sequence 19, Appl	972	10.6	37.9	17	4	US-09-866-108A-8927	Sequence 8927, Ap
C 900	10.8	40	3	US-09-484-850-19	Sequence 19, Appl	c 973	10.6	37.9	18	3	US-09-102-528-17	Sequence 17, Appl
C 901	10.8	40	3	US-09-408-392-19	Sequence 19, Appl	974	10.6	37.9	18	4	US-09-658-679A-5	Sequence 5, Appl
C 902	10.8	40	4	US-09-626-930-19	Sequence 19, Appl	975	10.6	37.9	18	4	US-09-422-978-4437	Sequence 4437, Ap
C 903	10.8	40	4	US-09-626-930-19	Sequence 19, Appl	c 976	10.6	37.9	18	4	US-09-422-978-6382	Sequence 6382, Ap



US-09-547-757-1

Query Match 100.0%; Score 28; DB 3; Length 47;  
Best Local Similarity 100.0%; Pred. No. 0.00022;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTTATCAGGCGAGTACCACAA 28  
Db 36 GCAAGCACCTTATCAGGCGAGTACCACAA 9

## RESULT 4

US-08-738-928-3

; Sequence 3, Application US/08738928  
; Patent No. 5837442  
; GENERAL INFORMATION:  
; APPLICANT: Tsang, Sue Y.  
; TITLE OF INVENTION: Oligonucleotide Primers for Amplifying  
; TITLE OF INVENTION: HCV Nucleic Acid  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hoffmann-La Roche Inc.  
; STREET: 340 Kingsland Street  
; CITY: Nutley  
; STATE: NJ  
; COUNTRY: U.S.A.  
; ZIP: 07110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/738,928  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Petry, Douglas A.  
; REGISTRATION NUMBER: 35,321  
; REFERENCE/DOCKET NUMBER: 9263  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 814-2974  
; TELEFAX: (510) 814-2977  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 27 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)

US-08-738-928-3

Query Match 96.4%; Score 27; DB 2; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.00059;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTTATCAGGCGAGTACCACA 27  
Db 1 GCAAGCACCTTATCAGGCGAGTACCACA 27

## RESULT 5

US-09-493-353-5

; Sequence 5, Application US/09493353  
; Patent No. 6638714  
; GENERAL INFORMATION:  
; APPLICANT: Johnson & Johnson  
; APPLICANT: Linnen, J.M.  
; TITLE OF INVENTION: OLIGONUCLEOTIDE PRIMERS FOR EFFICIENT  
; TITLE OF INVENTION: DETECTION OF HEPATITIS C VIRUS (HCV) AND METHODS OF USE  
; TITLE OF INVENTION: THEROF  
; FILE REFERENCE: 2094/1E286-US1

; CURRENT APPLICATION NUMBER: US/09/493,353  
; CURRENT FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/118,497  
; PRIOR FILING DATE: 1999-02-03  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 27  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer  
US-09-493-353-5

Query Match 96.4%; Score 27; DB 4; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.00059;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTTATCAGGCGAGTACCACA 27  
Db 1 GCAAGCACCTTATCAGGCGAGTACCACA 27

## RESULT 6

US-08-474-700B-12  
; Sequence 12, Application US/08474700B  
; Patent No. 6001990  
; GENERAL INFORMATION:  
; APPLICANT: Wands, Jack  
; APPLICANT: Wakita, Takaji  
; APPLICANT: Moradpour, Darius  
; TITLE OF INVENTION: ANTISENSE INHIBITION OF HEPATITIS C  
; TITLE OF INVENTION: VIRUS  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 502 or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/474,700B  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/240,382  
; FILING DATE: 10 May 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fraser, Janis K.  
; REGISTRATION NUMBER: 34,819  
; REFERENCE/DOCKET NUMBER: 00786/279001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 28  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

US-08-474-700B-12

Query Match 85.7%; Score 24; DB 3; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.016;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTTATCAGGCGAGTACC 24

Db 5 GCAAGCACCTATCAGGAGTACC 28  
|||||  
PCT-US95-05812-12  
RESULT 7  
PCT-US95-05812-12  
Sequence 12, Application PC/TUS9505812  
GENERAL INFORMATION:  
APPLICANT: Wakita, Takaji  
APPLICANT: Wands, Jack  
TITLE OF INVENTION: ANTISENSE INHIBITION OF  
TITLE OF INVENTION: HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/05812  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/240,382  
FILING DATE: 10 May 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00786/221001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
PCT-US95-05812-12  
Query Match 85.7%; Score 24; DB 5; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.016;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCAAGCACCTATCAGGAGTACC 24  
Db 5 GCAAGCACCTATCAGGAGTACC 28  
|||||  
RESULT 8  
US-08-438-639-51  
Sequence 51, Application US/08438639  
Patent No. 5712383  
GENERAL INFORMATION:  
APPLICANT: Sheridan, Patrick  
APPLICANT: Chang, Chu-An  
APPLICANT: Running, Joyce  
APPLICANT: Urdea, Michael S.  
TITLE OF INVENTION: PROBES FOR IMMOBILIZING NUCLEIC ACID  
TITLE OF INVENTION: PROBES ON POLYSTYRENE SURFACES  
NUMBER OF SEQUENCES: 70  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CHIRON CORPORATION - R440  
STREET: P.O. Box 8097  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94662-8097  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/813,338A  
FILING DATE: 23-DEC-1991  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Kenneth, M.  
REGISTRATION NUMBER: 34,174  
REFERENCE/DOCKET NUMBER: 0232.001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2719  
TELEFAX: (510) 655-3542  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-438-639-51  
Query Match 85.7%; Score 24; DB 1; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCAAGCACCTATCAGGAGTACC 24  
Db 10 GCAAGCACCTATCAGGAGTACC 33  
|||||  
RESULT 9  
US-07-813-338A-51  
Sequence 51, Application US/07813338A  
Patent No. 5747244  
GENERAL INFORMATION:  
APPLICANT: Sheridan, Patrick  
APPLICANT: Chang, Chu-An  
APPLICANT: Running, Joyce  
APPLICANT: Urdea, Michael S.  
TITLE OF INVENTION: PROCESS FOR IMMOBILIZING NUCLEIC ACID  
TITLE OF INVENTION: PROBES ON POLYSTYRENE SURFACES  
NUMBER OF SEQUENCES: 70  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CHIRON CORPORATION - R440  
STREET: P.O. Box 8097  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94662-8097  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/813,338A  
FILING DATE: 23-DEC-1991  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Kenneth, M.  
REGISTRATION NUMBER: 34,174  
REFERENCE/DOCKET NUMBER: 0232.001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2719  
TELEFAX: (510) 655-3542  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-438-639-51

TELEPHONE: (510) 601-2719  
TELEFAX: (510) 655-3542  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-07-813-338A-51

Query Match 85.7%; Score 24; DB 1; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTTATCAGGCGATACC 24  
Db 10 GCAAGCACCTTATCAGGCGATACC 33

## RESULT 10

US-08-470-124-61  
Sequence 61, Application US/08470124  
Patent No. 5849481

## GENERAL INFORMATION:

APPLICANT: Urdea, Michael S.  
APPLICANT: Horn, Thomas  
APPLICANT: Chang, Chu-An  
APPLICANT: Warner, Brian  
APPLICANT: Fultz, Timothy J.  
TITLE OF INVENTION: LARGE COMB-TYPE BRANCHED  
POLYNUCLEOTIDES  
NUMBER OF SEQUENCES: 87  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster  
STREET: 545 Middlefield Road, Suite 200  
CITY: Menlo Park  
STATE: California  
COUNTRY: USA  
ZIP: 94025

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/470,124  
FILING DATE:

## CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/813,588

FILING DATE: 23 December 1991

## ATTORNEY/AGENT INFORMATION:

NAME: Ciotti, Thomas E.

REGISTRATION NUMBER: 21,013

REFERENCE/DOCKET NUMBER: 22300-20104.20

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-813-5600

TELEFAX: 415-327-2951

TELEX: 706141

INFORMATION FOR SEQ ID NO: 61:

SEQUENCE CHARACTERISTICS:

LENGTH: 33 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-470-124-61

Query Match 85.7%; Score 24; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTTATCAGGCGATACC 24

Db 10 GCAAGCACCTTATCAGGCGATACC 33

## RESULT 11

US-08-441-971-127

Sequence 127, Application US/08441971

Patent No. 6071693

## GENERAL INFORMATION:

APPLICANT: Tai-An Cha

TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR

DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 147

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Avenue

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02210

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch

COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS Version 3.3

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/441,971

FILING DATE: 16-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/221,653

FILING DATE:

APPLICATION NUMBER: US/07/881,528

FILING DATE:

APPLICATION NUMBER: 07/697,326

FILING DATE: 8 May 1991

## ATTORNEY/AGENT INFORMATION:

NAME: Janiuk, Anthony J.

REGISTRATION NUMBER: 29,809

REFERENCE/DOCKET NUMBER: C0772/7000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 720-3500

TELEFAX: (617) 720-2441

TELEX: EZEKIEL

INFORMATION FOR SEQ ID NO: 127:

SEQUENCE CHARACTERISTICS:

LENGTH: 33 nucleotides

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-441-971-127

Query Match 85.7%; Score 24; DB 3; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTTATCAGGCGATACC 24

Db 10 GCAAGCACCTTATCAGGCGATACC 33

## RESULT 12

US-08-221-653-127

Sequence 127, Application US/08221653

Patent No. 6190864

## GENERAL INFORMATION:

APPLICANT: Tai-An Cha

TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR

DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 147

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 127:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-221-653-127

Query Match 85.7%; Score 24; DB 3; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 24; Conservative 0; Mismatches 0; Indels 0;

QY 1 GCAAGCACCTATCAGGCAGTACC 24  
DB 10 GCAAGCACCTATCAGGCAGTACC 33

RESULT 13  
US-08-442-144A-127  
Sequence 127, Application US/08442144A  
Patent No. 6214583  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
APPLICANT: Eileen Beall  
APPLICANT: Bruce Irvine  
APPLICANT: Janice Kolberg  
APPLICANT: Michael S. Urdea  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 Inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows NT  
SOFTWARE: Microsoft Word 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/442,144A  
FILING DATE: MAY 16, 1995

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/221,653  
FILING DATE: APRIL 1, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Doreen Yacko Trujillo  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CHIR-0121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
TELEX:  
INFORMATION FOR SEQ ID NO: 127:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 Nucleotides  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: DNA  
US-08-442-144A-127

Query Match 85.7%; Score 24; DB 3; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 24; Conservative 0; Mismatches 0; Indels 0;

QY 1 GCAAGCACCTATCAGGCAGTACC 24  
DB 10 GCAAGCACCTATCAGGCAGTACC 33

RESULT 14  
US-08-441-970-127  
Sequence 127, Application US/08441970  
Patent No. 6297370  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 127:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single



```
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-441-970-127

Query Match      85.7%; Score 24; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTTATCAGGAGTACC 24
Db 10 GCAAGCACCTTATCAGGAGTACC 33

RESULT 15
US-09-493-353-6
; Sequence 6, Application US/09493353
; Patent No. 6638714
; GENERAL INFORMATION:
; APPLICANT: Johnson & Johnson
; APPLICANT: Linnen, J.M.
; APPLICANT: Gorman, K.M.
; TITLE OF INVENTION: OLIGONUCLEOTIDE PRIMERS FOR EFFICIENT
; DETECTION OF HEPATITIS C VIRUS (HCV) AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 2094/1E286-US1
; CURRENT APPLICATION NUMBER: US/09/493,353
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/118,497
; PRIOR FILING DATE: 1999-02-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
US-09-493-353-6

Query Match      78.6%; Score 22; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTTATCAGGAGTACC 22
Db 6 GCAAGCACCTTATCAGGAGTACC 27

RESULT 16
PCT-US93-00928-1
; Sequence 1, Application PC/TUS9300928
; GENERAL INFORMATION:
; APPLICANT: TASSOPOULOS, NIC C.
; APPLICANT: HATZAKIS, ANGELOS E.
; APPLICANT: KUHN, MARY C.
; APPLICANT: TROONEN, HUGO
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS REAGENTS AND METH
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: ONE ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00928
; FILING DATE: 19930203
```

```
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5132.PC-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-937-9556
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US93-00928-1

Query Match      78.6%; Score 22; DB 5; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTTATCAGGAGTACC 22
Db 6 GCAAGCACCTTATCAGGAGTACC 27

RESULT 17
US-09-078-290A-10
; Sequence 10, Application US/09078290A
; Patent No. 6048696
; GENERAL INFORMATION:
; APPLICANT: Hoffman, Leslie M.
; APPLICANT: Hawkins, Gregory A.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING NUCLEIC ACID MOLECULES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/078,290A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Baker, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 310307.90100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5709
; TELEFAX: (414) 271-3552
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Oligonucleotide
US-09-078-290A-10

Query Match      75.0%; Score 21; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCCTATCAGGAGTACCACAA 28
; FILING DATE: 19930203
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Db      1  CCCTATCAGGCAGTACCACAA 21

RESULT 18
US-08-938-033-4
; Sequence 4, Application US/08938033
; Patent No. 6172046
; GENERAL INFORMATION:
; APPLICANT: Albrecht, Janice K.
; TITLE OF INVENTION: Combination Therapy For Eradicating
; Detectable HCV-RNA In Patients
; Having Chronic Hepatitis C Infection
;
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: 7.5.3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/938,033
; FILING DATE: 21-Sep-1997
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoffman, Thomas D.
; REGISTRATION NUMBER: 28,221
; REFERENCE/DOCKET NUMBER: IN0783-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-298-5037
; TELEFAX: 908-298-5388
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-938-033-4
;
; Query Match 75.0%; Score 21; DB 3; Length 21;
; Best Local Similarity 100.0%; Pred. No. 0.42;
; Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8  CCCTATCAGGCAGTACCACAA 28
Db      1  CCCTATCAGGCAGTACCACAA 21

RESULT 19
US-08-397-220B-17
; Sequence 17, Application US/08397220B
; Patent No. 6284458
; GENERAL INFORMATION:
; APPLICANT: Anderson et al.
; TITLE OF INVENTION: Compositions And Methods For Treatment
; Of Hepatitis C Virus-Associated Diseases
;
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM 486
;
; Query Match 75.0%; Score 21; DB 3; Length 21;
; Best Local Similarity 100.0%; Pred. No. 0.42;
; Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8  CCCTATCAGGCAGTACCACAA 28
Db      1  CCCTATCAGGCAGTACCACAA 21

RESULT 20
US-08-650-093C-17
; Sequence 17, Application US/08650093C
; Patent No. 6391542
; GENERAL INFORMATION:
; APPLICANT: Kevin P. Anderson et al.
; TITLE OF INVENTION: Compositions And Methods For Treatment Of
; Hepatitis C Virus-Associated Diseases
;
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LICATA & TYRRELL P.C.
; STREET: 66 E. Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WORDPERFECT 6.1 for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/650,093C
; FILING DATE: 17-May-1996
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/452,841
; FILING DATE: May 30, 1995
; APPLICATION NUMBER: 08/397,220
; FILING DATE: March 9, 1995
; APPLICATION NUMBER: 07/945,289
; FILING DATE: September 10, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,220B
; FILING DATE: 09-Mar-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/01293
; FILING DATE: 10-Sep-93
; APPLICATION NUMBER: JP 5-87195
; FILING DATE: 14-Apr-93
; APPLICATION NUMBER: 07/945,289
; FILING DATE: 10-Sep-92
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: nucleic acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-08-397-220B-17
;
; Query Match 75.0%; Score 21; DB 3; Length 21;
; Best Local Similarity 100.0%; Pred. No. 0.42;
; Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
;
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-08-650-093C-17

Query Match 75.0%; Score 21; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCCTATCAGGCAGTACCACAA 28
Db 1 CCCTATCAGGCAGTACCACAA 21

RESULT 21
US-08-823-895A-17
; Sequence 17, Application US/08823895A
; Patent No. 6433159
; GENERAL INFORMATION:
; APPLICANT: Kevin P. Anderson
; TITLE OF INVENTION: Compositions And Methods For
; TREATMENT OF HEPATITIS C VIRUS-ASSOCIATED DISEASES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: 66 E. Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM 486
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,895A
; FILING DATE: March 17, 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/453,085
; FILING DATE: May 30, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/945,289
; FILING DATE: September 10, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 810-1454
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: Nucleic
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
US-08-823-895A-17

Query Match 75.0%; Score 21; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.42;
```

```
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCCTATCAGGCAGTACCACAA 28
Db 1 CCCTATCAGGCAGTACCACAA 21

RESULT 22
US-09-311-487-4
; Sequence 4, Application US/09311487
; Patent No. 6472373
; GENERAL INFORMATION:
; APPLICANT: Albrecht, Janice K.
; TITLE OF INVENTION: Combination Therapy For Eradicating
; TITLE OF INVENTION: Detectable HCV-RNA In Patients
; TITLE OF INVENTION: Having Chronic Hepatitis C Infection
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: 7.5.3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/311,487
; FILING DATE: May 13, 1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoffman, Thomas D.
; REGISTRATION NUMBER: 28,221
; REFERENCE/DOCKET NUMBER: IN0878K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-298-5387
; TELEFAX: 908-298-5388
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
US-09-311-487-4

Query Match 75.0%; Score 21; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCCTATCAGGCAGTACCACAA 28
Db 1 CCCTATCAGGCAGTACCACAA 21

RESULT 23
PCT-US94-05407-13
; Sequence 13, Application PC/TUS9405407
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: "NUCLEIC ACID TAGGED IMMUNOASSAY"
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: Suite 1200, 127 Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05407
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/061,694
; FILING DATE: 13-MAY-1993
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
PCT-US94-05407-13

Query Match 75.0%; Score 21; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCTATCAGCAGTACACAA 28
Db 1 CCCTATCAGCAGTACACAA 21

RESULT 24
US-08-356-287-25
; Sequence 25, Application US/08356287
; Patent No. 5686272
; GENERAL INFORMATION:
; APPLICANT: Ronald L. Marshall
; APPLICANT: John J. Carrino
; APPLICANT: Joann Sustachek
; TITLE OF INVENTION: AMPLIFICATION OF RNA SEQUENCES USING
; TITLE OF INVENTION: THE LIGASE CHAIN REACTION
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,287
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/891,543
; FILING DATE: 29 MAY 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul D. Vaeger
; REGISTRATION NUMBER: 37,477
; REFERENCE/DOCKET NUMBER: 5172.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-2341
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid (synthetic DNA)
US-08-356-287-25

Query Match 75.0%; Score 21; DB 1; Length 23;
```

```

Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCTATCAGGCAGT 21
Db 3 GCAAGCACCTATCAGGCAGT 23

RESULT 25
PCT-US93-04863-25
; Sequence 25, Application PC/TUS9304863
; GENERAL INFORMATION:
; APPLICANT: Ronald L. Marshall
; APPLICANT: John J. Carrino
; APPLICANT: Joann C. Sustachek
; APPLICANT: ABBOTT LABORATORIES
; TITLE OF INVENTION: AMPLIFICATION OF RNA SEQUENCES
; TITLE OF INVENTION: USING THE LIGASE CHAIN REACTION
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: One Abbott Park Road
; CITY: Abbott Park
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/04863
; FILING DATE: 19930524
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/891,543
; FILING DATE: 29 MAY 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas D. Brainard
; REGISTRATION NUMBER: 32,459
; REFERENCE/DOCKET NUMBER: 5172.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-4884
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid (synthetic DNA)
PCT-US93-04863-25

Query Match 75.0%; Score 21; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCTATCAGGCAGT 21
Db 3 GCAAGCACCTATCAGGCAGT 23

RESULT 26
US-08-240-547-18
; Sequence 18, Application US/08240547
; Patent No. 5527669
; GENERAL INFORMATION:
; APPLICANT: Resnick, Robert M.
; APPLICANT: Young, Karen K.Y.
; TITLE OF INVENTION: Primers and Probes for Detection of
; TITLE OF INVENTION: Hepatitis C and No. 5527669el Variants
; NUMBER OF SEQUENCES: 43
```

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/240,547
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/918,844
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sias Ph.D., Stacey R.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER: 8586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2863
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-240-547-18

Query Match 75.0%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCCCTATCAGGCAGT 21
Db 4 GCAAGCACCCCTATCAGGCAGT 24

RESULT 28
US-08-332-616A-8
; Sequence 8, Application US/08332616A
; Patent No. 5620852
; GENERAL INFORMATION:
; APPLICANT: LIN, LILY
; APPLICANT: CIMINO, GEORGE
; APPLICANT: ZHU, YU SHENG
; TITLE OF INVENTION: NUCLEIC ACID PREPARATION METHODS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,616A
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,545
; FILING DATE: 19-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: HRI-01202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-332-616A-8

Query Match 75.0%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCCCTATCAGGCAGT 21
Db 4 GCAAGCACCCCTATCAGGCAGT 24

RESULT 29
US-08-317-220-8
```

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/240,547
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/918,844
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sias Ph.D., Stacey R.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER: 8586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2863
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-240-547-18

Query Match 75.0%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCCCTATCAGGCAGT 21
Db 4 GCAAGCACCCCTATCAGGCAGT 24

RESULT 27
US-08-449-050-16
; Sequence 16, Application US/08449050
; Patent No. 5561058
; GENERAL INFORMATION:
; APPLICANT: Gelfand, David
; APPLICANT: Myers, Thomas
; APPLICANT: Sigua, Christopher
; TITLE OF INVENTION: Reagents and Methods for Coupled High
; TITLE OF INVENTION: Temperature Reverse Transcription and Polymerase Chain
; TITLE OF INVENTION: Reactions
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,050
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 16:
```

; Sequence 8, Application US/08317220  
; Patent No. 5654179  
; GENERAL INFORMATION:  
; APPLICANT: LIN, LILY  
; TITLE OF INVENTION: NUCLEIC ACID PREPARATION METHODS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PETER G. CARROLL  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/317,220  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/044,649  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,545  
; FILING DATE: 19-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/614,921  
; FILING DATE: 14-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CARROLL, PETER G.  
; REGISTRATION NUMBER: 32,837  
; REFERENCE/DOCKET NUMBER: HRI-00542  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 24 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-317-220-8

Query Match 75.0%; Score 21; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.43;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCAGT 21  
Db 4 GCAAGCACCTATCAGGCAGT 24

RESULT 30  
US-08-675-153-8  
; Sequence 8, Application US/08675153  
; Patent No. 5677124  
; GENERAL INFORMATION:  
; APPLICANT: DuBois, Dwight  
; APPLICANT: Winkler, Matthew  
; APPLICANT: Pasloske, Brittan L.  
; TITLE OF INVENTION: RIBONUCLEASE RESISTANT VIRAL  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America

; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/675,153  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wilson, Mark B.  
; REGISTRATION NUMBER: 37,259  
; REFERENCE/DOCKET NUMBER: AMBI:026  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 24 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-675-153-8

Query Match 75.0%; Score 21; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.43;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCAGT 21  
Db 4 GCAAGCACCTATCAGGCAGT 24

RESULT 31  
US-08-244-116B-51/c  
; Sequence 51, Application US/08244116B  
; Patent No. 5763159  
; GENERAL INFORMATION:  
; APPLICANT: Simmonds, Peter  
; APPLICANT: Chan, Shiu-Wan  
; APPLICANT: Yap, Peng L.  
; TITLE OF INVENTION: Hepatitis-C Virus Testing  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bell, Seltzer, Park & Gibson, P.A.  
; STREET: 1211 East Morehead Street  
; CITY: Charlotte  
; STATE: No. 5763159th Carolina  
; COUNTRY: United States  
; ZIP: 28234

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/244,116B  
; FILING DATE: 15-JUL-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB92/02143  
; FILING DATE: 20-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sibley, Kenneth D.  
; REGISTRATION NUMBER: 31,665  
; REFERENCE/DOCKET NUMBER: 1749-125  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 704-377-1561  
; TELEFAX: 704-334-2014  
; INFORMATION FOR SEQ ID NO: 51:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 24 base pairs

```
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA
; DESCRIPTION: oligonucleotide"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Hepatitis-C virus
US-08-244-116B-51

Query Match          75.0%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCAAGCACCTATCAGGCAGT 21
Db      1 GCAAGCACCTATCAGGCAGT 1

RESULT 32
US-08-738-928-5
; Sequence 5, Application US/08738928
; Patent No. 5637442
; GENERAL INFORMATION:
; APPLICANT: Teang, Sue Y.
; TITLE OF INVENTION: Oligonucleotide Primers for Amplifying
; DESCRIPTION: HCV Nucleic Acid
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingeland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/738,928
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 9263
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-738-928-5

Query Match          75.0%; Score 21; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCAAGCACCTATCAGGCAGT 21
Db      4 GCAAGCACCTATCAGGCAGT 24

RESULT 33
US-08-841-252-8
; Sequence 8, Application US/08841252
; Patent No. 5919625
; GENERAL INFORMATION:
; APPLICANT: DUBOIS, DWIGHT
; APPLICANT: WINKLER, MATTHEW
; APPLICANT: PASLOSKE, BRITTAN L.
; TITLE OF INVENTION: RIBONUCLEASE RESISTANT VIRAL RNA
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/841,252
; FILING DATE: 29-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 5,677,124
; FILING DATE: 03-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARK B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: AMB1:026--1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-300
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-841-252-8

Query Match          75.0%; Score 21; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCAAGCACCTATCAGGCAGT 21
Db      4 GCAAGCACCTATCAGGCAGT 24

RESULT 34
US-08-881-571-8
; Sequence 8, Application US/08881571
; Patent No. 5939262
; GENERAL INFORMATION:
; APPLICANT: Pasloske, Brittan L.
; APPLICANT: DuBois, Dwight
; APPLICANT: Brown, David
; APPLICANT: Winkler, Matthew
; TITLE OF INVENTION: RIBONUCLEASE RESISTANT RNA PREPARATION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

Wed Nov 24 08:46:08 2004

```
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  FILING DATE: US/08/881,571
  FILING DATE: Concurrently Herewith
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/675,153
    FILING DATE: 03-JUL-1996
  APPLICATION DATA:
    APPLICATION NUMBER: US 60/021,145
    FILING DATE: 03-JUL-1996
  ATTORNEY/AGENT INFORMATION:
    NAME: Wilson, Mark B.
    REGISTRATION NUMBER: 37,259
    REFERENCE/DOCKET NUMBER: AMBI:033
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: 512/418-3000
      TELEFAX: 512/474-7577
    INFORMATION FOR SEQ ID NO: 8:
      SEQUENCE CHARACTERISTICS:
        LENGTH: 24 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: single
        TOPOLOGY: linear
      US-08-881-571-8

Query Match      75.0%; Score 21; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCCCTATCAGGCAGT 21
Db 4 GCAAGCACCCCTATCAGGCAGT 24

RESULT 35
US-09-282-054-8
; Sequence 8, Application US/09282054
; Patent No. 6214982
; GENERAL INFORMATION:
; APPLICANT: Pasloske, Brittan L.
; APPLICANT: DuBois, Dwight
; APPLICANT: Brown, David
; APPLICANT: Winkler, Matthew
; TITLE OF INVENTION: RIBONUCLEASE RESISTANT RNA PREPARATION
; TITLE OF INVENTION: AND UTILIZATION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/282,054
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,571
; FILING DATE:
; APPLICATION NUMBER: US 08/675,153
; FILING DATE: 03-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,145
; FILING DATE: 03-JUL-1996
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ATTORNEY/AGENT INFORMATION:
  NAME: Wilson, Mark B.
  REGISTRATION NUMBER: 37,259
  REFERENCE/DOCKET NUMBER: AMBI:033
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 512/418-3000
    TELEFAX: 512/474-7577
  INFORMATION FOR SEQ ID NO: 8:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 24 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
    US-09-282-054-8

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Best Local Similarity 100.0%; Pred. No. 0.43;
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Db 4 GCAAGCACCCCTATCAGGCAGT 24

RESULT 36
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; Sequence 8, Application US/09665638
; Patent No. 6399307
; GENERAL INFORMATION:
; APPLICANT: Pasloske, Brittan L.
; APPLICANT: DuBois, Dwight
; APPLICANT: Brown, David
; APPLICANT: Winkler, Matthew
; TITLE OF INVENTION: RIBONUCLEASE RESISTANT RNA PREPARATION
; TITLE OF INVENTION: AND UTILIZATION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/665,638
; FILING DATE: 19-Sep-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/881,571
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/021,145
; FILING DATE: 03-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: AMBI:033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 4 GCAAGCACCTATCAGGCAGT 24

RESULT 37
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; Sequence 5, Application US/10007389
; Patent No. 6727067
; GENERAL INFORMATION:
; APPLICANT: Russman, Eberhard
; APPLICANT: Meier, Thomas
; APPLICANT: Schmuck, Ranier
; APPLICANT: Staepels, Johnny
; APPLICANT: Wehnes, Uwe
; TITLE OF INVENTION: Methods for the analysis of non-proteinaceous
; FILE REFERENCE: Esperase
; CURRENT APPLICATION NUMBER: US/10/007,389
; CURRENT FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)
; OTHER INFORMATION: Biotin derivatization
US-10-007-389-5

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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 4 GCAAGCACCTATCAGGCAGT 24

RESULT 38
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; Sequence 19, Application US/08240547
; Patent No. 5527669
; GENERAL INFORMATION:
; APPLICANT: Resnick, Robert M.
; APPLICANT: Young, Karen K.Y.
; TITLE OF INVENTION: Primers and Probes for Detection of
; TITLE OF INVENTION: Hepatitis C and No. 5527669el Variants
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/918,844
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; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sias Ph.D., Stacey R.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER: 8586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2863
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-240-547-19

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; Sequence 4, Application US/08256568B
; Patent No. 5846704
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,568B
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410,004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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STRADEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: HCV  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: HCV  
MAP POSITION: Position -29 of 5' end  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..26  
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US-09-038-369B-4

Query Match 75.0%; Score 21; DB 3; Length 26;  
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCAGT 21  
Db 6 GCAAGCACCTATCAGGCAGT 26

TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: HCV  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: HCV  
MAP POSITION: Position -29 of 5' end  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..26  
OTHER INFORMATION: /standard name=  
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US-08-256-568B-4

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Best Local Similarity 100.0%; Pred.No. 0.44; 0; Indels 0;  
Matches 21; Conservative 0; Mismatches 0; Gaps 0;

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Db 6 GCAAGCACCTATCAGGCAGT 26

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RESULT 40  
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Sequence 4, Application US/09038369B  
Patent No. 6171784  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/038,369B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410,004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid

GenCore version 5.1.6  
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Perfect score: 28

Sequence: 1 gcaagcaccctatcaggcagctaccacaa 28

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Listing first 1000 summaries

Database : Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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4	25	89.3	47	14	US-10-225-501-11
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9	23	82.1	23	18	US-10-667-271-1407
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c 124	19	67.9	30	17	US-10-333-449A-5	Sequence 5, Appli	c 197	60.7	21	15	US-10-322-138-24	Sequence 65, Appl
c 125	19	67.9	32	15	US-10-111-817-6	Sequence 6, Appli	c 198	58.6	21	15	US-10-096-718-65	Sequence 23, Appl
c 126	19	67.9	39	17	US-10-318-416B-1	Sequence 1, Appli	c 199	58.6	33	10	US-09-770-158-25	Sequence 25, Appl
c 127	19	67.9	39	17	US-10-318-416B-9	Sequence 9, Appli	c 200	58.6	33	10	US-09-770-158-25	Sequence 34, Appl
c 128	18.4	65.7	26	15	US-10-396-964-23	Sequence 23, Appl	c 201	58.6	34	10	US-09-825-805-34	Sequence 63, Appl
c 129	18.2	65.0	32	15	US-10-111-817-4	Sequence 4, Appli	c 202	57.1	16	10	US-09-740-332-66	Sequence 66, Appl
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c 133	18	64.3	19	18	US-10-667-271-721	Sequence 721, App	c 206	57.1	17	17	US-10-669-841-2659	Sequence 18, Appl
c 134	18	64.3	20	17	US-10-475-025-18	Sequence 18, Appl	c 207	57.1	19	18	US-10-667-271-18	Sequence 27, Appl
c 135	18	64.3	21	15	US-10-322-138-21	Sequence 21, Appl	c 208	57.1	19	18	US-10-667-271-27	Sequence 714, App
c 136	18	64.3	21	18	US-10-444-853A-471	Sequence 471, App	c 209	57.1	19	18	US-10-667-271-714	Sequence 723, App
c 137	18	64.3	21	18	US-10-444-853A-472	Sequence 472, App	c 210	57.1	19	18	US-10-667-271-723	Sequence 1411, Ap
c 138	18	64.3	21	18	US-10-667-271-1503	Sequence 1503, App	c 211	57.1	23	18	US-10-667-271-1411	Sequence 1412, Ap
c 139	18	64.3	21	18	US-10-667-271-1515	Sequence 1515, Ap	c 212	57.1	23	18	US-10-667-271-1412	Sequence 33, Appl
c 140	18	64.3	21	18	US-10-667-271-1561	Sequence 1561, Ap	c 213	57.1	23	18	US-10-322-138-33	Sequence 30, Appl
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c 144	18	64.3	45	10	US-09-935-338-288	Sequence 288, App	c 217	55.0	15	9	US-09-504-231A-1517	Sequence 1517, Ap
c 145	18	64.3	45	17	US-10-475-025-19	Sequence 19, Appl	c 218	53.6	15	9	US-09-504-231A-1537	Sequence 1537, Ap
c 146	17.4	62.1	34	10	US-09-770-158-22	Sequence 22, Appl	c 219	53.6	15	9	US-09-504-231A-1538	Sequence 1538, Ap
c 147	17.4	62.1	34	10	US-09-770-158-24	Sequence 24, Appl	c 220	53.6	15	9	US-09-504-231A-1539	Sequence 1539, Ap
c 148	17.4	62.1	35	10	US-09-770-158-26	Sequence 26, Appl	c 221	53.6	15	9	US-09-504-231A-1540	Sequence 1540, Ap
c 149	17	60.7	17	10	US-09-740-332-64	Sequence 64, Appl	c 222	53.6	15	9	US-09-504-231A-1607	Sequence 1607, Ap
c 150	17	60.7	17	10	US-09-740-332-65	Sequence 65, Appl	c 223	53.6	15	9	US-09-504-231A-1607	Sequence 40, Appl
c 151	17	60.7	17	10	US-09-740-332-4490	Sequence 4490, Ap	c 224	53.6	15	9	US-09-274-553D-41	Sequence 41, Appl
c 152	17	60.7	17	10	US-09-740-332-4491	Sequence 4491, Ap	c 225	53.6	15	9	US-09-274-553D-41	Sequence 1517, Ap
c 153	17	60.7	17	10	US-09-740-332-4492	Sequence 4492, Ap	c 226	53.6	15	9	US-09-274-553D-1517	Sequence 1537, Ap
c 154	17	60.7	17	10	US-09-817-879-64	Sequence 64, Appl	c 227	53.6	15	9	US-09-274-553D-1537	Sequence 1538, Ap
c 155	17	60.7	17	10	US-09-817-879-65	Sequence 65, Appl	c 228	53.6	15	9	US-09-274-553D-1538	Sequence 1539, Ap
c 156	17	60.7	17	10	US-09-817-879-4490	Sequence 4490, Ap	c 229	53.6	15	9	US-09-274-553D-1539	Sequence 1539, Ap
c 157	17	60.7	17	10	US-09-817-879-4491	Sequence 4491, Ap	c 230	53.6	15	9	US-09-274-553D-1539	Sequence 1539, Ap
c 158	17	60.7	17	10	US-09-817-879-4492	Sequence 4492, Ap	c 231	53.6	15	9	US-09-274-553D-1539	Sequence 1539, Ap

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c 240	15	53.6	15	10	US-09-740-332-4712	Sequence 4712, Ap	c 312	14	50.0	19	18	US-10-667-271-741	Sequence 741, Appl
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c 242	15	53.6	15	10	US-09-740-332-4729	Sequence 4729, Ap	c 314	14	50.0	21	18	US-10-667-271-1523	Sequence 1523, Ap
c 243	15	53.6	15	10	US-09-740-332-4753	Sequence 4753, Ap	c 315	14	50.0	21	18	US-10-667-271-1560	Sequence 1560, Ap
c 244	15	53.6	15	10	US-09-817-879-4590	Sequence 4590, Ap	c 316	14	50.0	21	18	US-10-667-271-1569	Sequence 1569, Ap
c 245	15	53.6	15	10	US-09-817-879-4591	Sequence 4591, Ap	c 317	14	50.0	21	18	US-10-667-271-1572	Sequence 1572, Ap
c 246	15	53.6	15	10	US-09-817-879-4697	Sequence 4697, Ap	c 318	14	50.0	21	18	US-10-667-271-1581	Sequence 1581, Ap
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c 248	15	53.6	15	10	US-09-817-879-4711	Sequence 4711, Ap	c 320	14	50.0	26	9	US-09-877-526A-8	Sequence 8, Appl
c 249	15	53.6	15	10	US-09-817-879-4712	Sequence 4712, Ap	c 321	14	50.0	26	10	US-09-992-160-8	Sequence 8, Appl
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c 252	15	53.6	15	10	US-09-817-879-4753	Sequence 4753, Ap	c 324	14	50.0	30	9	US-09-037-657-48	Sequence 48, Appl
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c 258	15	53.6	15	17	US-10-669-841-7305	Sequence 7305, Ap	c 330	14	50.0	38	15	US-10-430-882-1364	Sequence 1364, Ap
c 259	15	53.6	15	17	US-10-669-841-7321	Sequence 7321, Ap	c 331	14	50.0	41	16	US-10-035-833A-529	Sequence 529, App
c 260	15	53.6	15	17	US-10-669-841-7322	Sequence 7322, Ap	c 332	14	50.0	41	16	US-10-035-833A-6096	Sequence 6096, Ap
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c 279	15	53.6	19	15	US-10-309-438-37	Sequence 37, Appl	c 349	14	50.0	43	14	US-10-012-755A-320	Sequence 320, App
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c 300	15	53.6	25	14	US-10-215-112-1725	Sequence 1725, Ap	c 370	14	50.0	43	15	US-10-015-671A-320	Sequence 320, App
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C 404	13.8	49.3	33	15	US-10-237-551-182	Sequence 182, App	C 477	13	46.4	13	18	US-10-667-271-41	Sequence 41, Appl
C 405	13.8	49.3	33	15	US-10-131-827-3008	Sequence 3008, App	C 478	13	46.4	13	18	US-10-667-271-708	Sequence 708, App
C 406	13.6	48.6	21	10	US-09-754-106-33	Sequence 33, Appl	C 479	13	46.4	13	18	US-10-667-271-737	Sequence 737, App
C 407	13.6	48.6	21	10	US-09-754-106-33	Sequence 33, Appl	C 480	13	46.4	13	18	US-10-174-771-17	Sequence 17, Appl
C 408	13.6	48.6	25	15	US-10-098-263B-41535	Sequence 41535, A	C 481	13	46.4	13	20	US-10-174-771-90	Sequence 90, Appl
C 409	13.6	48.6	38	10	US-09-827-395A-1566	Sequence 1566, App	C 482	13	46.4	13	20	US-10-215-112-90	Sequence 90, Appl
C 410	13.6	48.6	38	10	US-10-339-674-522	Sequence 522, App	C 483	13	46.4	13	25	US-10-215-112-9100	Sequence 9100, App
C 411	13.6	48.6	49	15	US-10-339-674-524	Sequence 524, App	C 484	13	46.4	13	25	US-10-098-263B-24140	Sequence 24140, A
C 412	13.6	48.6	50	16	US-10-131-827-5034	Sequence 5034, App	C 485	13	46.4	13	25	US-10-098-263B-49657	Sequence 49657, A
C 413	13.4	47.9	25	14	US-10-215-112-5997	Sequence 5997, App	C 486	13	46.4	13	27	US-10-096-718-66	Sequence 66, Appl
C 414	13.4	47.9	25	14	US-10-215-112-9130	Sequence 9130, App	C 487	13	46.4	13	27	US-10-096-718-73	Sequence 73, Appl
C 415	13.4	47.9	25	17	US-10-717-597-810	Sequence 810, App	C 488	13	46.4	13	27	US-10-096-718-78	Sequence 78, Appl
C 416	13.4	47.9	25	17	US-10-775-169-2809	Sequence 2809, App	C 489	13	46.4	13	30	US-10-309-290-243	Sequence 243, App
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C 418	13.4	47.9	27	17	US-10-316-667-7	Sequence 7, Appl	C 491	13	46.4	13	31	US-09-801-274-922	Sequence 922, App
C 419	13.4	47.9	40	18	US-10-469-851-209	Sequence 209, App	C 492	13	46.4	13	31	US-09-912-263-48	Sequence 48, Appl
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C 421	13.2	47.1	20	14	US-10-057-550-130	Sequence 130, App	C 494	13	46.4	13	35	US-10-339-674-2358	Sequence 2358, App
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C 423	13.2	47.1	20	15	US-10-173-225B-108	Sequence 108, App	C 496	13	46.4	13	37	US-09-504-231A-3129	Sequence 3129, App
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C 427	13.2	47.1	29	16	US-10-038-854-318	Sequence 318, App	C 500	13	46.4	13	38	US-09-827-395A-1193	Sequence 1193, App
C 428	13.2	47.1	31	10	US-09-912-263-370	Sequence 370, App	C 501	13	46.4	13	38	US-09-745-237A-2343	Sequence 2343, App
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ALIGNMENTS

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RESULT 1
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; Publication No. US20030054372A1
; GENERAL INFORMATION:
; APPLICANT: JAEGER, STEPHAN
; TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A
; FILE REFERENCE: 1803-335-999
; CURRENT APPLICATION NUMBER: US/10/087,631B
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 7
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: sequence
US-10-087-631B-7
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Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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; Sequence 7, Application US/10419022
; Publication No. US20030165982A1
; GENERAL INFORMATION:
; APPLICANT: JAEGER, STEPHAN
; TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A
; FILE REFERENCE: 1803-335-999
; CURRENT APPLICATION NUMBER: US/10/419,022
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US/10/087,631B
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 7
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ST778 HCV-specific primer
; OTHER INFORMATION: sequence
US-10-419-022-7
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Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-10-147-679A-16
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; Publication No. US2003024366A1
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; APPLICANT: Weindel, Kurt
; APPLICANT: Riedling, Michael
; APPLICANT: Geiger, Albert
; TITLE OF INVENTION: Magnetic glass particles, method for their preparation
; FILE REFERENCE: 1803-344-999
; CURRENT APPLICATION NUMBER: US/10/147,679A
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: EP99122853.7
; PRIOR FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 16
; LENGTH: 28
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide (HCV reverse)
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; OTHER INFORMATION: derivatization with a p-(t-butyl)benzyl-residue
US-10-147-679A-16
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Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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## RESULT 4

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; Sequence 11, Application US/10225501  
; Publication No. US20030059443A1  
; GENERAL INFORMATION:  
; APPLICANT: Ecker, David J.  
; TITLE OF INVENTION: Molecular Interaction Sites Of Hepatitis C Virus RNA And Methods  
; FILE OF INVENTION: Modulating The Same  
; FILE REFERENCE: IBIS0428  
; CURRENT APPLICATION NUMBER: US/10/225,501  
; CURRENT FILING DATE: 2002-08-19  
; PRIOR APPLICATION NUMBER: 60/314,236  
; PRIOR FILING DATE: 2001-08-22  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 47  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
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; OTHER INFORMATION: Synthetic construct  
US-10-225-501-11

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; Sequence 1398, Application US/10667271  
; Publication No. US20040209831A1  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics  
; APPLICANT: McSwiggen, James  
; APPLICANT: Macejak, Dennis  
; APPLICANT: Beigelman, Leonid  
; APPLICANT: Morrissey, David  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)  
; FILE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)  
; FILE REFERENCE: 400/129 (MBH02-763B)  
; CURRENT APPLICATION NUMBER: US/10/667,271  
; CURRENT FILING DATE: 2003-09-16  
; PRIOR APPLICATION NUMBER: US 10/444,853  
; PRIOR FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: PCT / US03/05043  
; PRIOR FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: PCT / US02/09187  
; PRIOR FILING DATE: 2002-03-26  
; PRIOR APPLICATION NUMBER: USSN 60/401,104  
; PRIOR FILING DATE: 2002-08-05  
; PRIOR APPLICATION NUMBER: USSN 60/358,580  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: USSN 60/363,124  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: USSN 60/386,782  
; PRIOR FILING DATE: 2002-06-06  
; PRIOR APPLICATION NUMBER: USSN 60/406,784  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: USSN 60/408,378  
; PRIOR FILING DATE: 2002-09-05  
; PRIOR APPLICATION NUMBER: USSN 60/409,293  
; PRIOR FILING DATE: 2002-09-09  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1705  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1398  
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; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense seq

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US-10-667-271-1398

Query Match 82.1%; Score 23; DB 18; Length 23;  
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Qy 6

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## RESULT 6

US-10-667-271-1404/c  
; Sequence 1404, Application US/10667271  
; Publication No. US20040209831A1  
; GENERAL INFORMATION:  
; APPLICANT: Sirna Therapeutics  
; APPLICANT: McSwiggen, James  
; APPLICANT: Macejak, Dennis  
; APPLICANT: Beigelman, Leonid  
; APPLICANT: Morrissey, David  
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)  
; FILE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)  
; FILE REFERENCE: 400/129 (MBH02-763B)  
; CURRENT APPLICATION NUMBER: US/10/667,271  
; CURRENT FILING DATE: 2003-09-16  
; PRIOR APPLICATION NUMBER: US 10/444,853  
; PRIOR FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: PCT / US03/05043  
; PRIOR FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: PCT / US02/09187  
; PRIOR FILING DATE: 2002-03-26  
; PRIOR APPLICATION NUMBER: USSN 60/401,104  
; PRIOR FILING DATE: 2002-08-05  
; PRIOR APPLICATION NUMBER: USSN 60/358,580  
; PRIOR FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: USSN 60/363,124  
; PRIOR FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: USSN 60/386,782  
; PRIOR FILING DATE: 2002-06-06  
; PRIOR APPLICATION NUMBER: USSN 60/406,784  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: USSN 60/408,378  
; PRIOR FILING DATE: 2002-09-05  
; PRIOR APPLICATION NUMBER: USSN 60/409,293  
; PRIOR FILING DATE: 2002-09-09  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1705  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1404  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense seq

US-10-667-271-1404

Query Match 82.1%; Score 23; DB 18; Length 23;  
Best Local Similarity 100.0%; Pred. No. 0.68;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5

GCACCTATCAGGCAGTACCA 27

Db 23

GCACCTATCAGGCAGTACCA 1

## RESULT 7

US-10-667-271-1405/c  
; Sequence 1405, Application US/10667271

Publication No. US20040209831A1  
GENERAL INFORMATION:  
APPLICANT: McSwiggen, James  
APPLICANT: Macejak, Dennis  
APPLICANT: Beigelman, Leonid  
APPLICANT: Morrissey, David  
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)  
FILE REFERENCE: 400/129 (WBH02-763B)  
CURRENT FILING DATE: 2003-09-16  
PRIOR APPLICATION NUMBER: US 10/444,853  
PRIOR FILING DATE: 2003-05-23  
PRIOR APPLICATION NUMBER: PCT / US03/05043  
PRIOR FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: PCT / US02/09187  
PRIOR FILING DATE: 2002-03-26  
PRIOR APPLICATION NUMBER: USSN 60/401,104  
PRIOR FILING DATE: 2002-08-05  
PRIOR APPLICATION NUMBER: USSN 60/358,580  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: USSN 60/363,124  
PRIOR FILING DATE: 2002-03-11  
PRIOR APPLICATION NUMBER: USSN 60/386,782  
PRIOR FILING DATE: 2002-06-06  
PRIOR APPLICATION NUMBER: USSN 60/406,784  
PRIOR FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: USSN 60/408,378  
PRIOR FILING DATE: 2002-09-05  
PRIOR APPLICATION NUMBER: USSN 60/409,293  
PRIOR FILING DATE: 2002-09-09  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 1705  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1406  
LENGTH: 23  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense seq  
US-10-667-271-1406

Query Match 82.1%; Score 23; DB 18; Length 23;  
Best Local Similarity 100.0%; Pred. No. 0.68;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AGCACCCCTATCAGGCAGTACCA 25  
|||||  
Db 23 AGCACCCCTATCAGGCAGTACCA 1

RESULT 9  
US-10-667-271-1407/c  
Sequence 1407, Application US/10667271  
Publication No. US20040209831A1  
GENERAL INFORMATION:  
APPLICANT: Sirna Therapeutics  
APPLICANT: McSwiggen, James  
APPLICANT: Macejak, Dennis  
APPLICANT: Beigelman, Leonid  
APPLICANT: Morrissey, David  
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)  
FILE REFERENCE: 400/129 (WBH02-763B)  
CURRENT FILING DATE: 2003-09-16  
PRIOR APPLICATION NUMBER: US 10/444,853  
PRIOR FILING DATE: 2003-05-23  
PRIOR APPLICATION NUMBER: PCT / US03/05043  
PRIOR FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: PCT / US02/09187  
PRIOR FILING DATE: 2002-03-26  
PRIOR APPLICATION NUMBER: USSN 60/401,104  
PRIOR FILING DATE: 2002-08-05  
PRIOR APPLICATION NUMBER: USSN 60/358,580  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: USSN 60/363,124  
PRIOR FILING DATE: 2002-03-11  
PRIOR APPLICATION NUMBER: USSN 60/386,782  
PRIOR FILING DATE: 2002-06-06  
PRIOR APPLICATION NUMBER: USSN 60/406,784  
PRIOR FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: USSN 60/408,378  
PRIOR FILING DATE: 2002-09-05  
PRIOR APPLICATION NUMBER: USSN 60/409,293  
PRIOR FILING DATE: 2002-09-09  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 1705  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1407

Publication No. US20040209831A1  
GENERAL INFORMATION:  
APPLICANT: Sirna Therapeutics  
APPLICANT: McSwiggen, James  
APPLICANT: Macejak, Dennis  
APPLICANT: Beigelman, Leonid  
APPLICANT: Morrissey, David  
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)  
FILE REFERENCE: 400/129 (WBH02-763B)  
CURRENT FILING DATE: 2003-09-16  
PRIOR APPLICATION NUMBER: US 10/444,853  
PRIOR FILING DATE: 2003-05-23  
PRIOR APPLICATION NUMBER: PCT / US03/05043  
PRIOR FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: PCT / US02/09187  
PRIOR FILING DATE: 2002-03-26  
PRIOR APPLICATION NUMBER: USSN 60/401,104  
PRIOR FILING DATE: 2002-08-05  
PRIOR APPLICATION NUMBER: USSN 60/358,580  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: USSN 60/363,124  
PRIOR FILING DATE: 2002-03-11  
PRIOR APPLICATION NUMBER: USSN 60/386,782  
PRIOR FILING DATE: 2002-06-06  
PRIOR APPLICATION NUMBER: USSN 60/406,784  
PRIOR FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: USSN 60/408,378  
PRIOR FILING DATE: 2002-09-05  
PRIOR APPLICATION NUMBER: USSN 60/409,293  
PRIOR FILING DATE: 2002-09-09  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 1705  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1405  
LENGTH: 23  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense seq  
US-10-667-271-1405

Query Match 82.1%; Score 23; DB 18; Length 23;  
Best Local Similarity 100.0%; Pred. No. 0.68;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AGCACCCCTATCAGGCAGTACCA 26  
|||||  
Db 23 AGCACCCCTATCAGGCAGTACCA 1

RESULT 8  
US-10-667-271-1406/c  
Sequence 1406, Application US/10667271  
Publication No. US20040209831A1  
GENERAL INFORMATION:  
APPLICANT: Sirna Therapeutics  
APPLICANT: McSwiggen, James  
APPLICANT: Macejak, Dennis  
APPLICANT: Beigelman, Leonid  
APPLICANT: Morrissey, David  
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)  
FILE REFERENCE: 400/129 (WBH02-763B)  
CURRENT FILING DATE: 2003-09-16  
PRIOR APPLICATION NUMBER: US 10/444,853  
PRIOR FILING DATE: 2003-05-23  
PRIOR APPLICATION NUMBER: PCT / US03/05043  
PRIOR FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: PCT / US02/09187  
PRIOR FILING DATE: 2002-03-26

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; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-1407
Query Match      82.1%; Score 23; DB 18; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CAAGCACCCCTATCAGGCAGTACC 24
Db 23 CAAGCACCCCTATCAGGCAGTACC 1

RESULT 10
US-10-182-126-6
; Sequence 6, Application US/10182126
; Publication No. US20030175691A1
; GENERAL INFORMATION:
; APPLICANT: ELAISSARI, Abdelhamid
; APPLICANT: MANDRAND, Bernard
; APPLICANT: DELAIR, Thierry
; APPLICANT: SPENCER, Doran
; APPLICANT: ARKIS, Ahmend
; TITLE OF INVENTION: METHOD FOR ISOLATING PROTEINS OR PROTEIN AND NUCLEIC ACID ASSOCIAT
; TITLE OF INVENTION: PARTICLE AND PROTEIN COMPLEXES, REAGENTS AND USES.
; FILE REFERENCE: 113339
; CURRENT APPLICATION NUMBER: US/10/182,126
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: PCT/FR01/00205
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: FR 00.00862
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-10-182-126-6
Query Match      82.1%; Score 23; DB 15; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCCCTATCAGGCAGTAC 23
Db 5 GCAAGCACCCCTATCAGGCAGTAC 27

RESULT 11
US-10-182-126-8
; Sequence 8, Application US/10182126
; Publication No. US20030175691A1
; GENERAL INFORMATION:
; APPLICANT: ELAISSARI, Abdelhamid
; APPLICANT: MANDRAND, Bernard
; APPLICANT: DELAIR, Thierry
; APPLICANT: SPENCER, Doran
; APPLICANT: ARKIS, Ahmend
; TITLE OF INVENTION: METHOD FOR ISOLATING PROTEINS OR PROTEIN AND NUCLEIC ACID ASSOCIAT
; TITLE OF INVENTION: PARTICLE AND PROTEIN COMPLEXES, REAGENTS AND USES.
; FILE REFERENCE: 113339
; CURRENT APPLICATION NUMBER: US/10/182,126
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: PCT/FR01/00205
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: FR 00.00862
; PRIOR FILING DATE: 2000-01-21
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; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-10-182-126-8
Query Match      82.1%; Score 23; DB 15; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCCCTATCAGGCAGTAC 23
Db 5 GCAAGCACCCCTATCAGGCAGTAC 27

RESULT 12
US-10-667-271-1399/c
; Sequence 1399, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrisey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/129 (MBHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1399
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-1399
Query Match      78.6%; Score 22; DB 18; Length 23;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ACCCTATCAGGCAGTACCACAA 28
Db 23 ACCCTATCAGGCAGTACCACAA 2
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```
RESULT 13
US-10-667-271-1408/c
; Sequence 1408, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/359,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1408
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siRNA sense re
US-10-667-271-1408

Query Match 78.6%; Score 22; DB 18; Length 23;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCAGTA 22
Db 22 GCAAGCACCTATCAGGCAGTA 1

RESULT 14
US-09-877-526A-10/c
; Sequence 10, Application US/09877526A
; Patent No. US20020102568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: Usman, Nassim
; APPLICANT: McSwiggen, Jim
; APPLICANT: Zinnen, Shawn
; APPLICANT: Seiwert, Scott
; APPLICANT: Haerberli, Pete
; APPLICANT: Chowrira, Bharat
; APPLICANT: Blatt, Larry
; APPLICANT: Vaish, Narendra
; TITLE OF INVENTION: A Process for the Detection of Nucleic Acid Using Nucleic Acid Ca
; FILE REFERENCE: MBHB00-816-C (700/002)
; CURRENT APPLICATION NUMBER: US/09/877,526A
;

US-10-087-631b-7.max.rnpb
```

```
; CURRENT FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/187,128
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 27
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic target signaling
US-09-877-526A-10

Query Match 78.6%; Score 22; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCAGTA 22
Db 22 GCAAGCACCTATCAGGCAGTA 1

RESULT 15
US-09-992-160-10/c
; Sequence 10, Application US/09992160
; Publication No. US20030008295A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: Usman, Nassim
; APPLICANT: McSwiggen, Jim
; APPLICANT: Zinnen, Shawn
; APPLICANT: Seiwert, Scott
; APPLICANT: Haerberli, Pete
; APPLICANT: Chowrira, Bharat
; APPLICANT: Blatt, Larry
; TITLE OF INVENTION: Nucleic Acid Sensor Molecules
; FILE REFERENCE: MBHB00-816-D (700/004)
; CURRENT APPLICATION NUMBER: US/09/992,160
; CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 27
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic target signaling
US-09-992-160-10

Query Match 78.6%; Score 22; DB 10; Length 27;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCAGTA 22
Db 22 GCAAGCACCTATCAGGCAGTA 1

RESULT 16
US-10-056-761-10/c
; Sequence 10, Application US/10056761
; Publication No. US20030065155A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: Usman, Nassim
; APPLICANT: McSwiggen, Jim
; APPLICANT: Zinnen, Shawn
; APPLICANT: Seiwert, Scott
; APPLICANT: Haerberli, Pete
; APPLICANT: Chowrira, Bharat
; APPLICANT: Blatt, Larry
```

```
; TITLE OF INVENTION: Nucleic Acid Sensor Molecules
; FILE REFERENCE: MBH00-816-E (700/005)
; CURRENT APPLICATION NUMBER: US/10/056,761
; CURRENT FILING DATE: 2002-01-23
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 27
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Target Signaling
US-10-056-761-10

Query Match      78.6%; Score 22; DB 14; Length 27;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCAGTA 22
Db 22 GCAAGCACCTATCAGGCAGTA 1

RESULT 17
US-10-422-050-10/c
; Sequence 10, Application US/10422050
; Publication No. US20040009510A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Seiwert, Scott
; APPLICANT: Zinnen, Shawn
; APPLICANT: Vaish, Narendra
; APPLICANT: Jadhav, Vasant
; APPLICANT: Kossen, Karl
; TITLE OF INVENTION: Allosteric Nucleic Acid Sensor Molecules
; FILE REFERENCE: 700/013 (MEHB 00-816-M)
; CURRENT APPLICATION NUMBER: US/10/422,050
; CURRENT FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: PCT/US 02/35529
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 10/286,492
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 10/283,858
; PRIOR FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: US 10/056,761
; PRIOR FILING DATE: 2002-01-23
; PRIOR APPLICATION NUMBER: US 09/992,160
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 09/877,526
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/800,594
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: US 60/187,128
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 27
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Target Signaling
US-10-422-050-10

Query Match      78.6%; Score 22; DB 16; Length 27;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTATCAGGCAGTA 22
Db 22 GCAAGCACCTATCAGGCAGTA 1
```

```
RESULT 18
US-09-464-426A-4
; Sequence 4, Application US/09464426A
; Publication No. US20020119122A1
; GENERAL INFORMATION:
; APPLICANT: Scalgis, Carlos O., Albrecht, Janice K., and Glue, Paul W.
; TITLE OF INVENTION: Ribavirin- Pegylated Interferon-Alfa
; Induction HCV Combination Therapy
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: 7.5.3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/464,426A
; FILING DATE: 16-Dec-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoffman, Thomas D.
; REGISTRATION NUMBER: 28,221
; REFERENCE/DOCKET NUMBER: IN0964Q
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-298-5037
; TELEFAX: 908-298-5388
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-464-426A-4

Query Match      75.0%; Score 21; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCCTATCAGGCAGTACCACAA 28
Db 1 CCCTATCAGGCAGTACCACAA 21

RESULT 19
US-09-981-215-4
; Sequence 4, Application US/09981215
; Patent No. US20020127203A1
; GENERAL INFORMATION:
; APPLICANT: Albrecht, Janice K.
; TITLE OF INVENTION: Ribavirin-Pegylated Interferon Alfa
; HCV Combination Therapy
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: 7.5.3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/981,215
; FILING DATE: 16-Oct-2001
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QY 7 ACCCTATCAGGCGATACCACA 27  
 Db 21 ACCCTATCAGGCGATACCACA 1

## RESULT 22

US-10-444-853A-196/c

; Sequence 196, Application US/10444853A

; Publication No. US20040192626A1

; GENERAL INFORMATION:

; APPLICANT: Sirna Therapeutics, Inc.

; APPLICANT: Haerberli, Peter

; APPLICANT: McSwiggen, James

; APPLICANT: Beigelman, Leonid

; APPLICANT: Macejak, Dennis

; APPLICANT: Zinnen, Shawn

; APPLICANT: Pavco, Pamela

; APPLICANT: Morrissey, David

; APPLICANT: Fosnaugh, Kathy

; APPLICANT: Mokler, Victor

; APPLICANT: Jamison, Sharon

; APPLICANT: Vaish, Nerendra

; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using  
 ; FILE REFERENCE: 400/114 (WBHB03-465)

; CURRENT APPLICATION NUMBER: US/10/444,853A

; PRIOR FILING DATE: 2003-05-23

; PRIOR APPLICATION NUMBER: US 10/417,012

; PRIOR FILING DATE: 2003-04-16

; PRIOR APPLICATION NUMBER: PCT/US03/05346

; PRIOR FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: PCT/US03/05028

; PRIOR FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: US 60/358,580

; PRIOR FILING DATE: 2002-02-20

; PRIOR APPLICATION NUMBER: US 60/363,124

; PRIOR FILING DATE: 2002-03-11

; PRIOR APPLICATION NUMBER: US 60/386,782

; PRIOR FILING DATE: 2002-06-06

; PRIOR APPLICATION NUMBER: US 60/406,784

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: US 60/408,378

; PRIOR FILING DATE: 2002-09-05

; PRIOR APPLICATION NUMBER: US 60/409,293

; PRIOR FILING DATE: 2002-09-09

; PRIOR APPLICATION NUMBER: US 60/440,129

; PRIOR FILING DATE: 2003-01-15

; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 626

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 196

; LENGTH: 21

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region

US-10-444-853A-196

## Query Match

Best Local Similarity 75.0%; Score 21; DB 18; Length 21;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## QY

6 CACCCCTATCAGGCGATACCAC 26

|||||

Db 21 CACCCCTATCAGGCGATACCAC 1

## RESULT 23

US-10-444-853A-203

; Sequence 203, Application US/10444853A

; Publication No. US20040192626A1

; GENERAL INFORMATION:

; APPLICANT: Sirna Therapeutics, Inc.

; APPLICANT: Haerberli, Peter  
 ; APPLICANT: McSwiggen, James  
 ; APPLICANT: Beigelman, Leonid  
 ; APPLICANT: Macejak, Dennis  
 ; APPLICANT: Zinnen, Shawn  
 ; APPLICANT: Pavco, Pamela  
 ; APPLICANT: Morrissey, David  
 ; APPLICANT: Fosnaugh, Kathy  
 ; APPLICANT: Mokler, Victor  
 ; APPLICANT: Jamison, Sharon  
 ; APPLICANT: Vaish, Nerendra  
 ; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Gene Expression Using  
 ; FILE REFERENCE: 400/114 (WBHB03-465)

; CURRENT APPLICATION NUMBER: US/10/444,853A

; PRIOR FILING DATE: 2003-05-23

; PRIOR APPLICATION NUMBER: US 10/417,012

; PRIOR FILING DATE: 2003-04-16

; PRIOR APPLICATION NUMBER: PCT/US03/05346

; PRIOR FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: PCT/US03/05028

; PRIOR FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: US 60/358,580

; PRIOR FILING DATE: 2002-02-20

; PRIOR APPLICATION NUMBER: US 60/363,124

; PRIOR FILING DATE: 2002-03-11

; PRIOR APPLICATION NUMBER: US 60/386,782

; PRIOR FILING DATE: 2002-06-06

; PRIOR APPLICATION NUMBER: US 60/406,784

; PRIOR FILING DATE: 2002-08-29

; PRIOR APPLICATION NUMBER: US 60/408,378

; PRIOR FILING DATE: 2002-09-05

; PRIOR APPLICATION NUMBER: US 60/409,293

; PRIOR FILING DATE: 2002-09-09

; PRIOR APPLICATION NUMBER: US 60/440,129

; PRIOR FILING DATE: 2003-01-15

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 626

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 203

; LENGTH: 21

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region

US-10-444-853A-203

## Query Match

Best Local Similarity 75.0%; Score 21; DB 18; Length 21;

Matches 18; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

## QY

8 CCCTATCAGGCGATACCACAA 28

|||||

Db 1 CCCTATCAGGCGATACCACAA 21

## RESULT 24

US-10-667-271-1451/c

; Sequence 1451, Application US/10667271

; Publication No. US20040209831A1

; GENERAL INFORMATION:

; APPLICANT: Sirna Therapeutics

; APPLICANT: McSwiggen, James

; APPLICANT: Macejak, Dennis

; APPLICANT: Beigelman, Leonid

; APPLICANT: Morrissey, David

; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)  
 ; FILE REFERENCE: 400/129 (WBHB02-763B)

; CURRENT APPLICATION NUMBER: US/10/667,271

; CURRENT FILING DATE: 2003-09-16

; PRIOR APPLICATION NUMBER: US 10/444,853

; PRIOR FILING DATE: 2003-05-23

```
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1451
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
US-10-667-271-1451

Query Match 75.0%; Score 21; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCCTATCAGCAGTACCACAA 28
Db 21 CCCTATCAGCAGTACCACAA 1

RESULT 25
US-10-667-271-1452/c
; Sequence 1452, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1451
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
US-10-667-271-1451

Query Match 75.0%; Score 21; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCCTATCAGCAGTACCACAA 28
Db 21 CCCTATCAGCAGTACCACAA 1
```

```
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1452
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
US-10-667-271-1452

Query Match 75.0%; Score 21; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ACCTATCAGCAGTACCACA 27
Db 21 ACCTATCAGCAGTACCACA 1

RESULT 26
US-10-667-271-1453/c
; Sequence 1453, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1453
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
US-10-667-271-1453

Query Match 75.0%; Score 21; DB 18; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CACCTATCAGCAGTACCAC 26
Db 21 CACCTATCAGCAGTACCAC 1
```

```
RESULT 27
US-10-667-271-1460
; Sequence 1460, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1460
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-667-271-1460

Query Match 75.0%; Score 21; DB 18; Length 21;
Best Local Similarity 85.7%; Pred. No. 5.8;
Matches 18; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCCTATCAGGCAGTACCACAA 28
Db 1 CCCUACAGGCAGUACCACAA 21

RESULT 28
US-10-667-271-1400/c
; Sequence 1400, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1460
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-667-271-1460

Query Match 75.0%; Score 21; DB 18; Length 21;
Best Local Similarity 85.7%; Pred. No. 5.8;
Matches 18; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCCTATCAGGCAGTACCACAA 28
Db 1 CCCUACAGGCAGUACCACAA 21

RESULT 29
US-10-667-271-1409/c
; Sequence 1409, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1400
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
```

```

; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1409
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-1409

Query Match          75.0%; Score 21; DB 18; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCCCTATCAGGCAGT 21
DB 21 GCAAGCACCCCTATCAGGCAGT 1

RESULT 30
US-09-880-945-2/c
; Sequence 2, Application US/09880945
; Patent No. US20020037868A1
; GENERAL INFORMATION:
; APPLICANT: BUDKOWSKA, Agata
; APPLICANT: MAILLARD, Patrick
; APPLICANT: BRONNERT, Christian
; APPLICANT: GOUNON, Pierre
; APPLICANT: NITKIEWICZ, Jadwiga
; APPLICANT: GRAINIC, Radu
; TITLE OF INVENTION: METHOD OF DETECTING HEPATITIS C
; FILE REFERENCE: 210017US0CIP
; CURRENT APPLICATION NUMBER: US/09/880,945
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US09/549,685
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US60/129,319
; PRIOR FILING DATE: 1999-04-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic DNA
US-09-880-945-2

Query Match          75.0%; Score 21; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCCCTATCAGGCAGT 21
DB 21 GCAAGCACCCCTATCAGGCAGT 1

RESULT 31
US-09-549-685A-2/c
; Sequence 2, Application US/09549685A
; Publication No. US20030022155A1
; GENERAL INFORMATION:
; APPLICANT: BUDKOWSKA, AGATA
; APPLICANT: MAILLARD, PATRICK
; APPLICANT: NITKIEWICZ, JADWIGA
; APPLICANT: CRAINIC, RADU
; TITLE OF INVENTION: METHOD FOR DETECTING HEPATITIS C VIRUS WITH HYBRIDOMAS
; FILE REFERENCE: 0660-0175-0
; CURRENT APPLICATION NUMBER: US/09/549,685A
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/129,319

```

```

; PRIOR FILING DATE: 1999-04-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
US-09-549-685A-2

Query Match          75.0%; Score 21; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCCCTATCAGGCAGT 21
DB 21 GCAAGCACCCCTATCAGGCAGT 1

RESULT 32
US-10-120-013-8
; Sequence 8, Application US/10120013
; Publication No. US20020192689A1
; GENERAL INFORMATION:
; APPLICANT: Pasloske, Brittan L.
; DuBois, David
; Brown, David
; Winkler, Matthew
; TITLE OF INVENTION: RIBONUCLEASE RESISTANT RNA PREPARATION
; AND UTILIZATION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/120,013
; FILING DATE: 10-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/881,571
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/675,153
; FILING DATE: 03-JUL-1996
; APPLICATION NUMBER: US 60/021,145
; FILING DATE: 03-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: AMBI:033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-120-013-8

Query Match          75.0%; Score 21; DB 13; Length 24;

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```
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTTATCAGGCAGT 21
Db 4 GCAAGCACCTTATCAGGCAGT 24

RESULT 33
US-10-011-855-2
; Sequence 2, Application US/10011855
; Publication No. US20030104582A1
; GENERAL INFORMATION:
; APPLICANT: BAUMANN, RUSSELL
; APPLICANT: HAMDAN, HASNAH
; APPLICANT: LEWINSKI, MICHAEL
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND METHODS FOR DETECTING HEPATITIS C
; FILE REFERENCE: 034827/0702
; CURRENT APPLICATION NUMBER: US/10/011,855
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Oligonucleotide
US-10-011-855-2

Query Match 75.0%; Score 21; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTTATCAGGCAGT 21
Db 4 GCAAGCACCTTATCAGGCAGT 24

RESULT 34
US-10-037-990-2
; Sequence 2, Application US/10037990
; Publication No. US20030124654A1
; GENERAL INFORMATION:
; APPLICANT: Sharma, Vijay
; APPLICANT: Kondiboyina, Venkat Ramana
; TITLE OF INVENTION: Method and Device for the Rapid Clinical Diagnosis of Hepatitis C
; FILE REFERENCE: Infection in Biological Samples
; FILE REFERENCE: RELIA P-106
; CURRENT APPLICATION NUMBER: US/10/037,990
; CURRENT FILING DATE: 2002-01-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-10-037-990-2

Query Match 75.0%; Score 21; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTTATCAGGCAGT 21
Db 4 GCAAGCACCTTATCAGGCAGT 24

RESULT 35
US-10-230-381-34/c
; Sequence 34, Application US/10230381
```

```
; Publication No. US20030152591A1
; GENERAL INFORMATION:
; APPLICANT: Immunogenetics N.V.
; TITLE OF INVENTION: New hepatitis C virus genotype 13, and its use as prophylactic,
; FILE REFERENCE: INNX-124-EP
; CURRENT APPLICATION NUMBER: US/10/230,381
; CURRENT FILING DATE: 2002-08-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: HCP# 666
US-10-230-381-34

Query Match 75.0%; Score 21; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTTATCAGGCAGT 21
Db 21 GCAAGCACCTTATCAGGCAGT 1

RESULT 36
US-10-007-389-5
; Sequence 5, Application US/10007389
; Publication No. US20030165855A1
; GENERAL INFORMATION:
; APPLICANT: Russman, Eberhard
; APPLICANT: Meier, Thomas
; APPLICANT: Schmuck, Ranier
; APPLICANT: Staepels, Johnny
; APPLICANT: Wehnes, Uwe
; TITLE OF INVENTION: Methods for the analysis of non-proteinaceous
; FILE REFERENCE: Esperase
; CURRENT APPLICATION NUMBER: US/10/007,389
; CURRENT FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)
; OTHER INFORMATION: Biotin derivatization
US-10-007-389-5

Query Match 75.0%; Score 21; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTTATCAGGCAGT 21
Db 4 GCAAGCACCTTATCAGGCAGT 24

RESULT 37
US-10-322-138-2
; Sequence 2, Application US/10322138
; Publication No. US2003017565A1
; GENERAL INFORMATION:
; APPLICANT: Kessler, Christoph
; APPLICANT: Haberhausen, Gerd
; APPLICANT: Bartl, Knut
; APPLICANT: Orum, Henrik
```

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; TITLE OF INVENTION: SPECIFIC AND SENSITIVE METHOD FOR DETECTING NUCLEIC ACIDS
; FILE REFERENCE: 4817/OQ
; CURRENT APPLICATION NUMBER: US/10/322,138
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US/09/530,746B
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 2
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amplification primer
US-10-322-138-2

Query Match          75.0%; Score 21; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCCCTATCAGGCAGT 21
    |||||
Db 4 GCAAGCACCCCTATCAGGCAGT 24

RESULT 38
US-10-396-964-51/c
; Sequence 51, Application US/10396964
; Publication No. US20030198946A1
; GENERAL INFORMATION:
; APPLICANT: Simmonds, Peter
; APPLICANT: Chan, Shiu-Wan
; APPLICANT: Yap, Peng L.
; TITLE OF INVENTION: Hepatitis-C Virus Testing
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seltzer, Park & Gibson, P.A.
; STREET: 1211 East Morehead Street
; CITY: Charlotte
; STATE: NO. US20030198946A1th Carolina
; COUNTRY: United States
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0. Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/396,964
; FILING DATE: 23-MARCH-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/244,116B
; FILING DATE: 15-JUL-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/02143
; FILING DATE: 20-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 1749-125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 704-377-1561
; TELEFAX: 704-334-2014
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
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; DESCRIPTION: oligonucleotide"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Hepatitis-C virus
US-10-396-964-51

Query Match          75.0%; Score 21; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCCCTATCAGGCAGT 21
    |||||
Db 21 GCAAGCACCCCTATCAGGCAGT 1

RESULT 39
US-10-147-679A-6
; Sequence 6, Application US/10147679A
; Publication No. US20030224366A1
; GENERAL INFORMATION:
; APPLICANT: Weindel, Kurt
; APPLICANT: Riedling, Michael
; APPLICANT: Geiger, Albert
; TITLE OF INVENTION: Magnetic glass particles, method for their preparation
; FILE OF INVENTION: and uses thereof
; FILE REFERENCE: 1803-344-999
; CURRENT APPLICATION NUMBER: US/10/147,679A
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: EP99122853.7
; PRIOR FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide primer (HCV reverse)
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)
; OTHER INFORMATION: Biotin derivatization
US-10-147-679A-6

Query Match          75.0%; Score 21; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCCCTATCAGGCAGT 21
    |||||
Db 4 GCAAGCACCCCTATCAGGCAGT 24

RESULT 40
US-10-655-508-5
; Sequence 5, Application US/10655508
; Publication No. US20040063155A1
; GENERAL INFORMATION:
; APPLICANT: Russman, Eberhard
; APPLICANT: Meier, Thomas
; APPLICANT: Schmuck, Ranier
; APPLICANT: Staepels, Johnny
; APPLICANT: Wehnes, Uwe
; TITLE OF INVENTION: Methods for the analysis of non-proteinaceous
; FILE REFERENCE: Esperase
; FILE REFERENCE: US/10/655,508
; CURRENT APPLICATION NUMBER: 2003-09-03
; PRIOR APPLICATION NUMBER: US/10/007,389
; PRIOR FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 12
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)
; OTHER INFORMATION: Biotin derivatization
US-10-655-508-5
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Query Match      75.0%; Score 21; DB 16; Length 24;
Best Local Similarity 100.0%; Pred.No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 GCAGCACCTTATCAGGCAGT 21
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Db      4 GCAGCACCTTATCAGGCAGT 24
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Job time : 139.396 secs
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:59:28 ; Search time 1342.43 Seconds  
(without alignments)  
760.051 Million cell updates/sec

Title: US-10-087-631B-7

Perfect score: 28  
Sequence: 1 gcaagcaccctatcagcgatgacacaa 28

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 158194

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

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2: gb\_est2.\*

3: gb\_hic.\*

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5: gb\_est4.\*

6: gb\_est5.\*

7: gb\_est6.\*

8: gb\_gss1.\*

9: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 4	13.8	49.3	50	7	CK136536 MM2_2_1_C
C 5	13.8	49.3	50	8	BH903991 SALK_1037
C 6	13.6	48.6	42	9	AJ981240 Danilo rer
C 7	13.4	47.9	47	1	AV965348 AV965348
C 8	13.2	47.1	28	1	AA932343 oo60c02.s
C 9	13.2	47.1	32	8	A2434394 1M0220F13
C 10	13.2	47.1	40	8	A2775335 2M0007G07
C 11	13.2	47.1	49	1	AI445901 t_j6gh01.x
C 12	13.2	47.1	49	1	AI965799 sc76e01.y
C 13	13	46.4	32	9	CL210926 A027F07 G
C 14	13	46.4	40	9	AG192612 Pan trogl
C 15	13	46.4	41	8	A2768376 1M0568P14
C 16	13	46.4	41	9	CG987124 RRS785_Ba
C 17	12.8	45.7	30	5	BX625891 BX625891
C 18	12.8	45.7	37	1	AI077338 oy65902.x
C 19	12.8	45.7	37	1	AI917811 wb53c07.x
C 20	12.8	45.7	38	9	CL679725 PRI0126G
C 21	12.8	45.7	40	8	CC183071 XG571_Bay
C 22	12.8	45.7	42	8	A2329441 1M0053M07
C 23	12.8	45.7	47	8	A2663255 1M0542K15
C 24	12.8	45.7	47	8	AZ797405 2M0053D08

49	8	AZ790187	2M0038N03
32	4	BI223057	602942007
35	9	AG200947	Pan trogl
43	8	AZ760045	1M0553K20
44	1	AA529852	vj13c07_r
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50	9	BX143358	Danio rer
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33	8	AZ766010	1M0563H13
38	8	AZ403184	1M0170C23
39	4	BJ063882	BJ063882
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50	8	AZ621023	1M045C04
39	8	AZ584738	1M0389A07
42	4	AZ282802	2M0105011
43	1	AI000180	oe45f08_b
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45	9	AL759189	Arabidops
48	9	CC894209	RRK023_Ba
50	1	AU105915	AU105915
33	9	AG195430	Pan trogl
36	8	AZ812410	2M0079M01
37	9	AL751473	Arabidops
39	7	T68192	YC40h05_81
39	8	BZ291626	SALK_1214
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43	8	AZ641546	1M0504F11
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50	1	AU102446	AU102446
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50	1	AU106020	AU106020
50	1	AU106304	AU106304
50	4	BI417997	LjNEST32e
50	9	CR217452	Reverse_8
26	8	AZ782009	2M0021F19
37	1	AJ666258	AJ666258
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33	4	BI524206	603051954
35	9	TA213F04Q	T_brucei
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37	9	CL436898	PST4053-N
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29	8	AZ787298	2M0033016
29	8	AZ661221	1M0539N07
31	9	CG724642	1119082B0
34	8	AQ025206	EP(3)1249
35	9	CL528704	ASV3G11.f
35	9	CL655250	PR10122d
36	2	AW247788	2820164_5
36	8	AZ453979	1M0255A13
37	4	PG393320	602411536
39	9	AJ590068	Arabidops
40	1	AA789732	vt78d02_r
40	8	AZ463268	1M0272B01
42	7	CF972652	PSU_2b1-a
42	7	CF972796	PSU_2b1c\

C 98	11.6	41.4	43	7	D44819	D44819 HUMSUPY271	171	11.2	40.0	44	9	CG710099	CG710099 1119015B0
C 99	11.6	41.4	43	9	TA38BD01P	AL498777 T. brucei	172	11.2	40.0	46	9	HSNC04F12	X88481 H. eapilens D
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C 101	11.6	41.4	46	6	CF334549	CF334549 JMT--03-O	C 174	11.2	40.0	47	8	AZ618994	AZ618994 1M0451C11
C 102	11.6	41.4	46	8	AZ324779	AZ324779 1M0406D22	C 175	11.2	40.0	47	8	AZ769994	AZ769994 1M0571A14
C 103	11.6	41.4	46	8	AQ254727	AQ254727 EP(3)3520	C 176	11.2	40.0	47	8	BH851581	BH851581 SALK_0732
C 104	11.6	41.4	47	8	AZ584664	AZ584664 1M0389A22	C 177	11.2	40.0	48	2	BF507210	BF507210 3659F-23
C 105	11.6	41.4	49	8	AZ497375	AZ497375 1M0334N10	C 178	11.2	40.0	48	2	AW497611	AW497611 RARGGSB34
C 106	11.6	41.4	49	8	AZ950523	AZ950523 2M0214G12	C 179	11.2	40.0	49	2	AY356299	AY356299 AY356299
C 107	11.6	41.4	50	1	AU103419	AU103419 AU103419	C 180	11.2	40.0	49	2	BE778801	BE778801 601463874
C 108	11.6	41.4	50	1	AU105582	AU105582 AU105582	C 181	11.2	40.0	49	8	AZ812510	AZ812510 2M0079A17
C 109	11.6	41.4	50	1	AU107620	AU107620 AU107620	C 182	11.2	40.0	50	1	AU1539113	AU1539113 2M0079A17
C 110	11.6	41.4	50	4	BH75539	BH75539 YW14112.81	C 183	11.2	40.0	50	1	AU103947	AU103947 AU103947
C 111	11.6	41.4	50	7	CG710737	CG710737 1119018F0	C 184	11.2	40.0	50	1	AU104141	AU104141 AU104141
C 112	11.6	41.4	50	9	AZ436588	AZ436588 1M0224H20	C 185	11.2	40.0	50	1	AU104173	AU104173 AU104173
C 113	11.4	40.7	24	8	AZ436588	N81476 TGESTZY47H0	C 186	11.2	40.0	50	1	AU106817	AU106817 AU106817
C 114	11.4	40.7	28	7	N81476	AZ592432 1M0403C19	C 187	11.2	40.0	50	1	AU107948	AU107948 AU107948
C 115	11.4	40.7	31	8	AZ592432	BH863404 SALK_0938	C 188	11.2	40.0	50	1	AU107953	AU107953 AU107953
C 116	11.4	40.7	35	8	BH863404	BH863405 SALK_0938	C 189	11.2	40.0	50	1	AU107959	AU107959 AU107959
C 117	11.4	40.7	35	8	BH863405	R37960 YC99G06.s1	C 190	11.2	40.0	50	1	AU107960	AU107960 AU107960
C 118	11.4	40.7	36	7	R37960	BF507311 8949P-20	C 191	11.2	40.0	50	8	AU107961	AU107961 AU107961
C 119	11.4	40.7	38	2	BF507311	AZ603310 1M0422N12	C 192	11.2	40.0	50	8	BH644632	BH644632 1008053H0
C 120	11.4	40.7	39	8	AZ603310	AZ992328 2M0276N21	C 193	11.2	40.0	50	9	CR035505	CR035505 Forward s
C 121	11.4	40.7	41	8	AZ992328	AZ770047 1M0571B19	C 194	11.2	40.0	50	9	CR210504	CR210504 Reverse s
C 122	11.4	40.7	42	8	AZ770047	AJ550295 AJ550295	C 195	11.2	40.0	50	9	CL437542	CL437542 PST5824-N
C 123	11.4	40.7	43	1	AJ550295	AA008276 mg9608.r	C 196	11.2	40.0	50	9	AZ815189	AZ815189 2M0083116
C 124	11.4	40.7	46	1	AA008276	C00602 HUMGS00814	C 197	11.2	40.0	50	8	AZ774487	AZ774487 2M0004D01
C 125	11.4	40.7	46	6	C00602	BZ353134 SALK_1198	C 198	11.2	40.0	50	8	AL473686	AL473686 T. brucei
C 126	11.4	40.7	46	9	BZ353134	AG189289 Pan trogl	C 199	11.2	40.0	50	8	CF328601	CF328601 NACL--03-
C 127	11.4	40.7	46	9	AG189289	AV970199 AV970199	C 200	11.2	40.0	50	8	AI416615	AI416615 8A17405.Y
C 128	11.4	40.7	47	1	AV970199	H33908 y054b03.r1	C 201	11.2	40.0	50	8	AZ661810	AZ661810 1M0540M06
C 129	11.4	40.7	48	7	H33908	AJ587603 Arabidops	C 202	11.2	40.0	50	8	BH847090	BH847090 SALK_0131
C 130	11.4	40.7	48	9	AJ587603	AI743359 w95208.x	C 203	11.2	40.0	50	8	AL979577	AL979577 Danilo rer
C 131	11.4	40.7	49	1	AI743359	AZ639320 1M0499E15	C 204	11.2	40.0	50	8	AI413707	AI413707 zn70h11.s
C 132	11.4	40.7	49	8	AZ639320	AU104921 AU104921	C 205	11.2	40.0	50	8	AI437342	AI437342 fb30d01.s
C 133	11.4	40.7	50	1	AU104921	AU105471 AU105471	C 206	11.2	40.0	50	8	BZ765843	BZ765843 SALK_1347
C 134	11.4	40.7	50	1	AU105471	AU107067 AU107067	C 207	11.2	40.0	50	8	AB082322	AB082322 Drosophila
C 135	11.4	40.7	50	1	AU107067	AU107892 AU107892	C 208	11.2	40.0	50	8	AL048715	AL048715 DFPZP566G
C 136	11.4	40.7	50	1	AU107892	BI407217 602918987	C 209	11.2	40.0	50	8	AA161946	AA161946 mr92a03.r
C 137	11.4	40.7	50	1	AU107962	AZ510728 1M0355120	C 210	11.2	40.0	50	8	BG178709	BG178709 602328612
C 138	11.4	40.7	50	8	BI407217	AZ765968 1M0563N12	C 211	11.2	40.0	50	8	CA796225	CA796225 Cac BL 32
C 139	11.4	40.7	50	8	AZ510728	EX985119 Reverse s	C 212	11.2	40.0	50	8	AZ769030	AZ769030 1M0569M13
C 140	11.4	40.7	50	8	AZ765968	AL458883 T. brucei	C 213	11.2	40.0	50	8	CF281514	CF281514 14FTL--08
C 141	11.4	40.7	50	9	EX985119	AZ309919 1M0017C19	C 214	11.2	40.0	50	8	H62327	H62327 Yr15F04.r1
C 142	11.4	40.7	50	9	TA101G05P	AJ678364 AJ678364	C 215	11.2	40.0	50	8	BZ379922	BZ379922 SALK_1142
C 143	11.2	40.0	25	8	AJ678364	AA670361 ad16e07.s	C 216	11.2	40.0	50	8	CF337251	CF337251 JMT--07-J
C 144	11.2	40.0	26	1	AA670361	AZ348137 1M0084O12	C 217	11.2	40.0	50	8	AZ537206	AZ537206 AST--2F027
C 145	11.2	40.0	31	8	AZ348137	AZ823090 2M0096122	C 218	11.2	40.0	50	8	BH641954	BH641954 1008051F1
C 146	11.2	40.0	31	8	AZ823090	AZ784432 2M0027E05	C 219	11.2	40.0	50	8	AZ509372	AZ509372 1M0352J17
C 147	11.2	40.0	32	8	AZ823432	AL485304 T. brucei	C 220	11.2	40.0	50	8	AZ833541	AZ833541 2M0115N08
C 148	11.2	40.0	33	9	TA266B04Q	BH792223 SALK_0630	C 221	11.2	40.0	50	8	BH641050	BH641050 1008039H1
C 149	11.2	40.0	34	8	BH792223	CC053711 SALK_0469	C 222	11.2	40.0	50	8	AA010457	AA010457 ze18e03.r
C 150	11.2	40.0	34	8	CC053711	AA628011 1M0476K12	C 223	11.2	40.0	50	8	AA120160	AA120160 mn33c12.r
C 151	11.2	40.0	34	8	AA628011	AA625816 zV87a04.s	C 224	11.2	40.0	50	8	AA1010457	AA1010457 ox02e11.s
C 152	11.2	40.0	36	8	AA625816	CC053707 SALK_0469	C 225	11.2	40.0	50	8	AA389458	AA389458 mp25e02.r
C 153	11.2	40.0	37	1	AA625816	AL497988 T. brucei	C 226	11.2	40.0	50	8	W07483	W07483 za96d11.r1
C 154	11.2	40.0	37	8	TA383E12Q	BJ082050 BJ082050	C 227	11.2	40.0	50	8	AZ768227	AZ768227 1M0568C08
C 155	11.2	40.0	37	9	TA383E12Q	AZ428906 1M0212C14	C 228	11.2	40.0	50	8	AZ795793	AZ795793 2M0051007
C 156	11.2	40.0	39	4	BJ082050	AI766423 wh49H03.x	C 229	11.2	40.0	50	8	BH909849	BH909849 SALK_0562
C 157	11.2	40.0	39	8	AZ428906	AJ600768 Arabidops	C 230	11.2	40.0	50	8	CC886323	CC886323 SALK_1484
C 158	11.2	40.0	40	1	AI766423	AG203784 Pan trogl	C 231	11.2	40.0	50	8	AZ801261	AZ801261 2M0059H08
C 159	11.2	40.0	40	9	AJ600768	BE872091 601448183	C 232	11.2	40.0	50	8	BT094799	BT094799 EP(2)0882
C 160	11.2	40.0	40	9	AG203784	AZ335532 1M0065H05	C 233	11.2	40.0	50	8	AZ300919	AZ300919 EST--CD34N
C 161	11.2	40.0	41	2	BE872091	AZ873114 2M0196B15	C 234	11.2	40.0	50	8	AZ759426	AZ759426 1M0551113
C 162	11.2	40.0	41	8	AZ873114	BE892628 601433437	C 235	11.2	40.0	50	8	AZ774612	AZ774612 2M0004O24
C 163	11.2	40.0	41	8	BE892628	AI047023 uh57e09.r	C 236	11.2	40.0	50	8	AZ786390	AZ786390 2M0031E19
C 164	11.2	40.0	42	1	AI047023	AQ025179 EP(3)1110	C 237	11.2	40.0	50	8	AL464659	AL464659 T. brucei
C 165	11.2	40.0	43	1	AQ025179	AJ599570 Arabidops	C 238	11.2	40.0	50	8	AZ333191	AZ333191 1M0062F09
C 166	11.2	40.0	43	8	AJ599570	CG740003 SILB06a25	C 239	11.2	40.0	50	8	BZ591175	BZ591175 3590.1.82
C 167	11.2	40.0	44	7	CG740003	CG709849 1119015B0	C 240	11.2	40.0	50	8	AJ600891	AJ600891 Arabidops
C 168	11.2	40.0	44	7	CG709849	CG709873 1119015C0	C 241	11.2	40.0	50	9	CG807819	CG807819 1118087C0
C 169	11.2	40.0	44	9	CG709873		C 242	11.2	40.0	50	9	AU102447	AU102447 AU102447
C 170	11.2	40.0	44	9			C 243	11.2	40.0	50	1		

C 244	11	39.3	50	1	AUI03013	AUI03013	317	10.6	38.6	50	1	AUI05458	AUI05458
C 245	11	39.3	50	1	AUI03014	AUI03014	318	10.8	38.6	50	1	AUI05460	AUI05460
C 246	11	39.3	50	1	AUI04142	AUI04142	319	10.8	38.6	50	1	AUI05461	AUI05461
C 247	11	39.3	50	1	AUI06298	AUI06298	320	10.8	38.6	50	1	AUI05462	AUI05462
C 248	11	39.3	50	1	AUI07101	AUI07101	321	10.8	38.6	50	1	AUI05464	AUI05464
C 249	11	39.3	50	8	A2875367	2M0189024	322	10.8	38.6	50	1	AUI05467	AUI05467
C 250	11	39.3	50	8	A2918083	1M06003B0	323	10.8	38.6	50	1	AUI05468	AUI05468
C 251	11	39.3	50	8	B2664361	SALK_0706	324	10.8	38.6	50	1	AUI05469	AUI05469
C 252	11	39.3	50	9	BX293332	Arabidops	325	10.8	38.6	50	1	AUI05470	AUI05470
C 253	11	39.3	50	9	CL518432	SAB9F09 F	C 326	10.8	38.6	50	1	AUI07175	AUI07175
C 254	10.8	38.6	21	8	A2460367	1M0265J10	C 327	10.8	38.6	50	1	AUI07265	AUI07265
C 255	10.8	38.6	23	8	A2316364	AZ6034E19	C 328	10.8	38.6	50	1	AUI07266	AUI07266
C 256	10.8	38.6	27	8	A2303426	1M0033A09	C 329	10.8	38.6	50	1	AUI07267	AUI07267
C 257	10.8	38.6	28	7	T72278	Yc65N03.S1	C 330	10.8	38.6	50	1	AUI07268	AUI07268
C 258	10.8	38.6	28	8	A2432111	1M0217E05	C 331	10.8	38.6	50	1	AUI07269	AUI07269
C 259	10.8	38.6	29	9	BH846412	SALK_0078	C 332	10.8	38.6	50	1	AUI07940	AUI07940
C 260	10.8	38.6	29	9	CL661015	PR10138C	C 333	10.8	38.6	50	1	AUI07942	AUI07942
C 261	10.8	38.6	30	8	A2601864	AZ601864	C 334	10.8	38.6	50	1	AUI07951	AUI07951
C 262	10.8	38.6	32	9	CL524584	DAA9C01 F	C 335	10.8	38.6	50	1	AUI07957	AUI07957
C 263	10.8	38.6	33	8	A2641117	1M0503A06	C 336	10.8	38.6	50	1	AUI07965	AUI07965
C 264	10.8	38.6	34	1	AI796749	wal4d11.x	C 337	10.8	38.6	50	1	AUI07966	AUI07966
C 265	10.8	38.6	34	8	A2422317	1M0200007	C 338	10.8	38.6	50	4	BJ036965	BJ036965
C 266	10.8	38.6	35	7	BE909856	601496143	C 339	10.8	38.6	50	7	N70569	N70569
C 267	10.8	38.6	35	7	N73542	z850B02.S1	C 340	10.8	38.6	50	9	BX662452	BX662452
C 268	10.8	38.6	37	1	AA492333	ng81C07.S	C 341	10.8	38.6	50	9	BX895538	BX895538
C 269	10.8	38.6	37	2	AW245295	2820036.3	C 342	10.8	38.6	50	9	CR134688	Forward s
C 270	10.8	38.6	37	8	AZ506198	1M0347C12	C 343	10.8	38.6	50	9	CR888380	SALK_1517
C 271	10.8	38.6	38	8	AZ998182	2M0285D01	C 344	10.6	37.9	21	8	AZ805948	2M0067R12
C 272	10.8	38.6	39	1	AV836734	AV836734	C 345	10.6	37.9	24	4	BM395763	5009-0-11
C 273	10.8	38.6	39	4	B1087730	602852286	C 346	10.6	37.9	29	8	BH853496	
C 274	10.8	38.6	39	7	U44319	ENU44319 As	C 347	10.6	37.9	30	8	AQ026392	1(3182976
C 275	10.8	38.6	39	9	TA306D11P		C 348	10.6	37.9	30	8	AZ784633	
C 276	10.8	38.6	40	8	BZ589649	3590_1_71	C 349	10.6	37.9	32	8	AZ482042	1M0306C20
C 277	10.8	38.6	41	6	CF298687	7LEAF--02	C 350	10.6	37.9	33	7	N67043	z850E12.S1
C 278	10.8	38.6	41	6	CF300723	7LEAF--05	C 351	10.6	37.9	33	9	BX662497	Arabidops
C 279	10.8	38.6	41	8	A2645689	1M0511H16	C 352	10.6	37.9	34	1	AA798808	vm43d09.r
C 280	10.8	38.6	41	8	A2645689	1M0511H16	C 353	10.6	37.9	34	1	AI790112	ue64902.r
C 281	10.8	38.6	41	8	A2645689	1M0511H16	C 354	10.6	37.9	34	1	AA237815	mx29a05.r
C 282	10.8	38.6	42	6	CS8084	CS8084_Yuji	C 355	10.6	37.9	34	8	AZ491530	1M0325H09
C 283	10.8	38.6	42	9	AG190850	Pan trogl	C 356	10.6	37.9	36	7	CF973738	PSU Joeca
C 284	10.8	38.6	42	9	AG190850	Pan trogl	C 357	10.6	37.9	36	8	AZ308346	1M0011C14
C 285	10.8	38.6	43	1	AI004121	ot54a09.s	C 358	10.6	37.9	36	8	BZ383557	SALK_1341
C 286	10.8	38.6	43	1	AI795121	sb77a11.y	C 359	10.6	37.9	37	8	AZ381090	1M0137J20
C 287	10.8	38.6	43	1	AJ649066	AJ649066	C 360	10.6	37.9	37	8	BZ383548	SALK_1340
C 288	10.8	38.6	43	9	CL436351	PS72795-N	C 361	10.6	37.9	38	1	AJ648502	AJ648502
C 289	10.8	38.6	44	6	CF298909	7LEAF--02	C 362	10.6	37.9	38	6	CO1982	HUMGS000400
C 290	10.8	38.6	44	8	A2823752	2M0098A04	C 363	10.6	37.9	38	9	CR400428	Arabidops
C 291	10.8	38.6	44	9	A2823752	2M0098A04	C 364	10.6	37.9	38	9	CL528419	ASV10F01
C 292	10.8	38.6	44	9	AV960508	AV960508	C 365	10.6	37.9	39	4	BI559436	603252932
C 293	10.8	38.6	45	8	AZ310900	1M0026N04	C 366	10.6	37.9	39	4	BI838507	603083494
C 294	10.8	38.6	45	8	AZ796408	2M0052E12	C 367	10.6	37.9	39	6	CF113888	Shultzomi
C 295	10.8	38.6	46	1	AI019594	u91a06.r	C 368	10.6	37.9	39	6	CF290826	14ROOT--0
C 296	10.8	38.6	46	1	AI144303	qb59h11.x	C 369	10.6	37.9	39	8	AZ663490	1M0543G11
C 297	10.8	38.6	46	1	AI45519	ms06f11.r	C 370	10.6	37.9	39	8	AJ598250	Arabidops
C 298	10.8	38.6	46	8	AZ498067	1M0335J12	C 371	10.6	37.9	40	1	AA746897	nx63a09.s
C 299	10.8	38.6	46	8	AZ781445	2M0019N18	C 372	10.6	37.9	40	1	AA937425	oj09b08.s
C 300	10.8	38.6	46	8	BH171419	SALK_0042	C 373	10.6	37.9	40	1	AI138679	ta49g08.x
C 301	10.8	38.6	46	8	BH611947	BH611947	C 374	10.6	37.9	40	7	H79514	YU44g02.S1
C 302	10.8	38.6	46	9	DR85D1T	Danio rer	C 375	10.6	37.9	40	8	AZ346802	1M0082011
C 303	10.8	38.6	47	8	AZ209567	1M0016F07	C 376	10.6	37.9	41	8	AZ436596	1M0224122
C 304	10.8	38.6	47	8	BZ768669	SALK_1405	C 377	10.6	37.9	41	9	EX203165	Danio rer
C 305	10.8	38.6	47	9	AL940725	Arabidops	C 378	10.6	37.9	42	8	AZ383427	1M0141N02
C 306	10.8	38.6	48	7	U44313	ENU44313 As	C 379	10.6	37.9	42	8	AZ977990	2M0254P06
C 307	10.8	38.6	48	7	W10946	ms46b10.r1	C 380	10.6	37.9	43	1	AA616908	AL6669008
C 308	10.8	38.6	48	8	AZ784814	2M0028M02	C 381	10.6	37.9	43	1	AA613679	no38b05.s
C 309	10.8	38.6	48	8	AZ805973	2M0067M10	C 382	10.6	37.9	44	8	AZ760412	1M0554110
C 310	10.8	38.6	48	8	BZ766237	SALK_1369	C 383	10.6	37.9	44	9	TA308F05Q	
C 311	10.8	38.6	49	1	AA995234	ou17a05.s	C 384	10.6	37.9	44	9	CG271761	T. brucei
C 312	10.8	38.6	49	7	CN752480	ApHL3LD-I	C 385	10.6	37.9	44	9	CG722451	1119068H0
C 313	10.8	38.6	50	1	AUI02362	AUI02362	C 386	10.6	37.9	45	1	AA276118	vc36d12.r
C 314	10.8	38.6	50	1	AUI02695	AUI02695	C 387	10.6	37.9	45	6	CF054916	OCN34f07.r
C 315	10.8	38.6	50	1	AUI02702	AUI02702	C 388	10.6	37.9	46	1	AA722219	zh21a09.s
C 316	10.8	38.6	50	1	AUI03416	AUI03416	C 389	10.6	37.9	46	1	AI545027	Fb73907.x

C 390	10.6	37.9	46	4	B1829941	B1829941	6030800075
C 391	10.6	37.9	46	8	AZ759592	AZ759592	1M0552D23
C 392	10.6	37.9	46	8	AZ792431	AZ792431	2M0043E21
C 393	10.6	37.9	46	8	AZ821566	AZ821566	2M00094F21
C 394	10.6	37.9	46	8	AZ831192	AZ831192	2M0112L06
C 395	10.6	37.9	46	9	BX231478	BX231478	Danio rer
C 396	10.6	37.9	46	9	CG722939	CG722939	1119074B0
C 397	10.6	37.9	47	1	CG570265	CG570265	nf39F06.s
C 398	10.6	37.9	47	1	CG716081	CG716081	1119044E0
C 399	10.6	37.9	47	9	CL665793	CL665793	PR1014d.A
C 400	10.6	37.9	48	1	AA602253	AA602253	mp13c0d1.s
C 401	10.6	37.9	48	8	AZ496155	AZ496155	1M0332K15
C 402	10.6	37.9	48	8	BZ230752	BZ230752	SALK_0912
C 403	10.6	37.9	49	1	AA936278	AA936278	on75e07.s
C 404	10.6	37.9	49	1	AJ746758	AJ746758	AJ746758
C 405	10.6	37.9	49	4	BG099459	BG099459	naq44e02.
C 406	10.6	37.9	49	4	B1113311	B1113311	602900277
C 407	10.6	37.9	49	4	B1873153	B1873153	603397612
C 408	10.6	37.9	49	6	CAB45431	CAB45431	hab999g11.
C 409	10.6	37.9	49	7	H14049	H14049	vm5h05.r1
C 410	10.6	37.9	49	9	CG799286	CG799286	1118001F0
C 411	10.6	37.9	50	1	AU102669	AU102669	AU102669
C 412	10.6	37.9	50	1	AU102768	AU102768	AU102768
C 413	10.6	37.9	50	1	AU102773	AU102773	AU102773
C 414	10.6	37.9	50	1	AU102788	AU102788	AU102788
C 415	10.6	37.9	50	1	AU102792	AU102792	AU102792
C 416	10.6	37.9	50	1	AU103069	AU103069	AU103069
C 417	10.6	37.9	50	1	AU103398	AU103398	AU103398
C 418	10.6	37.9	50	1	AU103417	AU103417	AU103417
C 419	10.6	37.9	50	1	AU104386	AU104386	AU104386
C 420	10.6	37.9	50	1	AU104854	AU104854	AU104854
C 421	10.6	37.9	50	1	AU107087	AU107087	AU107087
C 422	10.6	37.9	50	1	AA589316	AA589316	vm36402.f
C 423	10.6	37.9	50	7	D20656	D20656	HUMG501632
C 424	10.6	37.9	50	8	CC456525	CC456525	SALK_0989
C 425	10.4	37.1	22	1	A1269362	A1269362	1M0134L02
C 426	10.4	37.1	22	9	TA134B10Q	TA134B10Q	q174g03.x
C 427	10.4	37.1	22	9	TA70B11Q	TA70B11Q	T. brucei
C 428	10.4	37.1	24	6	CF329168	CF329168	NaCL--04-
C 429	10.4	37.1	25	9	TA133B01P	TA133B01P	T. brucei
C 430	10.4	37.1	26	8	AZ435264	AZ435264	1M0222G12
C 431	10.4	37.1	26	9	TA129A07P	TA129A07P	T. brucei
C 432	10.4	37.1	29	8	AZ598234	AZ598234	1M0412O23
C 433	10.4	37.1	30	9	AJ593242	AJ593242	ArabiIdops
C 434	10.4	37.1	31	1	AA977899	AA977899	oq62b09.s
C 435	10.4	37.1	31	9	CG707724	CG707724	1119003E1
C 436	10.4	37.1	31	9	CG707746	CG707746	1119003F0
C 437	10.4	37.1	31	9	CL682876	CL682876	PR10135b-
C 438	10.4	37.1	32	1	AJ790259	AJ790259	AJ790259
C 439	10.4	37.1	32	8	AZ513928	AZ513928	1M0360G15
C 440	10.4	37.1	32	8	AZ654189	AZ654189	1M0528B14

536	10.2	36.4	30	9	AG204931	Pan trogl	609	10.2	36.4	49	1	AI185705	AI185705	
c 537	10.2	36.4	31	8	AZ794691	2M0048N04	c 610	10.2	36.4	49	1	AJ649956	AJ649956	
538	10.2	36.4	32	9	CG720047	1119060D0	611	10.2	36.4	49	1	AA410762	zt35ell.r	
c 539	10.2	36.4	33	8	AZ828702	2M0105P14	c 612	10.2	36.4	49	2	BF203474	601865731	
c 540	10.2	36.4	34	1	AA889919	aj87g07.s	613	10.2	36.4	49	4	BG099520	na953c01	
541	10.2	36.4	34	1	AI367422	qW18h03.x	c 614	10.2	36.4	49	7	DI8209	MUSGS00479	
c 542	10.2	36.4	34	4	BH396017	5009-0-15	c 615	10.2	36.4	49	7	HI4959	Ym19c11.s1	
c 543	10.2	36.4	34	6	CA587274	LBE10p42	616	10.2	36.4	49	7	H28255	Yl6e0e3.r1	
c 544	10.2	36.4	34	8	AZ761910	1M0556C05	c 617	10.2	36.4	49	7	T56757	ya71d06.r1	
c 545	10.2	36.4	34	8	AZ804148	2M0064G23	618	10.2	36.4	49	8	AZ578707	26C12 Sho	
546	10.2	36.4	35	8	AZ448253	1M0245013	619	10.2	36.4	49	8	AZ615333	1M0444D09	
c 547	10.2	36.4	35	9	DME545696	Drosophil	c 620	10.2	36.4	49	9	BX120175	Danio rer	
c 548	10.2	36.4	36	9	CC888822	SALK_1524	c 621	10.2	36.4	50	1	AJ652427	AJ652427	
549	10.2	36.4	37	1	AI790648	u103a07.x	c 622	10.2	36.4	50	1	AUI02661	AUI02661	
c 550	10.2	36.4	37	8	AZ444497	1M0239A16	c 623	10.2	36.4	50	1	AUI02956	AUI02956	
c 551	10.2	36.4	37	8	AZ789783	2M0037H19	c 624	10.2	36.4	50	1	AUI03410	AUI03410	
c 552	10.2	36.4	37	8	AZ972111	2M0245A22	c 625	10.2	36.4	50	1	AUI03415	AUI03415	
553	10.2	36.4	37	8	CC053865	SALK_0494	c 626	10.2	36.4	50	1	AUI03418	AUI03418	
c 554	10.2	36.4	37	9	DR43028	AL977257	Danio rer	c 627	10.2	36.4	50	1	AUI05156	AUI05156
c 555	10.2	36.4	38	1	AB088499	AB088499	c 628	10.2	36.4	50	1	AUI05553	AUI05553	
556	10.2	36.4	38	4	BG912318	602806861	c 629	10.2	36.4	50	1	AUI05839	AUI05839	
c 557	10.2	36.4	38	8	AZ811787	2M0078N06	630	10.2	36.4	50	1	AUI07908	AUI07908	
c 558	10.2	36.4	39	2	BE874819	601488760	631	10.2	36.4	50	1	AUI07909	AUI07909	
c 559	10.2	36.4	40	1	AA160572	zq46d11.x	632	10.2	36.4	50	1	AUI07910	AUI07910	
560	10.2	36.4	40	2	BF026645	601672360	633	10.2	36.4	50	1	AUI07937	AUI07937	
c 561	10.2	36.4	40	7	T18543	hbc2020 Hum	c 634	10.2	36.4	50	2	AW424126	sh61c07.y	
c 562	10.2	36.4	40	9	AL753199	AL753199	c 635	10.2	36.4	50	8	AZ765968	1M0563M12	
c 563	10.2	36.4	40	9	TA253H01Q	Arabidops	c 636	10.2	36.4	50	8	AZ862310	2M0169022	
c 564	10.2	36.4	40	9	CG869712	CG869712	c 637	10.2	36.4	50	9	BX123067	Danio rer	
565	10.2	36.4	41	1	AA976917	Qq35h04.s	638	10.2	36.4	50	9	CR236244	Forward s	
c 566	10.2	36.4	41	1	AI568481	tn39g09.x	c 639	10.2	36.4	50	9	AG194315	Pan trogl	
567	10.2	36.4	41	8	AF039768	AF039768	c 640	10.2	36.4	50	6	CD531370	10103 Ara	
c 568	10.2	36.4	41	8	AZ612511	1M0439006	c 641	10.2	36.4	50	21	TA45E03Q	T. brucei	
569	10.2	36.4	42	7	R84748	vt68h09.r1	642	10.2	36.4	50	9	BG896918	HOA59-1-B	
c 570	10.2	36.4	42	8	AZ815699	2M0084C13	643	10.2	36.4	50	9	AJ587708	Arabidops	
c 571	10.2	36.4	42	9	BX157082	Danio rer	644	10.2	36.4	50	9	AJ587708	Arabidops	
572	10.2	36.4	42	9	AB082313	Drosophil	c 645	10.2	36.4	50	8	AZ307549	1M0009024	
c 573	10.2	36.4	42	9	AG203402	Pan trogl	c 646	10.2	36.4	50	8	AZ318715	1M0038D08	
574	10.2	36.4	43	1	AI020994	ua98e01.r	647	10.2	36.4	50	28	AA974354	Qq14f03.s	
c 575	10.2	36.4	43	9	CG779709	CG779709	648	10.2	36.4	50	1	AI218854	QG75g06.x	
576	10.2	36.4	43	9	CL212287	G037D05.G	649	10.2	36.4	50	8	AZ647786	1M0514P23	
577	10.2	36.4	44	7	H39421	DR115 IFNga	c 650	10.2	36.4	50	8	AZ661529	1M0540U01	
c 578	10.2	36.4	44	7	H97472	H97472	c 651	10.2	36.4	50	8	BH901129	SALK_0731	
c 579	10.2	36.4	44	7	T68451	Yc42f02.b1	c 652	10.2	36.4	50	8	BZ769424	SALK_1421	
c 580	10.2	36.4	44	8	BH811570	SALK_0591	653	10.2	36.4	50	3	CL439155	PST8752-N	
581	10.2	36.4	44	8	BZ663210	Q268	c 654	10.2	36.4	50	3	CA587688	LBE14p53P	
c 582	10.2	36.4	44	9	TA83E04Q	T. brucei	c 655	10.2	36.4	50	3	BZ355049	SALK_1262	
583	10.2	36.4	45	4	BH862028	BI862028	c 656	10.2	36.4	50	3	DR19J3S	Danio rer	
c 584	10.2	36.4	45	8	BH848020	hbc2020 SALK_0673	c 657	10.2	36.4	50	31	AA781776	ai51a12.s	
585	10.2	36.4	46	1	AA027616	mi08c08.r	c 658	10.2	36.4	50	31	AU256721	AU256721	
586	10.2	36.4	46	1	AA062105	mj84d05.r	c 659	10.2	36.4	50	31	AZ789801	2M0037L19	
c 587	10.2	36.4	46	1	AA906763	oi16a08.s	660	10.2	36.4	50	31	BX893918	Arabidops	
588	10.2	36.4	46	1	AI021500	ub12f02.r	661	10.2	36.4	50	32	BF316607	601903146	
c 589	10.2	36.4	46	1	AI182421	uc24h04.r	c 662	10.2	36.4	50	32	BE277972	601179981	
590	10.2	36.4	46	2	BE778884	601465146	663	10.2	36.4	50	32	T92842	ye27a08.r1	
c 591	10.2	36.4	46	8	BH848546	SALK_0685	664	10.2	36.4	50	32	T92862	ye27e08.r1	
c 592	10.2	36.4	47	9	BX658078	Arabidops	665	10.2	36.4	50	32	TA326F02Q	T. brucei	
c 593	10.2	36.4	47	9	AA651618	ns65g11.s	666	10.2	36.4	50	32	AZ424156	1M0203C09	
594	10.2	36.4	48	4	BJ034532	BJ034532	667	10.2	36.4	50	32	AZ514079	1M0360F07	
c 595	10.2	36.4	48	4	BM285362	EST00003	668	10.2	36.4	50	32	AZ834737	2M0117006	
c 596	10.2	36.4	48	4	BM493234	EST000017	669	10.2	36.4	50	33	CC889158	SALK_1528	
597	10.2	36.4	48	5	BQ094078	040802_37	c 670	10.2	36.4	50	33	AG199552	Pan trogl	
c 598	10.2	36.4	48	5	BQ094080	040802_39	671	10.2	36.4	50	33	AG199552	Pan trogl	
599	10.2	36.4	48	5	BQ094081	040802_40	c 672	10.2	36.4	50	34	AA954884	op20e10.s	
600	10.2	36.4	48	5	BQ094082	040802_41	c 673	10.2	36.4	50	34	AI142664	ok38h07.s	
c 601	10.2	36.4	48	5	BQ094086	040802_45	674	10.2	36.4	50	34	BJ040736	BJ040736	
602	10.2	36.4	48	5	BQ094088	040802_47	c 675	10.2	36.4	50	34	BX659099	Arabidops	
603	10.2	36.4	48	9	BX122790	Danio rer	c 676	10.2	36.4	50	34	TA196C06P	T. brucei	
604	10.2	36.4	48	9	CL517714	SAAGA01.F	c 677	10.2	36.4	50	35	AI044927	DKFZp434N	
605	10.2	36.4	48	9	CL528747	ASV7F07.f	678	10.2	36.4	50	35	BH812616	SALK_0621	
606	10.2	36.4	49	1	AA870263	vq13g11.r	c 679	10.2	36.4	50	36	BG765238	602738656	
c 607	10.2	36.4	49	1	AA990502	ua62g06.s	680	10.2	36.4	50	36	BX654718	Arabidops	
c 608	10.2	36.4	49	1	AI052522	oz27f05.x	c 681	10.2	36.4	50	36	CL684480	PRI0139C_	

682	10	35.7	37	1	AA706652	AA706652 ag90g06.i	c 755	10	35.7	49	1	AA717442	AA717442 vvl9406.i
683	10	35.7	37	1	A1047840	A1047840 u64a04.x	756	10	35.7	49	1	A1098407	A1098407 uc05d10.i
684	10	35.7	37	1	A1119228	A1119228 ue24a02.y	c 757	10	35.7	49	1	A1185705	A1185705 q6e0h06.x
685	10	35.7	37	8	A2597440	A2597440 IM0411i23	758	10	35.7	49	1	A1326039	A1326039 mr-66c09.x
686	10	35.7	38	9	AZ463776	AZ463776 IM0272P15	759	10	35.7	49	1	A1385645	A1385645 m74c04.x
687	10	35.7	38	9	AG195969	AG195969 Pan trogl	c 760	10	35.7	49	1	A1719563	A1719563 as54d09.x
688	10	35.7	39	8	AZ346424	AZ346424 IM0081N12	761	10	35.7	49	1	A1883392	A1883392 as54d09.x
689	10	35.7	39	8	AZ379756	AZ379756 IM0135C18	c 762	10	35.7	49	4	AG058867	AG058867 f6c3d06.y
690	10	35.7	39	8	AZ797170	AZ797170 2M0053C18	763	10	35.7	49	4	AG058867	AG058867 f6c3d06.y
691	10	35.7	40	1	A1583366	A1583366 ts15906.x	764	10	35.7	49	4	AG058867	AG058867 f6c3d06.y
692	10	35.7	40	1	A1609582	A1609582 tw28c02.x	c 765	10	35.7	49	6	CD533308	CD533308 ag49e04.
693	10	35.7	40	1	A1900047	A1900047 sb98b08.y	c 766	10	35.7	49	8	CO780197	CO780197 BL0009A.A0
694	10	35.7	40	1	A1959989	A1959989 sc36b11.x	767	10	35.7	49	9	CG729392	CG729392 31B7 Arab
695	10	35.7	40	1	AJ7281519	AJ7281519 4A3A-P5D7	c 768	10	35.7	49	1	CG729392	CG729392 31B7 Arab
696	10	35.7	40	1	AV851018	AV851018 AV851018	769	10	35.7	49	1	CG729392	CG729392 31B7 Arab
697	10	35.7	40	1	AV851018	AV851018 AV851018	c 770	10	35.7	49	1	CG729392	CG729392 31B7 Arab
698	10	35.7	40	7	CO793322	CO793322 NT017C.A0	c 771	10	35.7	49	1	CG729392	CG729392 31B7 Arab
699	10	35.7	40	8	AZ479725	AZ479725 IM0300002	c 772	10	35.7	49	1	CG729392	CG729392 31B7 Arab
700	10	35.7	40	8	AZ490766	AZ490766 IM0323N19	c 773	10	35.7	49	1	CG729392	CG729392 31B7 Arab
701	10	35.7	40	8	AZ810561	AZ810561 2M0076110	c 774	10	35.7	49	1	CG729392	CG729392 31B7 Arab
702	10	35.7	40	8	BH847602	BH847602 SALK_0548	c 775	10	35.7	49	1	CG729392	CG729392 31B7 Arab
703	10	35.7	40	8	BH850455	BH850455 SALK_0713	c 776	10	35.7	49	1	CG729392	CG729392 31B7 Arab
704	10	35.7	40	8	BH850455	BH850455 SALK_0932	c 777	10	35.7	49	1	CG729392	CG729392 31B7 Arab
705	10	35.7	40	9	BX230948	BX230948 Arabidops	c 778	10	35.7	49	1	CG729392	CG729392 31B7 Arab
706	10	35.7	40	9	BX230948	BX230948 Arabidops	c 779	10	35.7	49	1	CG729392	CG729392 31B7 Arab
707	10	35.7	40	9	BX230948	BX230948 Arabidops	c 780	10	35.7	49	1	CG729392	CG729392 31B7 Arab
708	10	35.7	40	9	BX230948	BX230948 Arabidops	c 781	10	35.7	49	1	CG729392	CG729392 31B7 Arab
709	10	35.7	40	9	BX230948	BX230948 Arabidops	c 782	10	35.7	49	1	CG729392	CG729392 31B7 Arab
710	10	35.7	40	9	BX230948	BX230948 Arabidops	c 783	10	35.7	49	1	CG729392	CG729392 31B7 Arab
711	10	35.7	40	9	BX230948	BX230948 Arabidops	c 784	10	35.7	49	1	CG729392	CG729392 31B7 Arab
712	10	35.7	40	9	BX230948	BX230948 Arabidops	c 785	10	35.7	49	1	CG729392	CG729392 31B7 Arab
713	10	35.7	40	9	BX230948	BX230948 Arabidops	c 786	10	35.7	49	1	CG729392	CG729392 31B7 Arab
714	10	35.7	40	9	BX230948	BX230948 Arabidops	c 787	10	35.7	49	1	CG729392	CG729392 31B7 Arab
715	10	35.7	40	9	BX230948	BX230948 Arabidops	c 788	10	35.7	49	1	CG729392	CG729392 31B7 Arab
716	10	35.7	40	9	BX230948	BX230948 Arabidops	c 789	10	35.7	49	1	CG729392	CG729392 31B7 Arab
717	10	35.7	40	9	BX230948	BX230948 Arabidops	c 790	10	35.7	49	1	CG729392	CG729392 31B7 Arab
718	10	35.7	40	9	BX230948	BX230948 Arabidops	c 791	10	35.7	49	1	CG729392	CG729392 31B7 Arab
719	10	35.7	40	9	BX230948	BX230948 Arabidops	c 792	10	35.7	49	1	CG729392	CG729392 31B7 Arab
720	10	35.7	40	9	BX230948	BX230948 Arabidops	c 793	10	35.7	49	1	CG729392	CG729392 31B7 Arab
721	10	35.7	40	9	BX230948	BX230948 Arabidops	c 794	10	35.7	49	1	CG729392	CG729392 31B7 Arab
722	10	35.7	40	9	BX230948	BX230948 Arabidops	c 795	10	35.7	49	1	CG729392	CG729392 31B7 Arab
723	10	35.7	40	9	BX230948	BX230948 Arabidops	c 796	10	35.7	49	1	CG729392	CG729392 31B7 Arab
724	10	35.7	40	9	BX230948	BX230948 Arabidops	c 797	10	35.7	49	1	CG729392	CG729392 31B7 Arab
725	10	35.7	40	9	BX230948	BX230948 Arabidops	c 798	10	35.7	49	1	CG729392	CG729392 31B7 Arab
726	10	35.7	40	9	BX230948	BX230948 Arabidops	c 799	10	35.7	49	1	CG729392	CG729392 31B7 Arab
727	10	35.7	40	9	BX230948	BX230948 Arabidops	c 800	10	35.7	49	1	CG729392	CG729392 31B7 Arab
728	10	35.7	40	9	BX230948	BX230948 Arabidops	c 801	10	35.7	49	1	CG729392	CG729392 31B7 Arab
729	10	35.7	40	9	BX230948	BX230948 Arabidops	c 802	10	35.7	49	1	CG729392	CG729392 31B7 Arab
730	10	35.7	40	9	BX230948	BX230948 Arabidops	c 803	10	35.7	49	1	CG729392	CG729392 31B7 Arab
731	10	35.7	40	9	BX230948	BX230948 Arabidops	c 804	10	35.7	49	1	CG729392	CG729392 31B7 Arab
732	10	35.7	40	9	BX230948	BX230948 Arabidops	c 805	10	35.7	49	1	CG729392	CG729392 31B7 Arab
733	10	35.7	40	9	BX230948	BX230948 Arabidops	c 806	10	35.7	49	1	CG729392	CG729392 31B7 Arab
734	10	35.7	40	9	BX230948	BX230948 Arabidops	c 807	10	35.7	49	1	CG729392	CG729392 31B7 Arab
735	10	35.7	40	9	BX230948	BX230948 Arabidops	c 808	10	35.7	49	1	CG729392	CG729392 31B7 Arab
736	10	35.7	40	9	BX230948	BX230948 Arabidops	c 809	10	35.7	49	1	CG729392	CG729392 31B7 Arab
737	10	35.7	40	9	BX230948	BX230948 Arabidops	c 810	10	35.7	49	1	CG729392	CG729392 31B7 Arab
738	10	35.7	40	9	BX230948	BX230948 Arabidops	c 811	10	35.7	49	1	CG729392	CG729392 31B7 Arab
739	10	35.7	40	9	BX230948	BX230948 Arabidops	c 812	10	35.7	49	1	CG729392	CG729392 31B7 Arab
740	10	35.7	40	9	BX230948	BX230948 Arabidops	c 813	10	35.7	49	1	CG729392	CG729392 31B7 Arab
741	10	35.7	40	9	BX230948	BX230948 Arabidops	c 814	10	35.7	49	1	CG729392	CG729392 31B7 Arab
742	10	35.7	40	9	BX230948	BX230948 Arabidops	c 815	10	35.7	49	1	CG729392	CG729392 31B7 Arab
743	10	35.7	40	9	BX230948	BX230948 Arabidops	c 816	10	35.7	49	1	CG729392	CG729392 31B7 Arab
744	10	35.7	40	9	BX230948	BX230948 Arabidops	c 817	10	35.7	49	1	CG729392	CG729392 31B7 Arab
745	10	35.7	40	9	BX230948	BX230948 Arabidops	c 818	10	35.7	49	1	CG729392	CG729392 31B7 Arab
746	10	35.7	40	9	BX230948	BX230948 Arabidops	c 819	10	35.7	49	1	CG729392	CG729392 31B7 Arab
747	10	35.7	40	9	BX230948	BX230948 Arabidops	c 820	10	35.7	49	1	CG729392	CG729392 31B7 Arab
748	10	35.7	40	9	BX230948	BX230948 Arabidops	c 821	10	35.7	49	1	CG729392	CG729392 31B7 Arab
749	10	35.7	40	9	BX230948	BX230948 Arabidops	c 822	10	35.7	49	1	CG729392	CG729392 31B7 Arab
750	10	35.7	40	9	BX230948	BX230948 Arabidops	c 823	10	35.7	49	1	CG729392	CG729392 31B7 Arab
751	10	35.7	40	9	BX230948	BX230948 Arabidops	c 824	10	35.7	49	1	CG729392	CG729392 31B7 Arab
752	10	35.7	40	9	BX230948	BX230948 Arabidops	c 825	10	35.7	49	1	CG729392	CG729392 31B7 Arab
753	10	35.7	40	9	BX230948	BX230948 Arabidops	c 826	10	35.7	49	1	CG729392	CG729392 31B7 Arab
754	10	35.7	40	9	BX230948	BX230948 Arabidops	c 827	10	35.7	49	1	CG729392	CG729392 31B7 Arab

C 828	9.8	35.0	29	8	BZ382171	901	9.8	35.0	43	9	DME547032	AJ547032 Drosophil
C 829	9.8	35.0	30	8	AZ331753	C 902	9.8	35.0	44	6	C00309	C00309 HUMG000601
C 830	9.8	35.0	30	9	TAl114A09Q	C 903	9.8	35.0	44	6	CD530465	CD530465 06H11 Ara
C 831	9.8	35.0	30	9	CL521210P	C 904	9.8	35.0	44	8	AZ772309	AZ772309 1M0583P03
C 832	9.8	35.0	30	9	CL5211134	C 905	9.8	35.0	44	8	AZ862141	AZ862141 2M0169M04
C 833	9.8	35.0	31	1	A8666806	C 906	9.8	35.0	44	8	BH864323	BH864323 SALK_0957
C 834	9.8	35.0	31	8	AZ796042	C 907	9.8	35.0	44	8	BZ353313	BZ353313 SALK_1201
C 835	9.8	35.0	32	4	BQ419594	C 908	9.8	35.0	44	9	AL771575	AL771575 Arabidops
C 836	9.8	35.0	32	8	AZ467339	C 909	9.8	35.0	44	9	CL320A09Q	CL320A09 T. brucei
C 837	9.8	35.0	32	8	AZ779073	C 910	9.8	35.0	44	9	CL528676	CL528676 ASV26H06
C 838	9.8	35.0	32	9	DR10M115	C 911	9.8	35.0	44	9	AG215899	AG215899 Drosophil
C 839	9.8	35.0	32	9	T882C07Q	C 912	9.8	35.0	45	4	BI755939	BI755939 G03030159
C 840	9.8	35.0	33	1	AU267504	C 913	9.8	35.0	45	4	CC249630	CC249630 X1363 Bay
C 841	9.8	35.0	33	8	AZ509017	C 914	9.8	35.0	45	9	BX210693	BX210693 Danilo rer
C 842	9.8	35.0	33	8	AZ629731	C 915	9.8	35.0	45	9	CC884757	CC884757 SALK_1352
C 843	9.8	35.0	33	8	AZ841576	C 916	9.8	35.0	46	1	AA639421	AA639421 nq89C05.s
C 844	9.8	35.0	33	9	TA215H02P	C 917	9.8	35.0	46	1	AA719000	AA719000 zh22b04.s
C 845	9.8	35.0	33	9	TA215H02P	C 918	9.8	35.0	46	1	AA828900	AA828900 od75h11.s
C 846	9.8	35.0	34	1	AA939151	C 919	9.8	35.0	46	1	AU014238	AU014238 AU014238
C 847	9.8	35.0	34	1	AA222577	C 920	9.8	35.0	46	4	AJ050218	AJ050218 BJ050218
C 848	9.8	35.0	34	8	AZ622092	C 921	9.8	35.0	46	8	AQ025695	AQ025695 1(2)k0100
C 849	9.8	35.0	34	8	AZ824067	C 922	9.8	35.0	46	8	AQ232570	AQ232570 1M0048H21
C 850	9.8	35.0	34	8	AZ957635	C 923	9.8	35.0	46	8	AZ328369	AZ328369 1M0052B09
C 851	9.8	35.0	35	4	BJ034483	C 924	9.8	35.0	46	8	BH856922	BH856922 SALK_0775
C 852	9.8	35.0	35	4	BW401165	C 925	9.8	35.0	46	8	BH892168	BH892168 3526_1_20
C 853	9.8	35.0	35	9	BX660083	C 926	9.8	35.0	46	9	BX121139	BX121139 Danilo rer
C 854	9.8	35.0	35	9	BX660083	C 927	9.8	35.0	46	9	BX293301	BX293301 Arabidops
C 855	9.8	35.0	35	9	TA129B11P	C 928	9.8	35.0	46	9	TA296G08Q	TA296G08 T. brucei
C 856	9.8	35.0	36	1	AV833092	C 929	9.8	35.0	46	9	CG779295	CG779295 1123032H0
C 857	9.8	35.0	36	4	B045071	C 930	9.8	35.0	46	9	CL212822	CL212822 G023A04 G
C 858	9.8	35.0	36	8	AZ760285	C 931	9.8	35.0	47	1	AV741604	AV741604 AV741604
C 859	9.8	35.0	36	8	AZ818349	C 932	9.8	35.0	47	1	AV956136	AV956136 AV956136
C 860	9.8	35.0	37	4	BG915991	C 933	9.8	35.0	47	4	BG522577	BG522577 24-43 Ste
C 861	9.8	35.0	37	4	BG915991	C 934	9.8	35.0	47	8	AZ493275	AZ493275 1M0327D24
C 862	9.8	35.0	37	9	AZ775936	C 935	9.8	35.0	47	8	AZ588201	AZ588201 1M0396R22
C 863	9.8	35.0	38	2	B570996	C 936	9.8	35.0	47	8	BH620863	BH620863 100709C0
C 864	9.8	35.0	38	7	CO781885	C 937	9.8	35.0	47	8	BZ593018	BZ593018 SALK_0550
C 865	9.8	35.0	38	8	AZ436860	C 938	9.8	35.0	47	8	CC156016	CC156016 NPX242 Ba
C 866	9.8	35.0	39	8	AZ402088	C 939	9.8	35.0	48	4	BI753336	BI753336 603026191
C 867	9.8	35.0	39	8	AZ768302	C 940	9.8	35.0	48	4	BI756103	BI756103 603023994
C 868	9.8	35.0	39	8	BZ665489	C 941	9.8	35.0	48	7	H21537	H21537 Y132f09_81
C 869	9.8	35.0	39	9	AG194343	C 942	9.8	35.0	48	8	AZ598247	AZ598247 1M0412M21
C 870	9.8	35.0	40	1	A1023350	C 943	9.8	35.0	48	8	AZ766335	AZ766335 1M0563P13
C 871	9.8	35.0	40	1	A1080507	C 944	9.8	35.0	48	8	AZ785009	AZ785009 2M0028B05
C 872	9.8	35.0	40	1	AA086682	C 945	9.8	35.0	48	8	BZ660760	BZ660760 SALK_0242
C 873	9.8	35.0	40	1	A1882509	C 946	9.8	35.0	48	8	BZ660761	BZ660761 SALK_0242
C 874	9.8	35.0	40	1	AA544934	C 947	9.8	35.0	48	8	BZ766924	BZ766924 SALK_1380
C 875	9.8	35.0	40	2	B5960473	C 948	9.8	35.0	48	9	DME546992	DME546992 Drosophil
C 876	9.8	35.0	40	4	BM399990	C 949	9.8	35.0	49	1	AA028816	AA028816 mn87d03.r
C 877	9.8	35.0	40	8	AZ798767	C 950	9.8	35.0	49	1	AA878633	AA878633 Oj21f04.s
C 878	9.8	35.0	40	8	BZ767723	C 951	9.8	35.0	49	1	AA922785	AA922785 cm62h01.s
C 879	9.8	35.0	41	9	BX896855	C 952	9.8	35.0	49	1	AA146415	AA146415 mr66c08.r
C 880	9.8	35.0	41	1	AJ680173	C 953	9.8	35.0	49	1	AI680543	AI680543 tw82c11.x
C 881	9.8	35.0	41	5	BX621835	C 954	9.8	35.0	49	2	BEG15718	BEG15718 601379R32
C 882	9.8	35.0	41	8	AZ794084	C 955	9.8	35.0	49	6	CF302478	CF302478 7LEAF--08
C 883	9.8	35.0	41	8	BH791218	C 956	9.8	35.0	49	8	AZ346989	AZ346989 1M0082E01
C 884	9.8	35.0	41	9	AL760282	C 957	9.8	35.0	49	8	AZ769616	AZ769616 1M0570H06
C 885	9.8	35.0	41	9	BX292797	C 958	9.8	35.0	49	8	AZ784737	AZ784737 2M0027L14
C 886	9.8	35.0	41	9	BX661505	C 959	9.8	35.0	49	8	BH752880	BH752880 SALK_0194
C 887	9.8	35.0	42	1	AA095986	C 960	9.8	35.0	49	8	BH791914	BH791914 SALK_0619
C 888	9.8	35.0	42	6	CF308435	C 961	9.8	35.0	49	8	CC456020	CC456020 SALK_0911
C 889	9.8	35.0	42	9	BX222960	C 962	9.8	35.0	49	9	TA366A08P	TA366A08P
C 890	9.8	35.0	43	1	AA971669	C 963	9.8	35.0	49	9	CL520169	CL520169 T. brucei
C 891	9.8	35.0	43	1	AI098177	C 964	9.8	35.0	49	9	AG202665	AG202665 Pan trogl
C 892	9.8	35.0	43	6	CA965921	C 965	9.8	35.0	50	1	AU102352	AU102352 AU102352
C 893	9.8	35.0	43	6	CA969808	C 966	9.8	35.0	50	1	AU102353	AU102353 AU102353
C 894	9.8	35.0	43	7	H94728	C 967	9.8	35.0	50	1	AU102356	AU102356 AU102356
C 895	9.8	35.0	43	7	H87658	C 968	9.8	35.0	50	1	AU102586	AU102586 AU102586
C 896	9.8	35.0	43	8	AZ393328	C 969	9.8	35.0	50	1	AU102591	AU102591 AU102591
C 897	9.8	35.0	43	8	AZ467394	C 970	9.8	35.0	50	1	AU102595	AU102595 AU102595
C 898	9.8	35.0	43	8	BH609433	C 971	9.8	35.0	50	1	AU102737	AU102737 AU102737
C 899	9.8	35.0	43	8	BZ352392	C 972	9.8	35.0	50	1	AU102921	AU102921 AU102921
C 900	9.8	35.0	43	9	AJ591815	C 973	9.8	35.0	50	1	AU102954	AU102954 AU102954



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c 974 9.8 35.0 50 1 AUI103409 AUI103409
c 975 9.8 35.0 50 1 AUI103411 AUI103411
c 976 9.8 35.0 50 1 AUI103420 AUI103420
c 977 9.8 35.0 50 1 AUI104146 AUI104146
c 978 9.8 35.0 50 1 AUI104147 AUI104147
c 979 9.8 35.0 50 1 AUI104149 AUI104149
c 980 9.8 35.0 50 1 AUI104157 AUI104157
c 981 9.8 35.0 50 1 AUI104161 AUI104161
c 982 9.8 35.0 50 1 AUI104265 AUI104265
c 983 9.8 35.0 50 1 AUI104267 AUI104267
c 984 9.8 35.0 50 1 AUI104268 AUI104268
c 985 9.8 35.0 50 1 AUI104270 AUI104270
c 986 9.8 35.0 50 1 AUI104272 AUI104272
c 987 9.8 35.0 50 1 AUI104273 AUI104273
c 988 9.8 35.0 50 1 AUI104971 AUI104971
c 989 9.8 35.0 50 1 AUI105622 AUI105622
c 990 9.8 35.0 50 1 AUI105623 AUI105623
c 991 9.8 35.0 50 1 AUI105803 AUI105803
c 992 9.8 35.0 50 1 AUI105855 AUI105855
c 993 9.8 35.0 50 1 AUI105978 AUI105978
c 994 9.8 35.0 50 1 AUI106388 AUI106388
c 995 9.8 35.0 50 1 AUI106828 AUI106828
c 996 9.8 35.0 50 1 AUI106975 AUI106975
c 997 9.8 35.0 50 1 AUI107053 AUI107053
c 998 9.8 35.0 50 1 AUI107054 AUI107054
c 999 9.8 35.0 50 1 AUI107055 AUI107055
c1000 9.8 35.0 50 1 AUI107056 AUI107056
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## ALIGNMENTS

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RESULT 1
LOCUS AZ822723/c 28 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0096009F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0096009 F, genomic survey sequence.
ACCESSION AZ822723 GI:12992631
VERSION AZ822723.1
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 28)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0096 row: 0 column: 09
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 28.
FEATURES
source Location/Qualifiers
1..28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0096009"
/sex="Male"
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/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"/
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

```
Query Match 50.7%; Score 14.2; DB 8; Length 28;
Best Local Similarity 70.4%; Pred. No. 9.7e+04;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 2 CAAGCACCCCTATCAGGCGAGTACCACAA 28
Db 28 CAAGCACCCCTATCAGTATACGAAA 2
```

```
RESULT 2
LOCUS AZ437906 38 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0226A08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0226A08 R, genomic survey sequence.
ACCESSION AZ437906
VERSION AZ437906.1
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 38)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0226 row: A column: 08
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 38.
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FEATURES
source Location/Qualifiers
1..38
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0226A08"
/sex="Male"
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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 49.3%; Score 13.8; DB 8; Length 38;  
 Best Local Similarity 88.2%; Pred. No. 1.5e+05;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 ATCAGGCGAGTACCACAA 28  
 |||||  
 Db 13 ATCAGGCGAGTACCACAA 29

## RESULT 3

AZ402707

LOCUS

DEFINITION AZ402707 45 bp DNA linear GSS 03-OCT-2000  
 clone UUC1M0170E08 F, genomic virus sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 45)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0170 row: E column: 08

Seq primer: CGTTGTAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 45.

Location/Qualifiers

1. .45

FEATURES

source

/organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUC1M0170E08"  
 /sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 49.3%; Score 13.8; DB 8; Length 45;  
 Best Local Similarity 72.0%; Pred. No. 1.6e+05;  
 Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 AGCACCTCTACGAGTACCACAA 28  
 |||||  
 Db 7 AGCACCTCTCTGGCAGATCCAAA 31

## RESULT 4

CK136536

LOCUS

DEFINITION MM2\_2\_1\_C04 Sugar beet 10-week GH root cDNA Beta vulgaris cDNA 5',  
 mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.  
 1 (bases 1 to 50)

REFERENCE

AUTHORS

Klotz, K.L. and McGrath, J.M.  
 ESTs from 10-week old greenhouse grown sugar beet roots  
 Unpublished (2003)

JOURNAL

COMMENT

Contact: J. Mitchell McGrath  
 Sugar Beet Genetics Lab., USDA/ARS/Sugar Beet and Bean Research  
 Unit

Michigan State University

494 Plant and Soil Sci. Bldg., East Lansing MI 48824, USA

Tel: 517 353 9262

Fax: (517)-337-6782

Email: mitchmcgmsu.edu

Plate: MM2\_2\_1 row: C column: 04

Seq primer: 5'-GCATACATATACGAGTATCAG-3'.

Location/Qualifiers

1. .50

FEATURES

source

/organism="Beta vulgaris"  
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 /db\_xref="taxon:161934"  
 /tissue\_type="whole root"  
 /dev\_stage="1- week old"  
 /lab\_host="DH5-alpha"  
 /clone\_lib="Sugar beet 10-week GH root cDNA"  
 /note="Organ: root; Vector: pDNR-LIB; Site 1: SfiI A;  
 Site 2: SfiI B; cDNAs were derived from reverse  
 transcription of mRNA samples from greenhouse grown whole  
 roots frozen in liquid nitrogen, freeze-dried, and ground



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Query Match      47.9%; Score 13.4; DB 1; Length 47;
Best Local Similarity 73.9%; Pred. NO. 2.4e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 5 GCACCCCTATCAGGAGTACCACA 27
DB 41 GCACCAATCAGGCATATCCCA 19

RESULT 8
AA932343
LOCUS      28 bp mRNA linear EST 07-JUL-1998
DEFINITION oos0c02.s1 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1570562 3'
similar to SW:RUZA_HUMAN P46776 60S RIBOSOMAL PROTEIN L27A. ; mRNA
sequence.
ACCESSION  AA932343
VERSION     AA932343.1 GI:3086581
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens

REFERENCE
AUTHORS    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL    National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT    Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E.B. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
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Seq primer: -40ml3 fwd ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. .28
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/db_xref="taxon:9606"
/clone="IMAGE:1570562"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu5"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
neuroendocrine lung carcinoid, and was then primed with a
Not I - oligo(dT) primer. Double-stranded cDNA was ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT7T3 vector. Library is normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN
Query Match      47.1%; Score 13.2; DB 1; Length 28;
Best Local Similarity 83.3%; Pred. NO. 2.7e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 10 CTATCAGGAGTACCACA 27
DB 9 CTATGAGCATTACCACA 26

RESULT 9
A2434394/c

LOCUS      32 bp DNA linear GSS 03-OCT-2000
DEFINITION iM0220F13R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG1M0220F13 R, genomic survey sequence.
ACCESSION  A2434394
VERSION     A2434394.1 GI:10558407
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus

REFERENCE
AUTHORS    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 32)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Kelly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhauser, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0220 row: F column: 13
Seq primer: CACACAGGAAACAGCTATGACC
Class: Plasmid ends
High quality sequence stop: 32.
Location/Qualifiers
1. .32
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0220F13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match      47.1%; Score 13.2; DB 8; Length 32;
Best Local Similarity .69.2%; Pred. NO. 2.8e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 2 CAAGCACCCTATCAGGAGTACCACA 27
DB 32 CCACCCCTTAATAGGCATACCACA 7

RESULT 10
A2775335/c

```

LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
source  
ORIGIN  
Query Match  
Best Local Similarity  
Matches  
QY  
Db  
RESULT 11  
AI445901

40 bp DNA linear GSS 16-FEB-2001  
2M0007G07R Mouse 10kb plasmid UUGCLM library Mus musculus genomic  
clone UUGC2M0007G07 R, genomic survey sequence.  
AZ775335  
AZ775335.1 GI:12901711  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 40)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dduun@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0007 row: G column: 07  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 40.  
Location/Qualifiers  
1. 40  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0007G07"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Ti-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGCLM library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (G14732114[gb]/AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
source  
ORIGIN  
Query Match  
Best Local Similarity  
Matches  
QY  
Db  
RESULT 12  
AI965799  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

49 bp mRNA linear EST 13-APR-1999  
tj06h01.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2140753 3'  
similar to TR:P93237 P93237 PROLINE-RICH PROTEIN PRP2 PRECURSOR.  
; contains MSRI.b3 MSRI repetitive element ;, mRNA sequence.  
AI445901  
AI445901.1 GI:4291451  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 49)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapsb-remail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Trace considered overall poor quality  
Insert Length: 1393 Std Error: 0.00  
Seq primer: -400P from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers  
1. 49  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2140753"  
/tissue\_type="poorly differentiated adenocarcinoma with  
signet ring cell features"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Gas4"  
/note="Organ: stomach; Vector: pCMV-SPORT6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"

Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

# Public Soybean EST Project

Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. Trace considered overall poor quality possible reversed clone: similarity on wrong strand This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)

Insert Length: 723 Std Error: 0.00

High quality sequence stop: 1.

Location/Qualifiers

1. 49

/organism="Glycine max"

/mol\_type="mRNA"

/cultivar="Williams 82"

/db\_xref="taxon:3847"

/clone="GENOME SYSTEMS CLONE ID: Gm-cl018-817"

/tissue\_type="leaves of greenhouse grown plants"

/dev\_stages="2-3 weeks old"

/lab\_host="DH10B (Gibco BRL)"

/clone\_libs="Gm-cl018"

/note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2: XhoI; This cDNA library was constructed from mRNA isolated from 2-3 week old greenhouse grown plants. The cDNA library was prepared using the Stratagene pBluescript II XR library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelting."

## ORIGIN

Query Match 47.1%; Score 13.2; DB 1; Length 49;

Best Local Similarity 69.2%; Pred. No. 3e+05;

Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GCACGACCCCTATCAGGCAGTACCAC 26

Db 11 GCAAAACCCCTAACGGGTACACAC 36

## RESULT 13

### CL210926

LOCUS A027F07 GGTG Gene Trap Library GV03C04 Mus musculus cDNA clone

DEFINITION A027F07, mRNA sequence.

ACCESSION CL210926

VERSION CL210926.2 GI:49489590

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 32)

REFERENCE Hansen,J., Floss,T., van Sloun,P., Fuchtbauer,E.M., Vauti,F., Arnold,H.H., Schnutgen,F., Wurst,W., Von Melchner,H. and Ruiz,P.

## TITLE

### JOURNAL

### MEDLINE

### PUBMED

### COMMENT

On Jun 30, 2004 this sequence version replaced gi:40727827.

Contact: GGTC

German Genetrap Consortium (GGTC)

Email: info@genetrap.de

Pribetago gene trap. Sequence tag generated by 5'RACE. Additional sequence information can be found at:

'http://genetrap.gsf.de/project/web\_new/database/result\_clone.html?clone\_id=A027F07' ES cell line harboring insertion mutation of

target gene is available at:

'http://genetrap.gsf.de/project/web\_new/order\_clones/howtoorder.htm'

1' Inhouse Sequence Identifier: 08052

Class: Gene Trap.

## FEATURES

### source

1..32

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="129 Sv"

/db\_xref="taxon:10090"

/clone="A027F07"

/sex="Male"

/cell\_type="Embryonic stem cell"

/cell\_lines="ES cells 129S2 (formerly 129/SvPas)"

/clone\_libs="GGTC Gene Trap Library GV03C04"

/note="Vector: pribetago"

## ORIGIN

Query Match 46.4%; Score 13; DB 9; Length 32;

Best Local Similarity 76.2%; Pred. No. 3.4e+05;

Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 6 CACCTATCAGGCAGTACCAC 26

Db 1 CTCCTATCAAAACAGTACCTC 21

## RESULT 14

### AG192612/c

### LOCUS

AG192612 40 bp DNA linear GSS 06-MAR-2004

DEFINITION Pan troglodytes DNA, clone: RP43-069E06.T7, genomic survey

sequence.

ACCESSION AG192612

VERSION AG192612.1 GI:45224788

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Homnidae; Pan.

1

Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,

Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.

BAC end sequences of Library RP-43

2 (bases 1 to 40)

Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,

Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.

Direct Submission

Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of

Bioscience and Biotechnology (KRIIBB), Genome Research Center (GRC);

52, Oun-dong, Yuseong-gu, Daejeon 305-333, Korea

(E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,

Tel:82-42-866-7181, Fax:82-42-860-4409)

Clones are derived from the chimpanzee BAC library RP-43 This BAC

end was generated during the R&D process and may have higher chance

of clone tracking errors.

PRIMERS

Sequencing: T7

LIBRARY Vector : pBACe3.6

ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

ORIGIN

Query Match 46.4%; Score 13; DB 8; Length 41;  
Best Local Similarity 100.0%; Pred. No. 3.5e+05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGCACCCTAT 13  
|||||  
Db 25 GCAAGCACCCTAT 13

RESULT 16

CG887124/c 41 bp mRNA linear GSS 16-JUN-2004  
LOCUS RRS785 BayGenomics Gene Trap Library pGT0Lxf Mus musculus cDNA,  
DEFINITION mRNA sequence.

ACCESSION CG887124.1 GI:38641534

VERSION CG887124.1

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 41)

AUTHORS BayGenomics.

TITLE http://baygenomics.ucsf.edu/

JOURNAL Unpublished (2001)

COMMENT Contact: BayGenomics  
Bay Area Functional Genomics Consortium (BayGenomics)  
Email: info@baygenomics.ucsf.edu

Sequence tag generated by 5' RACE of total RNA from gene trap ES  
cell line. ES cell lines harboring insertion mutation of target  
gene are available upon request from BayGenomics. Annotation  
information available from  
http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=CELL\_LINE&KEY=RRS785  
Class: Gene Trap.

FEATURES

Location/Qualifiers  
1..41  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129 ola"  
/db\_xref="taxon:10090"  
/sex="Male"  
/cell\_type="Embryonic stem cell"  
/clone\_lib="BayGenomics Gene Trap Library pGT0Lxf"  
/note="Vector: pGT0Lxf"

ORIGIN

Query Match 46.4%; Score 13; DB 9; Length 41;  
Best Local Similarity 76.2%; Pred. No. 3.5e+05;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6 CACCCTATCAGGAGTACCAC 26  
|||||  
Db 24 CACACACTCAGGAGTACCAC 4

RESULT 17

EX625891/c 30 bp mRNA linear EST 08-AUG-2003  
LOCUS EX625891 NAP1 Anopheles gambiae cDNA clone ANGNP1163B01T7, mRNA  
DEFINITION

R.Site 1 : ECORI.  
R.Site 2 : ECORI.

FEATURES source

Location/Qualifiers  
1..40  
/organism="pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/clone="RP43-069E06.T7"  
/sex="male"  
/cell\_type="lymphocytes"  
/clone\_lib="RP-43 Chimpanzee Male BAC Library"

ORIGIN

Query Match 46.4%; Score 13; DB 9; Length 40;  
Best Local Similarity 76.2%; Pred. No. 3.5e+05;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 CAAGCACCCTATCAGGAGT 22  
|||||  
Db 21 CAAGAAACTTACCAGCCAGT 1

RESULT 15

AZ768376/c 41 bp DNA linear GSS 16-FEB-2001  
LOCUS IM0568P14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0568P14 F, genomic survey sequence.

ACCESSION AZ768376

VERSION AZ768376.1 GI:12887417

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 41)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Ielam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Kelly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0568 row: p column: 14  
Seq primer: GGTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 41.

FEATURES

Location/Qualifiers  
1..41  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0568P14"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pMD22nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were





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source
1..37
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2309388"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_lib="NCI CGAP GC6"
/note="Vector: pTV3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA
from the normalized library NCI CGAP GC4 was prepared, and
ss circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 45.7%; Score 12.8; DB 1; Length 37;
Best Local Similarity 70.8%; Pred. No. 4.3e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GCAAGCACCTATCAGGCAGTACC 24
Db 27 GGAGAACCTGTCTGCGCGCCCC 4

RESULT 20
LOCUS CL679725 38 bp DNA linear GSS 09-JUL-2004
DEFINITION PR10126d.D08.2 - PR10126d.BR (38) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION CL679725.1 GI:50186437
VERSION CL679725
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 38)
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppADB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
FEATURES
source
1..38
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"

ORIGIN
Query Match 45.7%; Score 12.8; DB 9; Length 38;
Best Local Similarity 70.8%; Pred. No. 4.3e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GCAAGCACCTATCAGGCAGTACC 24

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Db 15 GCACGGCTCCTATGCTGCAGACC 38
|||||
|||||
|||||
|||||
|||||

RESULT 21
LOCUS CC183071/c 40 bp mRNA linear GSS 08-MAY-2003
DEFINITION XG571 BayGenomics Gene Trap Library pGTL1xf Mus musculus cDNA, mRNA
sequence.
ACCESSION CC183071.1 GI:30426971
VERSION CC183071.1
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
BayGenomics.
http://baygenomics.ucsf.edu/
Unpublished (2001)
Contact: BayGenomics
Bay Area Functional Genomics Consortium (BayGenomics)
Email: info@baygenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
information available from
http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=
CELL_LINE&KEY=XG571
Class: Gene Trap.
FEATURES
source
1..40
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 ola"
/db_xref="taxon:10090"
/sex="Male"
/cell_type="Embryonic stem cell"
/clone_lib="BayGenomics Gene Trap Library pGTL1xf"
/note="Vector: pGTL1xf"

ORIGIN
Query Match 45.7%; Score 12.8; DB 8; Length 40;
Best Local Similarity 87.5%; Pred. No. 4.3e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 TCAGGCAGTACCACAA 28
Db 24 TCAGGCAGTACCACCA 9

RESULT 22
LOCUS AZ329441 42 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0053M07R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0053M07 R, genomic survey sequence.
ACCESSION AZ329441
VERSION AZ329441.1 GI:10390156
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 42)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

```



University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0053 row: M column: 07  
Seq primer: CACACGAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 42.

#### FEATURES

Location/Qualifiers  
1..42  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clones="UUGC1M0053M07"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

#### ORIGIN

Query Match 45.7%; Score 12.8; DB 8; Length 42;  
Best Local Similarity 70.8%; Pred. No. 4.4e+05;  
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GCAAGCACCCCTATCAGGCAGTACC 24  
Db 2 GCAGGCGGCGAGCGGCGGGCC 25

#### RESULT 23

AZ663255  
LOCUS 47 bp DNA linear GSS 14-DEC-2000  
DEFINITION IM0542K15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0542K15 R, genomic survey sequence.

ACCESSION AZ663255

VERSION AZ663255.1 GI:11800401

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

#### ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 47)

REFERENCE  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0542 row: K column: 15  
Seq primer: CACACGAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 47.

#### FEATURES

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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clones="UUGC1M0542K15"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

#### ORIGIN

Query Match 45.7%; Score 12.8; DB 8; Length 47;  
Best Local Similarity 70.8%; Pred. No. 4.5e+05;  
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4 AGCACCCCTATCAGGCAGTACCACA 27  
Db 23 AGGACCTATCATGGCTTACACA 46

#### RESULT 24

AZ797405/c  
LOCUS 47 bp DNA linear GSS 16-FEB-2001  
DEFINITION 2M0053D08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0053D08 R, genomic survey sequence.

ACCESSION AZ797405

VERSION AZ797405.1 GI:12946449

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

#### ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 47)

REFERENCE  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0053 row: D column: 08  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 47.

# FEATURES

Location/Qualifiers  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0053D08"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|GB|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

# ORIGIN

Query Match 45.7%; Score 12.6; DB 8; Length 47;  
Best Local Similarity 70.8%; Pred. No. 4.5e+05;  
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
QY 1 GCAAGCACCCTATCAGGAGTACC 24  
DB 29 GGAAGCAGCCGAGAGCTGTACC 6

RESULT 25  
LOCUS A2790187 49 bp DNA linear GSS 16-FEB-2001  
DEFINITION 2M0038N03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0038N03 R, genomic survey sequence.  
ACCESSION A2790187  
VERSION A2790187.1 GI:12931784  
SOURCE GSS.  
ORGANISM Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 49)  
REFERENCE 1 (bases 1 to 49)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0038 row: N column: 03  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 49.

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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0038N03"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|GB|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

# ORIGIN

Query Match 45.7%; Score 12.8; DB 8; Length 49;  
Best Local Similarity 70.8%; Pred. No. 4.5e+05;  
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
QY 3 AAGCACCCTATCAGGAGTACCAC 26  
DB 1 ATGCATCCATTGAGGAGTCTCTC 24

RESULT 26  
LOCUS BI223057/c 32 bp mRNA linear EST 11-JUL-2001  
DEFINITION 602942007F1 NIH\_MGC\_12 Homo sapiens cDNA clone IMAGE:5105089 5', mRNA sequence.  
ACCESSION BI223057  
VERSION BI223057.1 GI:14676501  
SOURCE EST.  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 32)  
REFERENCE 1 (bases 1 to 32)  
AUTHORS NIH-MGC http://mgs.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgabbs@mail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: Incyte Genomics, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E.B. Consortium/LLNL at:  
http://image.llnl.gov

Plate: LLAM11253 row: n column: 01

High quality sequence stop: 32.

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/clone="IMAGE:5105088"  
/tissue type="cervical carcinoma cell line"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_12"  
/note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.4 kb. Library prepared by Life Technologies."

## ORIGIN

Query Match 45.0%; Score 12.6; DB 4; Length 32;  
Best Local Similarity 78.9%; Pred. No. 5.2e+05;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTTACGCGCA 19  
Db 31 GCAAGCAGCGCTGCTTGA 13

## RESULT 27

AG200947/c  
LOCUS  
DEFINITION Pan troglodytes DNA, clone: RP43-083D01.TJ, genomic survey sequence.

ACCESSION AG200947

VERSION AG200947.1 GI:45233122

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM

REFERENCE  
AUTHORS Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C. J., Hoon, S. T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.

TITLE BAC end sequences of Library RP-43

REFERENCE  
AUTHORS Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C. J., Hoon, S. T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.

TITLE Direct Submission

REFERENCE  
AUTHORS Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C. J., Hoon, S. T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.

TITLE Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KRIIBB), Genome Research Center (GRC);

52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea

(E-mail: redstone@mail.kribb.re.kr, URL: http://phs.grc.kribb.re.kr/)

Tel: 82-42-866-7181, Fax: 82-42-860-4409

Clones are derived from the chimpanzee BAC library RP-43 This BAC

end was generated during the R&D process and may have higher chance

of clone tracking errors.

PRIMERS

Sequencing: TJ

LIBRARY

Vector : pBACe3.6

R.Site 1 : EcoRI

R.Site 2 : EcoRI.

Location/Qualifiers

1..35

/organism="Pan troglodytes"

/mol\_type="genomic DNA"

/db\_xref="taxon:9598"

/clone="RP43-083D01.TJ"

/sex="male"

/cell\_type="lymphocytes"

/clone\_lib="RP-43 Chimpanzee Male BAC Library"

FEATURES  
source

## ORIGIN

Query Match 45.0%; Score 12.6; DB 9; Length 35;

Best Local Similarity 66.7%; Pred. No. 5.2e+05;

Matches 18; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GCAAGCACCTTACGCGCAGTACCACA 27  
Db 29 GCATGCAACCTTATGGTGAATAAACA 3

## RESULT 28

AG2760045

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0553 row: K column: 20

Seq primer: CGTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 43.

Location/Qualifiers

1..43

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0553K20"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 [gi|4732114|gb|AF129072.1], a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Db	15	CCACACCCCTATCTCGAAGAAATATAAAA	41
RESULT 30			
LOCUS			
DEFINITION			
ACCESSION			
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ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
ORIGIN			
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Best Local Similarity			
Matches			
Qy			
Db			
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BX143358			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
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REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
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AUTHORS			
TITLE			
JOURNAL			
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AUTHORS			
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AUTHORS			
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JOURNAL			
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AUTHORS			
TITLE			
JOURNAL			
COMMENT			
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BX143358			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES</			

DEFINITION Danio rerio genomic clone DKEY-109K22, genomic survey sequence.  
 ACCESSION BX143358  
 VERSION BX143358.1 GI:27974696  
 KEYWORDS GSS.  
 SOURCE Danio rerio (zebrafish)  
 ORGANISM Danio rerio  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.  
 REFERENCE 1 (bases 1 to 50)  
 AUTHORS Humphray, S.J., Huckle, E. and Durham, J.L.  
 TITLE Direct Submission  
 JOURNAL Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk Unpublished  
 COMMENT This sequence was generated from the T7 end of BAC 109K22. 109K22 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygens. Further details: [http://www.sanger.ac.uk/Projects/D\\_rerio/](http://www.sanger.ac.uk/Projects/D_rerio/).  
 FEATURES  
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 Location/Qualifiers  
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 /db\_xref="taxon:7955"  
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 /tissue\_type="Testis"  
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 Query Match 45.0%; Score 12.6; DB 9; Length 50;  
 Best Local Similarity 66.7%; Pred. No. 5.5e+05;  
 Matches 18; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 Qy 2 CAAGCACCCCTATCAGGCAGTACCACAA 28  
 |||||  
 Db 22 CAAGCACCCCTACCTAGAAAGCGCAAAA 48  
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 RESULT 32  
 LOCUS CR397867 50 bp DNA linear GSS 02-MAY-2004  
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-530E06-025923, genomic survey sequence.  
 CR397867  
 ACCESSION CR397867  
 VERSION CR397867.1 GI:46938595  
 KEYWORDS GSS.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
 REFERENCE 1  
 AUTHORS Li, Y., Rosso M.G., Strizhov, N., Viehoever, P. and Weissshaar, B.  
 TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana  
 JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)  
 MEDLINE 22755829  
 PUBMED 12674060  
 REFERENCE 2  
 AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weissshaar, B.  
 TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics  
 JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)  
 MEDLINE 23117147  
 PUBMED 14756321  
 REFERENCE 3  
 AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and Weissshaar, B.  
 TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines  
 JOURNAL Biotechniques 35 (6), 1164-1168 (2003)

14682050  
 REFERENCE 4 (bases 1 to 50)  
 AUTHORS Strizhov, N., Rosso, M.G., Li, Y. and Weissshaar, B.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-MAY-2004) Weissshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
 COMMENT This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone fca all. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.  
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 Location/Qualifiers  
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 ORIGIN  
 Query Match 45.0%; Score 12.6; DB 9; Length 50;  
 Best Local Similarity 78.9%; Pred. No. 5.5e+05;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 Qy 9 CCTATCAGGCAGTACCACA 27  
 |||||  
 Db 22 CCCATAAGGCGCTAACACA 4  
 |||||  
 RESULT 33  
 LOCUS AZ402223 32 bp DNA linear GSS 03-OCT-2000  
 DEFINITION IM0169L21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0169L21 F, genomic survey sequence.  
 AZ402223  
 ACCESSION AZ402223  
 VERSION AZ402223.1 GI:10517297  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 32)  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Ismail, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: [rdunn@genetics.utah.edu](mailto:rdunn@genetics.utah.edu)  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0169 row: L column: 21  
 Seq primer: CGTTGTAACGACGCGCCAGT  
 Class: plasmid ends

High quality sequence stop: 33.  
Location/Qualifiers  
1..33  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0169L21"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 44.3%; Score 12.4; DB 8; Length 33;  
Best Local Similarity 92.9%; Pred. No. 6.4e+05;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 CAGCAGTACCACA 27  
||| ||||| |||||  
Db 19 CAGCCAGTACCACA 32

RESULT 35  
AZ403184/c  
LOCUS  
DEFINITION  
1M0170C23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0170C23 R, genomic survey sequence.

ACCESSION  
AZ403184  
VERSION  
AZ403184.1 GI:10518258  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 38)  
REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0170 row: C column: 23  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends

High quality sequence stop: 32.  
Location/Qualifiers  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 44.3%; Score 12.4; DB 8; Length 32;  
Best Local Similarity 72.7%; Pred. No. 6.4e+05;  
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 CAAGCACCTATCAGGCAGTAC 23  
||| ||||| |||||  
Db 5 CCAGACCTTAAAGCAGTGC 26

RESULT 34  
AZ766010  
LOCUS  
DEFINITION  
A2766010 Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0563H13 F, genomic survey sequence.

ACCESSION  
A2766010  
VERSION  
A2766010.1 GI:12882629  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 32)  
REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0563 row: H column: 13  
Seq primer: CGTTGTAACAGCGGCAGT  
Class: plasmid ends

High quality sequence stop: 38.  
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 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
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 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGCLM library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 44.3%; Score 12.4; DB 8; Length 38;  
 Best Local Similarity 92.9%; Pred. No. 6.5e+05;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CCTATCAGGAGTA 22  
 |||||  
 Db 34 CCTATCAGGAGTA 21

RESULT 36  
 LOCUS BJ063882 39 bp mRNA linear EST 29-SEP-2003  
 DEFINITION BJ063882 NIBB Mochii normalized Xenopus tailbud library Xenopus laevis cDNA clone XL077k13 5', mRNA sequence.  
 ACCESSION BJ063882  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Xenopus laevis (African clawed frog)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopodinae; Xenopus; Xenopus.  
 1 (bases 1 to 39)  
 Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara, Y.

Expressed genes in X. laevis embryo  
 Unpublished (2001)  
 Contact: Tadasu Shin-i  
 Center For Genetic Resource Information  
 National Institute of Genetics  
 1111 Yata, Mishima, Shizuoka 411-8540, Japan  
 Tel: 81-559-81-6856  
 Fax: 81-559-81-6855  
 Email: tshini@genes.nig.ac.jp  
 The information of this clone is available through the following URL.  
 http://xenopus.nibb.ac.jp.

## FEATURES

source  
 1..39  
 /organism="Xenopus laevis"  
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/db\_xref="taxon:8355"  
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## ORIGIN

Query Match 44.3%; Score 12.4; DB 4; Length 39;  
 Best Local Similarity 72.7%; Pred. No. 6.6e+05;  
 Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 AGCACCCCTATCAGGAGTACCA 25  
 |||||  
 Db 30 AGCACTCGGTATACAGAACCA 9

RESULT 37  
 LOCUS BJ077137 44 bp mRNA linear EST 29-SEP-2003  
 DEFINITION BJ077137 NIBB Mochii normalized Xenopus tailbud library Xenopus laevis cDNA clone XL059p19 3', mRNA sequence.  
 ACCESSION BJ077137  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Xenopus laevis (African clawed frog)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopodinae; Xenopus; Xenopus.  
 1 (bases 1 to 44)  
 Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara, Y.

Expressed genes in X. laevis embryo  
 Unpublished (2001)  
 Contact: Tadasu Shin-i  
 Center For Genetic Resource Information  
 National Institute of Genetics  
 1111 Yata, Mishima, Shizuoka 411-8540, Japan  
 Tel: 81-559-81-6856  
 Fax: 81-559-81-6855  
 Email: tshini@genes.nig.ac.jp  
 The information of this clone is available through the following URL.  
 http://xenopus.nibb.ac.jp.

Location/Qualifiers  
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 /organism="Xenopus laevis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:8355"  
 /clone="XL059p19"  
 /tissue type="whole embryo"  
 /dev stage="stage 25"  
 /clone\_lib="NIBB Mochii normalized Xenopus tailbud library"

## REFERENCE

AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

## FEATURES

source  
 1..44  
 /organism="Xenopus laevis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:8355"  
 /clone="XL059p19"  
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 /dev stage="stage 25"  
 /clone\_lib="NIBB Mochii normalized Xenopus tailbud library"

## ORIGIN

Query Match 44.3%; Score 12.4; DB 4; Length 44;  
 Best Local Similarity 69.6%; Pred. No. 6.7e+05;  
 Matches 16; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 AGCACCCCTATCAGGAGTACCA 26  
 |||||  
 Db 33 AGTATGGTATCAAGGAGNACCAC 11

RESULT 38  
 LOCUS AZ621023 50 bp DNA linear GSS 13-DEC-2000  
 DEFINITION 1M0454C04F Mouse 10kb plasmid UUGCLM library Mus musculus genomic clone UUGCLM0454C04 F, genomic survey sequence.  
 ACCESSION AZ621023  
 VERSION AZ621023.1 GI:11743213

## FEATURES

source  
 1..39  
 /organism="Xenopus laevis"  
 /mol\_type="mRNA"



KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS

TITLE

JOURNAL  
COMMENT

FEATURES  
source

ORIGIN

Query Match 44.3%; Score 12.4; DB 8; Length 50;  
Best Local Similarity 72.7%; Pred. No. 6.8e+05;  
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 CACCCTATCAGGCAGTACCACA 27  
|||  
DB 50 CATATTATGAGGCAGTAGCCCA 29  
|||

RESULT 39  
AZ584738/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 50)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0454 row: C column: 04  
Seq primer: CGTTGTAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 50.  
Location/Qualifiers  
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/db\_xref="taxon:10090"  
/clone="UUGC1M0454C04"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, P-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

39  
AZ584738  
1M0389A07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0389A07 R, genomic survey sequence.  
AZ584738  
AZ584738.1 GI:11705925

KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS

TITLE

JOURNAL  
COMMENT

FEATURES  
source

ORIGIN

Query Match 43.6%; Score 12.2; DB 8; Length 39;  
Best Local Similarity 68.0%; Pred. No. 8.1e+05;  
Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 AAGCACCCTATCAGGCAGTACCACA 27  
|||  
DB 38 AATACCCCTGGAGGAGTACCAGA 14  
|||

RESULT 40  
AZ828302/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 39)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0389 row: A column: 07  
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/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

39  
AZ828302  
2M0105011F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0105011 F, genomic survey sequence.  
AZ828302  
AZ828302.1 GI:12998210



KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 42)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112 USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0105 row: O column: 11  
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Class: plasmid ends  
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High quality sequence stop: 42.  
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/note="Vector: FWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

ORIGIN  
Query Match 43.6%; Score 12.2; DB 8; Length 42;  
Best Local Similarity 68.0%; Pred. No. 8.2e+05;  
Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
Qy 1 GCAAGCACCTCATCAGGACGTACCA 25  
Db 42 GTAACCACTCATCACTCACTCCCA 18

Search completed: November 23, 2004, 22:24:28  
Job time : 1371.43 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:50:22 ; Search time 468.195 Seconds  
(without alignments)  
2626.113 Million cell updates/sec

Title: US-10-087-631B-8

Perfect score: 26  
Sequence: 1 cgtcttcgcagatcggtacctcaat 26

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 1785872

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 1000 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_htg.\*

3: gb\_in.\*

4: gb\_on.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_ats.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	26	100.0	26	6	AX523949
3	26	100.0	26	6	AX524847
C 4	15.2	58.5	44	6	I38537 Sequence 5
C 5	14.6	56.2	41	6	AR053999
C 6	14.6	56.2	41	6	AR146175
C 7	14.4	55.4	40	6	BD263605
C 8	14.4	55.4	40	6	AX343106
C 9	14.2	54.6	30	6	AX454034
10	14	53.8	48	14	MLMLTRB1
C 11	13.8	53.1	24	6	AX445171
12	13.6	52.3	34	6	AR182869
13	13.6	52.3	40	6	BD190521
14	13.6	52.3	40	6	AX038843
C 15	13.4	51.5	24	6	CQ824393
C 16	13.4	51.5	25	6	AR448717
17	13.4	51.5	31	6	AR101054
C 18	13.4	51.5	39	6	AR099751
C 19	13.4	51.5	39	6	BD064614

20	13.4	51.5	48	6	AX305162	AX305162 Sequence
21	13.4	51.5	50	4	AY124654S3	AY124656 Equus cab
22	13.4	51.5	50	4	AY124657S3	AY124659 Equus cab
23	13.4	51.5	50	4	AY124660S3	AY124662 Equus cab
24	13.4	51.5	50	4	AY124663S3	AY124665 Equus cab
25	13.4	51.5	50	4	AY124666S3	AY124668 Equus cab
26	13.4	51.5	50	4	AY124669S3	AY124671 Equus prz
27	13.4	51.5	50	4	AY124672S3	AY124674 Equus asi
28	13.4	51.5	50	4	AY124675S3	AY124677 Equus asi
29	13.4	51.5	50	4	AY124678S3	AY124680 Equus asi
30	13.4	51.5	50	4	AY124681S3	AY124683 Equus asi
31	13.4	51.5	50	4	AY124684S3	AY124686 Equus asi
32	13.4	51.5	50	4	AY124687S3	AY124689 Equus bur
33	13.4	51.5	50	4	AY124690S3	AY124692 Equus bur
34	13.4	51.5	50	4	AY124693S3	AY124695 Equus bur
35	13.4	51.5	50	4	AY124696S3	AY124698 Equus gre
36	13.4	51.5	50	4	AY124699S3	AY124701 Equus zeb
37	13.2	50.8	30	6	BD189528	BD189528 Method of
38	13.2	50.8	30	6	BD189534	BD189534 Method of
39	13.2	50.8	30	6	BD017630	BD017630 Method fo
40	13.2	50.8	30	6	BD017636	BD017636 Method fo
41	13.2	50.8	32	6	AR310570	AR310570 Sequence
42	13.2	50.8	32	6	AX150251	AX150251 Sequence
C 43	13.2	50.8	40	6	E07010	E07010 Primer. 9/1
44	13	50.0	24	6	AX289779	AX289779 Sequence
C 45	13	50.0	26	6	A04044	A04044 Synthetic o
46	13	50.0	27	6	E33244	E33244 HTLV-1 reco
47	13	50.0	27	6	E33247	E33247 HTLV-1 reco
48	13	50.0	30	6	AR243738	AR243738 Sequence
49	13	50.0	32	6	BD251198	BD251198 Cells for
50	13	50.0	32	6	AX025203	AX025203 Sequence 6
C 51	13	50.0	37	6	A82363	A82363 Sequence 6
C 52	13	50.0	50	6	AR032971	AR032971 Sequence 58
C 53	13	50.0	50	6	I29711	I29711 Sequence 58
C 54	13	50.0	50	6	I91385	I91385 Sequence 58
C 55	13	50.0	50	6	AR209635	AR209635 Sequence
56	12.8	49.2	17	6	AX781701	AX781701 Sequence
57	12.8	49.2	17	6	AX781702	AX781702 Sequence
58	12.8	49.2	25	6	AX610233	AX610233 Sequence
59	12.8	49.2	25	6	AX782447	AX782447 Sequence
60	12.8	49.2	25	6	AX782448	AX782448 Sequence
61	12.8	49.2	25	6	AX782449	AX782449 Sequence
62	12.8	49.2	25	6	AX782450	AX782450 Sequence
63	12.8	49.2	25	6	AX782451	AX782451 Sequence
64	12.8	49.2	25	6	AX782452	AX782452 Sequence
65	12.8	49.2	25	6	AX782453	AX782453 Sequence
66	12.8	49.2	30	6	AX018685	AX018685 Sequence
C 67	12.8	49.2	33	6	AL12129	AL12129 oligonucleo
C 68	12.8	49.2	38	6	AR020203	AR020203 Sequence
C 69	12.8	49.2	38	6	AR032155	AR032155 Sequence
C 70	12.8	49.2	38	6	AR043820	AR043820 Sequence
C 71	12.8	49.2	38	6	AR072132	AR072132 Sequence
C 72	12.8	49.2	38	6	AR095986	AR095986 Sequence
C 73	12.8	49.2	38	6	AR136646	AR136646 Sequence
C 74	12.8	49.2	38	6	AR157181	AR157181 Sequence
C 75	12.8	49.2	38	6	AR164130	AR164130 Sequence
C 76	12.8	49.2	38	6	I32816	I32816 Sequence 12
C 77	12.8	49.2	38	6	I59630	I59630 Sequence 12
C 78	12.8	49.2	38	6	AX127253	AX127253 Sequence
C 79	12.8	49.2	38	6	AX800784	AX800784 Sequence
80	12.8	49.2	39	6	I05259	I05259 Sequence 21
C 81	12.8	49.2	50	6	AX157008	AX157008 Sequence
C 82	12.6	48.5	21	6	BD013408	BD013408 Method fo
C 83	12.6	48.5	26	6	BD273463	BD273463 High sens
C 84	12.6	48.5	26	6	AX824496	AX824496 Sequence
C 85	12.6	48.5	30	6	CQ847068	CQ847068 Sequence
86	12.6	48.5	30	6	AX428445	AX428445 Sequence
87	12.6	48.5	30	6	AX428477	AX428477 Sequence
88	12.6	48.5	30	6	BD097490	BD097490 Process f
C 89	12.6	48.5	32	6	AX622937	AX622937 Sequence
90	12.6	48.5	34	6	A21294	A21294 Nucleotide
91	12.6	48.5	40	6	BD132037	BD132037 Fibroblas
92	12.6	48.5	42	6	A09949	A09949 Nucleotide

93	12.6	48.5	43	6	BD181430	BD181430 Method fo	166	12	45.2	27	6	BD1813640	BD1813640 Process f
94	12.6	48.5	43	6	BD091643	BD091643 Method fo	167	12	46.2	27	6	AX343658	AX343658 Sequence
95	12.6	48.5	48	6	I07867	I07867 Sequence 7	168	12	46.2	28	6	EX2356	EX2356 Plant havin
96	12.4	47.7	17	6	AX722703	AX722703 Sequence	169	12	46.2	30	6	CQ814749	CQ814749 Sequence
97	12.4	47.7	17	6	AX781699	AX781699 Sequence	170	12	46.2	32	6	AR217261	AR217261 Sequence
98	12.4	47.7	17	6	AX781700	AX781700 Sequence	171	12	46.2	32	6	BD000511	BD000511 Protein,
99	12.4	47.7	20	6	AX295269	AX295269 Sequence	172	12	46.2	33	6	CQ812759	CQ812759 Transgeni
100	12.4	47.7	24	6	AX164372	AX164372 Sequence	173	12	46.2	35	6	BD243702	BD243702 Sequence
101	12.4	47.7	24	6	AX290636	AX290636 Sequence	174	12	46.2	36	6	AR006796	AR006796 Sequence
102	12.4	47.7	24	6	AX291378	AX291378 Sequence	175	12	46.2	36	6	AR135404	AR135404 Sequence
103	12.4	47.7	27	6	E32354	E32354 Plant havin	176	12	46.2	36	6	I71308	I71308 Sequence 46
104	12.4	47.7	28	6	AX399202	AX399202 Sequence	177	12	46.2	38	6	AR000580	AR000580 Sequence
105	12.4	47.7	28	6	AX108668	AX108668 Sequence	178	12	46.2	38	6	BD267995	BD267995 Polynucle
106	12.4	47.7	33	6	I00040	I00040 Sequence 3	179	12	46.2	38	6	AR208893	AR208893 Sequence
107	12.4	47.7	35	6	AR201623	AR201623 Sequence	180	12	46.2	38	6	BD003632	BD003632 A polynuc
108	12.4	47.7	35	6	AR491606	AR491606 Sequence	181	12	46.2	38	6	BD057133	BD057133 Polynucle
109	12.4	47.7	37	6	AR411038	AR411038 Sequence	182	12	46.2	42	6	AX525430	AX525430 Sequence
110	12.4	47.7	40	6	AR364170	AR364170 Sequence	183	12	46.2	42	6	AX525431	AX525431 Sequence
111	12.4	47.7	41	6	AX515174	AX515174 Sequence	184	12	46.2	43	6	AR19038	AR19038 Sequence
112	12.4	47.7	41	6	AX517968	AX517968 Sequence	185	12	46.2	43	6	AR179154	AR179154 Sequence
113	12.4	47.7	42	6	AR104422	AR104422 Sequence	186	12	46.2	48	6	AX305162	AX305162 Sequence
114	12.4	47.7	42	6	BD262362	BD262362 Bacterici	187	12	46.2	48	6	AX305167	AX305167 Sequence
115	12.4	47.7	45	6	BD102842	BD102842 Beta-Lipo	188	12	46.2	48	6	AX612167	AX612167 Sequence
116	12.4	47.7	45	6	BD102842	BD102842 Beta-Lipo	189	12	46.2	48	6	AX612168	AX612168 Sequence
117	12.4	47.7	45	9	HS224296	HS224296 Homo sapi	190	12	46.2	50	1	FVBFOXIF	FVBFOXIF
118	12.4	47.7	50	6	CQ008630	CQ008630 Sequence	191	12	46.2	50	6	AR381690	AR381690 Sequence
119	12.4	47.7	50	6	CQ008631	CQ008631 Sequence	192	12	46.2	50	6	AX395202	AX395202 Sequence
120	12.2	46.9	19	6	CQ757898	CQ757898 Sequence	193	12	46.2	50	6	AX781703	AX781703 Sequence
121	12.2	46.9	19	6	CQ757899	CQ757899 Sequence	194	11.8	45.4	17	6	AX822204	AX822204 Sequence
122	12.2	46.9	20	6	AX293269	AX293269 Sequence	195	11.8	45.4	18	6	AX825844	AX825844 Sequence
123	12.2	46.9	24	6	AR217186	AR217186 Sequence	196	11.8	45.4	22	6	AX231093	AX231093 Sequence
124	12.2	46.9	24	6	AX288636	AX288636 Sequence	197	11.8	45.4	22	6	AX231554	AX231554 Sequence
125	12.2	46.9	28	6	BD161136	BD161136 Method fo	198	11.8	45.4	22	6	AX232205	AX232205 Sequence
126	12.2	46.9	30	6	AX600867	AX600867 Sequence	199	11.8	45.4	22	6	AX232214	AX232214 Sequence
127	12.2	46.9	30	6	AX642344	AX642344 Sequence	200	11.8	45.4	22	6	AX233339	AX233339 Sequence
128	12.2	46.9	31	6	AR411312	AR411312 Sequence	201	11.8	45.4	22	6	AX233348	AX233348 Sequence
129	12.2	46.9	33	6	CQ770998	CQ770998 Sequence	202	11.8	45.4	23	6	E09823	E09823 Antisense p
130	12.2	46.9	33	6	AR474321	AR474321 Sequence	203	11.8	45.4	23	6	BD249648	BD249648 Pi-ta gen
131	12.2	46.9	33	6	AR474335	AR474335 Sequence	204	11.8	45.4	24	6	AR254321	AR254321 Sequence
132	12.2	46.9	33	6	AR474342	AR474342 Sequence	205	11.8	45.4	24	6	AR277969	AR277969 Sequence
133	12.2	46.9	33	6	AX282625	AX282625 Sequence	206	11.8	45.4	24	6	AX081035	AX081035 Sequence
134	12.2	46.9	33	6	AX282629	AX282629 Sequence	207	11.8	45.4	25	6	AR209035	AR209035 Sequence
135	12.2	46.9	33	6	AX282646	AX282646 Sequence	208	11.8	45.4	25	6	AR002992	AR002992 Sequence
136	12.2	46.9	35	6	AX655221	AX655221 Sequence	209	11.8	45.4	25	6	AR482104	AR482104 Sequence
137	12.2	46.9	35	6	AX231285	AX231285 Sequence	210	11.8	45.4	25	6	AX782454	AX782454 Sequence
138	12.2	46.9	36	6	AR268971	AR268971 Sequence	211	11.8	45.4	25	6	AX930018	AX930018 Sequence
139	12.2	46.9	36	6	BD009830	BD009830 Compositi	212	11.8	45.4	25	6	BD132732	BD132732 Regulator
140	12.2	46.9	42	6	BD209223	BD209223 Enzymatic	213	11.8	45.4	25	6	AX105562	AX105562 Sequence
141	12.2	46.9	43	6	BD217529	BD217529 Glucoamy1	214	11.8	45.4	27	6	A46165	A46165 Sequence 3
142	12.2	46.9	43	6	CQ770999	CQ770999 Sequence	215	11.8	45.4	30	6	A46166	A46166 Sequence 4
143	12.2	46.9	43	6	AR198409	AR198409 Sequence	216	11.8	45.4	30	6	AR361090	AR361090 Sequence
144	12.2	46.9	48	6	AX093110	AX093110 Sequence	217	11.8	45.4	30	6	AR361091	AR361091 Sequence
145	12.2	46.9	48	6	AX522764	AX522764 Sequence	218	11.8	45.4	30	6	AX431480	AX431480 Sequence
146	12.2	46.9	48	6	BD009934	BD009934 BH3 inter	219	11.8	45.4	31	6	AR195952	AR195952 Sequence
147	12.2	46.9	48	6	AX314113	AX314113 Sequence 9	220	11.8	45.4	31	6	AR89684	AR89684 Sequence 16
148	12.2	46.2	20	6	A85350	A85350 Sequence	221	11.8	45.4	32	6	AR002996	AR002996 Sequence
149	12.2	46.2	21	6	AR098956	AR098956 Sequence	222	11.8	45.4	32	6	AR151699	AR151699 Sequence
150	12.2	46.2	21	6	AR154843	AR154843 Sequence	223	11.8	45.4	32	6	AR209038	AR209038 Sequence
151	12.2	46.2	21	6	AR170540	AR170540 Sequence	224	11.8	45.4	32	6	AR336822	AR336822 Sequence
152	12.2	46.2	21	6	AR170704	AR170704 Sequence	225	11.8	45.4	32	6	AR482107	AR482107 Sequence
153	12.2	46.2	21	6	AR174772	AR174772 Sequence	226	11.8	45.4	32	6	BD132735	BD132735 Regulator
154	12.2	46.2	21	6	E65368	E65368 Genome DNA	227	11.8	45.4	32	6	AX183828	AX183828 Sequence
155	12.2	46.2	21	6	I79796	I79796 Sequence 92	228	11.8	45.4	33	6	AR016829	AR016829 Sequence
156	12.2	46.2	23	6	AX802122	AX802122 Sequence	229	11.8	45.4	34	6	AR020855	AR020855 Sequence
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158	12.2	46.2	25	6	AX448094	AX448094 Sequence	231	11.8	45.4	34	6	AR038465	AR038465 Sequence
159	12.2	46.2	25	6	AX690086	AX690086 Sequence	232	11.8	45.4	34	6	AR064607	AR064607 Sequence
160	12.2	46.2	25	6	AX690087	AX690087 Sequence	233	11.8	45.4	34	6	AR067532	AR067532 Sequence
161	12.2	46.2	25	6	AX690088	AX690088 Sequence	234	11.8	45.4	34	6	I07358	I07358 Sequence 10
162	12.2	46.2	25	6	AX690089	AX690089 Sequence	235	11.8	45.4	34	6	I38484	I38484 Sequence 58
163	12.2	46.2	25	6	AX690090	AX690090 Sequence	236	11.8	45.4	34	6	I56959	I56959 Sequence 58
164	12.2	46.2	25	6	AX690091	AX690091 Sequence	237	11.8	45.4	34	6	I59825	I59825 Sequence 58
165	12.2	46.2	25	6	CQ818874	CQ818874 Sequence	238	11.8	45.4	34	6		

C 239	11.8	45.4	34	6	I75152	I75152 Sequence 58	312	11.6	44.6	20	6	AR312363	AR312363 Sequence
C 240	11.8	45.4	34	6	AR409700	AR409700 Sequence	C 313	11.6	44.6	20	6	AR382864	AR382864 Sequence
C 241	11.8	45.4	36	6	I35618	I35618 Sequence 4	C 314	11.6	44.6	20	6	AX294379	AX294379 Sequence
C 242	11.8	45.4	37	6	AR2991	AR2991 Sequence 1	C 315	11.6	44.6	20	6	BD012499	BD012499 Guanosine
C 243	11.8	45.4	37	6	AR2993	AR2993 Sequence 3	C 316	11.6	44.6	23	6	AX172363	AX172363 Sequence
C 244	11.8	45.4	37	6	AR175560	AR175560 Sequence	C 317	11.6	44.6	23	6	AX394772	AX394772 Sequence
C 245	11.8	45.4	37	6	AR175562	AR175562 Sequence	C 318	11.6	44.6	24	6	AR229825	AR229825 Sequence
C 246	11.8	45.4	37	6	CQ774687	CQ774687 Sequence	C 319	11.6	44.6	24	6	AX289746	AX289746 Sequence
C 247	11.8	45.4	37	6	AX207717	AX207717 Sequence	C 320	11.6	44.6	25	6	BD245283	BD245283 Developme
C 248	11.8	45.4	37	6	BD106502	BD106502 Method fo	C 321	11.6	44.6	25	6	BD245360	BD245360 Developme
C 249	11.8	45.4	37	6	BD106504	BD106504 Method fo	C 322	11.6	44.6	25	6	AX690084	AX690084 Sequence
C 250	11.8	45.4	38	6	AR018828	AR018828 Sequence	C 323	11.6	44.6	25	6	AX690085	AX690085 Sequence
C 251	11.8	45.4	38	6	AR020854	AR020854 Sequence	C 324	11.6	44.6	25	6	AX690092	AX690092 Sequence
C 252	11.8	45.4	38	6	AR027177	AR027177 Sequence	C 325	11.6	44.6	25	6	AX690093	AX690093 Sequence
C 253	11.8	45.4	38	6	AR038464	AR038464 Sequence	C 326	11.6	44.6	27	6	CQ788626	CQ788626 Sequence
C 254	11.8	45.4	38	6	AR064606	AR064606 Sequence	C 327	11.6	44.6	27	6	I08539	I08539 Sequence 1
C 255	11.8	45.4	38	6	AR067531	AR067531 Sequence	C 328	11.6	44.6	28	6	AX404949	AX404949 Sequence
C 256	11.8	45.4	38	6	I07357	I07357 Sequence 9	C 329	11.6	44.6	28	6	BD006148	BD006148 Methods a
C 257	11.8	45.4	38	6	I38483	I38483 Sequence 57	C 330	11.6	44.6	29	6	A99074	A99074 Sequence 82
C 258	11.8	45.4	38	6	I56958	I56958 Sequence 57	C 331	11.6	44.6	29	6	AR195389	AR195389 Sequence 9
C 259	11.8	45.4	38	6	I59824	I59824 Sequence 57	C 332	11.6	44.6	30	6	A49494	A49494 Sequence 9
C 260	11.8	45.4	38	6	I75151	I75151 Sequence 57	C 333	11.6	44.6	30	6	AR087700	AR087700 Sequence
C 261	11.8	45.4	38	6	AR409699	AR409699 Sequence	C 334	11.6	44.6	30	6	I87172	I87172 Sequence 7
C 262	11.8	45.4	40	6	AR8998	AR8998 Sequence 6	C 335	11.6	44.6	31	6	E59841	E59841 Method for
C 263	11.8	45.4	40	6	AR195315	AR195315 Sequence	C 336	11.6	44.6	31	6	I52169	I52169 Sequence 12
C 264	11.8	45.4	40	6	AX514618	AX514618 Sequence	C 337	11.6	44.6	31	6	AR196031	AR196031 Sequence
C 265	11.8	45.4	40	6	AX520560	AX520560 Sequence	C 338	11.6	44.6	31	6	AR340186	AR340186 Sequence
C 266	11.8	45.4	40	6	AX538378	AX538378 Sequence	C 339	11.6	44.6	31	6	AR408584	AR408584 Sequence
C 267	11.8	45.4	41	6	AX515336	AX515336 Sequence	C 340	11.6	44.6	31	6	AX151283	AX151283 Sequence
C 268	11.8	45.4	41	6	AX517833	AX517833 Sequence	C 341	11.6	44.6	31	6	BD002480	BD002480 Gene comp
C 269	11.8	45.4	42	6	A09950	A09950 Nucleotide	C 342	11.6	44.6	31	6	BD002532	BD002532 Gene comp
C 270	11.8	45.4	44	6	E09822	E09822 Antisense p	C 343	11.6	44.6	32	6	AR016831	AR016831 Sequence
C 271	11.8	45.4	44	6	E27278	E27278 Method for	C 344	11.6	44.6	32	6	AR020857	AR020857 Sequence
C 272	11.8	45.4	44	6	AR411399	AR411399 Sequence	C 345	11.6	44.6	32	6	AR027180	AR027180 Sequence
C 273	11.8	45.4	45	6	AR042820	AR042820 Sequence	C 346	11.6	44.6	32	6	AR038467	AR038467 Sequence
C 274	11.8	45.4	45	6	BD262796	BD262796 Diagnosti	C 347	11.6	44.6	32	6	AR064609	AR064609 Sequence
C 275	11.8	45.4	45	6	AR476977	AR476977 Sequence	C 348	11.6	44.6	32	6	AR067534	AR067534 Sequence
C 276	11.8	45.4	45	6	AX046232	AX046232 Sequence	C 349	11.6	44.6	32	6	I06799	I06799 Sequence 9
C 277	11.8	45.4	47	6	AR288427	AR288427 Sequence	C 350	11.6	44.6	32	6	I07360	I07360 Sequence 12
C 278	11.8	45.4	47	6	AR194985	AR194985 Sequence	C 351	11.6	44.6	32	6	I38486	I38486 Sequence 60
C 279	11.8	45.4	48	6	AX234365	AX234365 Sequence	C 352	11.6	44.6	32	6	I56961	I56961 Sequence 60
C 280	11.8	45.4	48	6	AX234385	AX234385 Sequence	C 353	11.6	44.6	32	6	I59827	I59827 Sequence 60
C 281	11.8	45.4	48	6	AX305153	AX305153 Sequence	C 354	11.6	44.6	32	6	I75154	I75154 Sequence 60
C 282	11.8	45.4	48	6	AX305154	AX305154 Sequence	C 355	11.6	44.6	32	6	AR409702	AR409702 Sequence
C 283	11.8	45.4	48	6	AX305155	AX305155 Sequence	C 356	11.6	44.6	33	6	AR209734	AR209734 Sequence
C 284	11.8	45.4	48	6	AX305156	AX305156 Sequence	C 357	11.6	44.6	33	6	AX574356	AX574356 Sequence
C 285	11.8	45.4	48	6	AX305159	AX305159 Sequence	C 358	11.6	44.6	33	6	AX597443	AX597443 Sequence
C 286	11.8	45.4	48	6	AX305163	AX305163 Sequence	C 359	11.6	44.6	35	6	I52170	I52170 Sequence 13
C 287	11.8	45.4	48	6	AX305164	AX305164 Sequence	C 360	11.6	44.6	35	6	AR381716	AR381716 Sequence
C 288	11.8	45.4	48	6	AX305166	AX305166 Sequence	C 361	11.6	44.6	35	6	AX006374	AX006374 Sequence
C 289	11.8	45.4	48	6	AX305168	AX305168 Sequence	C 362	11.6	44.6	35	6	AX019932	AX019932 Sequence
C 290	11.8	45.4	48	6	AX305170	AX305170 Sequence	C 363	11.6	44.6	35	6	AX590521	AX590521 Sequence
C 291	11.8	45.4	48	6	AX305175	AX305175 Sequence	C 364	11.6	44.6	36	6	AR209737	AR209737 Sequence
C 292	11.8	45.4	48	6	AX305178	AX305178 Sequence	C 365	11.6	44.6	36	6	AX794109	AX794109 Sequence
C 293	11.8	45.4	49	6	AX305179	AX305179 Sequence	C 366	11.6	44.6	37	6	E40796	E40796 Antihuman F
C 294	11.8	45.4	49	6	AR125772	AR125772 Sequence	C 367	11.6	44.6	37	6	AX581930	AX581930 Sequence
C 295	11.8	45.4	49	6	I47184	I47184 Sequence 11	C 368	11.6	44.6	39	6	E36951	E36951 Human telom
C 296	11.8	45.4	50	6	AR151515	AR151515 Sequence	C 369	11.6	44.6	39	6	E36953	E36953 Human telom
C 297	11.8	45.4	50	6	AR151516	AR151516 Sequence	C 370	11.6	44.6	39	6	E36955	E36955 Human telom
C 298	11.8	45.4	50	6	AR151517	AR151517 Sequence	C 371	11.6	44.6	39	6	E36957	E36957 Human telom
C 299	11.8	45.4	50	6	AR151518	AR151518 Sequence	C 372	11.6	44.6	39	6	AR243472	AR243472 Sequence
C 300	11.8	45.4	50	6	AR151519	AR151519 Sequence	C 373	11.6	44.6	39	6	AR243474	AR243474 Sequence
C 301	11.8	45.4	50	6	AR151520	AR151520 Sequence	C 374	11.6	44.6	39	6	AR243476	AR243476 Sequence
C 302	11.8	45.4	50	6	AR151521	AR151521 Sequence	C 375	11.6	44.6	39	6	AR243478	AR243478 Sequence
C 303	11.8	45.4	50	6	AR151522	AR151522 Sequence	C 376	11.6	44.6	39	6	AR390628	AR390628 Sequence
C 304	11.8	45.4	50	6	I42213	I42213 Sequence 26	C 377	11.6	44.6	39	6	AR390630	AR390630 Sequence
C 305	11.8	45.4	50	6	I47182	I47182 Sequence 11	C 378	11.6	44.6	39	6	AR390632	AR390632 Sequence
C 306	11.8	45.4	50	6	AX156795	AX156795 Sequence	C 379	11.6	44.6	39	6	AR390634	AR390634 Sequence
C 307	11.8	45.4	50	6	AX305160	AX305160 Sequence	C 380	11.6	44.6	39	6	AR393242	AR393242 Sequence
C 308	11.8	45.4	50	6	AX305160	AX305160 Sequence	C 381	11.6	44.6	39	6	AR393244	AR393244 Sequence
C 309	11.8	45.4	50	6	BD014158	BD014158 Probe for	C 382	11.6	44.6	39	6	AR393246	AR393246 Sequence
C 310	11.6	44.6	19	6	AX815569	AX815569 Sequence	C 383	11.6	44.6	39	6	AR393248	AR393248 Sequence
C 311	11.6	44.6	20	6	BD196073	BD196073 Antisense	C 384	11.6	44.6	39	6	AX810533	AX810533 Sequence

385	11.6	44.6	39	6	AX810535	Sequence	458	11.4	43.8	33	6	BD011030	BD011030 HIV probe
386	11.6	44.6	39	6	AX810537	Sequence	459	11.4	43.8	33	6	BD061585	BD061585 Peptide h
387	11.6	44.6	39	6	AX810539	Sequence	460	11.4	43.8	34	6	AX1791	AX1791 Sequence 14
388	11.6	44.6	39	6	BD011202	Human tel	C 461	11.4	43.8	34	6	CQ840153	CQ840153 Sequence
389	11.6	44.6	39	6	BD011204	Human tel	462	11.4	43.8	34	6	AX353829	AX353829 Sequence
390	11.6	44.6	39	6	BD011206	Human tel	463	11.4	43.8	34	6	AX358614	AX358614 Sequence
391	11.6	44.6	39	6	BD011208	Human tel	C 464	11.4	43.8	35	6	AR099783	AR099783 Sequence
392	11.6	44.6	40	6	AX052782	Sequence 10	C 465	11.4	43.8	35	6	AR159970	AR159970 Sequence
393	11.6	44.6	41	6	I06800	Sequence 10	C 466	11.4	43.8	35	6	AR210049	AR210049 Sequence
394	11.6	44.6	41	6	AX516903	Sequence	C 467	11.4	43.8	35	6	AX028956	AX028956 Sequence
395	11.6	44.6	41	6	AX519414	Sequence	C 468	11.4	43.8	35	6	AX028956	AX028956 Sequence
396	11.6	44.6	41	6	BD137163	Autonomou	469	11.4	43.8	35	6	AX684159	AX684159 Sequence
397	11.6	44.6	42	6	AR490210	Sequence	470	11.4	43.8	35	6	BD136770	BD136770 Human pla
398	11.6	44.6	42	6	AX018715	Sequence	C 471	11.4	43.8	37	6	AR3835	AR3835 Sequence 4
399	11.6	44.6	44	6	AR104030	Sequence	C 472	11.4	43.8	37	6	AR360582	AR360582 Sequence
400	11.6	44.6	44	6	AR104118	Sequence	C 473	11.4	43.8	37	6	AX000221	AX000221 Sequence
401	11.6	44.6	44	6	AR104119	Sequence	C 474	11.4	43.8	38	6	CQ821251	CQ821251 Sequence
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404	11.6	44.6	45	6	AX404956	Sequence	C 477	11.4	43.8	40	6	BD240782	BD240782 Substanti
405	11.6	44.6	45	6	AX513776	Sequence	C 478	11.4	43.8	40	6	CQ772558	CQ772558 Sequence
406	11.6	44.6	46	6	AR032405	Sequence	C 479	11.4	43.8	41	6	I06806	I06806 Sequence 16
407	11.6	44.6	46	6	I29145	Sequence 17	C 480	11.4	43.8	41	6	AX514784	AX514784 Sequence
408	11.6	44.6	46	6	I90819	Sequence 17	C 481	11.4	43.8	41	6	AX520794	AX520794 Sequence
409	11.6	44.6	46	6	AR209069	Sequence	482	11.4	43.8	42	3	SCAFNCNII	J03789 S.americana
410	11.6	44.6	46	6	AX357202	Sequence	483	11.4	43.8	43	6	E14886	E14886 DNA contain
411	11.6	44.6	47	6	CQ753988	Sequence	C 484	11.4	43.8	44	6	BD181482	BD181482 Poxvirus
412	11.6	44.6	47	6	AR230918	Sequence	485	11.4	43.8	45	6	CQ772690	CQ772690 Sequence
413	11.6	44.6	48	3	DME300022	Sequence 6	C 487	11.4	43.8	45	6	CQ772698	CQ772698 Sequence
414	11.6	44.6	50	6	CQ004570	Sequence	C 488	11.4	43.8	45	6	AX092135	AX092135 Sequence
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416	11.6	44.6	50	6	AX781698	Sequence	C 490	11.4	43.8	47	6	AX138315	AX138315 Sequence
417	11.4	43.8	17	6	AX781698	Sequence	C 491	11.4	43.8	49	6	AR162095	AR162095 Sequence
418	11.4	43.8	20	6	AX718426	Sequence	C 492	11.4	43.8	49	6	AR166620	AR166620 Sequence
419	11.4	43.8	20	6	AX823896	Sequence	C 493	11.4	43.8	49	6	E09371	E09371 DNA fragmen
420	11.4	43.8	21	6	BD228617	Sequence	C 494	11.4	43.8	49	6	AR279828	AR279828 Sequence
421	11.4	43.8	21	6	E35039	Sequence 1	C 495	11.4	43.8	50	6	AR148168	AR148168 Sequence
422	11.4	43.8	21	6	I19720	Sequence 1	C 496	11.2	43.1	17	6	CQ006611	CQ006611 Sequence
423	11.4	43.8	21	6	AR404579	Sequence	C 497	11.2	43.1	17	6	AX688587	AX688587 Sequence
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426	11.4	43.8	23	6	AX0279190	Sequence	C 500	11.2	43.1	18	6	BD250478	BD250478 Identific
427	11.4	43.8	23	6	AX021131	Sequence	C 501	11.2	43.1	19	6	E49440	E49440 Screening m
428	11.4	43.8	23	6	BD082764	Sequence	C 502	11.2	43.1	19	6	AX129020	AX129020 Sequence
429	11.4	43.8	25	6	AX042816	Sequence	C 503	11.2	43.1	19	6	AX100076	AX100076 Sequence
430	11.4	43.8	26	6	BD262681	Sequence	C 504	11.2	43.1	20	6	I24530	I24530 Sequence 10
431	11.4	43.8	26	6	AX038104	Sequence	C 505	11.2	43.1	20	6	I33872	I33872 Sequence 10
432	11.4	43.8	26	6	AX127109	Sequence	C 506	11.2	43.1	20	6	I83696	I83696 Sequence 26
433	11.4	43.8	26	6	BD165726	Novel pol	C 507	11.2	43.1	20	6	AR312047	AR312047 Sequence
434	11.4	43.8	27	6	AX039574	Sequence	C 508	11.2	43.1	20	6	AR315986	AR315986 Sequence
435	11.4	43.8	28	6	AX088623	Sequence	C 509	11.2	43.1	20	6	AX020814	AX020814 Sequence
436	11.4	43.8	28	6	AX088624	Sequence	510	11.2	43.1	20	6	AX296011	AX296011 Sequence
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438	11.4	43.8	28	6	BD223222	Isolated	C 512	11.2	43.1	21	6	BD251424	BD251424 Ion chann
439	11.4	43.8	28	6	E55115	DNA encodin	513	11.2	43.1	21	6	AX023788	AX023788 Sequence
440	11.4	43.8	28	6	AX024607	Sequence	514	11.2	43.1	21	6	AR071135	AR071135 Sequence
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443	11.4	43.8	30	6	AX093846	Sequence	C 517	11.2	43.1	25	6	AX487007	AX487007 Sequence
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446	11.4	43.8	30	6	BD061403	Peptide h	C 520	11.2	43.1	25	6	AX610232	AX610232 Sequence
447	11.4	43.8	30	6	BD096247	Process f	C 521	11.2	43.1	26	6	A68453	A68453 Sequence 26
448	11.4	43.8	31	6	AR087440	Sequence	C 522	11.2	43.1	26	6	AX34133	AX34133 Synthetic H
449	11.4	43.8	31	6	E33094	Tetrahydroc	523	11.2	43.1	27	6	A35388	A35388 Synthetic H
450	11.4	43.8	31	6	E55109	DNA encodin	C 524	11.2	43.1	27	6	BD191571	BD191571 ChimERIC
451	11.4	43.8	31	6	AR184333	Sequence	C 525	11.2	43.1	27	6	BD141082	BD141082 Transform
452	11.4	43.8	32	6	AX203866	Sequence	C 526	11.2	43.1	27	6	BD141086	BD141086 Transform
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454	11.4	43.8	32	6	AX522092	Sequence	C 528	11.2	43.1	28	6	AR053744	AR053744 Sequence
455	11.4	43.8	33	6	AR106458	Sequence	529	11.2	43.1	28	6	AR085756	AR085756 Sequence
456	11.4	43.8	33	6	AR106460	Sequence	530	11.2	43.1	28	6		
457	11.4	43.8	33	6	AR368998	Sequence							

C 531	11.2	43.1	28	6	AR091029 Sequence	AR091029 Sequence	C 604	11.2	43.1	40	6	AR258517 Sequence
C 532	11.2	43.1	28	6	AR146244 Sequence	AR146244 Sequence	C 605	11.2	43.1	40	6	AR258566 Sequence
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C 534	11.2	43.1	28	6	CQ812750 Sequence	CQ812750 Sequence	C 607	11.2	43.1	40	6	AX685572 Sequence
C 535	11.2	43.1	28	6	I73323 Sequence 19	I73323 Sequence 19	C 608	11.2	43.1	40	6	BD062539 ICM-6 ma
C 536	11.2	43.1	28	6	AR198064 Sequence	AR198064 Sequence	C 609	11.2	43.1	41	6	BD274163 Identific
C 537	11.2	43.1	28	6	AR214480 Sequence	AR214480 Sequence	C 610	11.2	43.1	41	6	BD274167 Identific
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C 542	11.2	43.1	28	6	AR280451 Sequence	AR280451 Sequence	C 615	11.2	43.1	42	6	BD209178 Enzymatic
C 543	11.2	43.1	28	6	AX068944 Sequence	AX068944 Sequence	C 616	11.2	43.1	42	6	AR229150 Sequence
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C 546	11.2	43.1	28	6	AX704517 Sequence	AX704517 Sequence	C 619	11.2	43.1	42	9	LUHIGHABS
C 547	11.2	43.1	28	6	AR172331 Sequence	AR172331 Sequence	C 620	11.2	43.1	43	6	I17032 Homo sapien
C 548	11.2	43.1	29	6	BD191557 Sequence	BD191557 Sequence	C 621	11.2	43.1	43	6	AX484541 Sequence
C 549	11.2	43.1	29	6	AR361346 Sequence	AR361346 Sequence	C 622	11.2	43.1	43	6	BD017540 Short-cha
C 550	11.2	43.1	29	6	AX528934 Sequence	AX528934 Sequence	C 623	11.2	43.1	44	9	HUMTCVJ6
C 551	11.2	43.1	30	6	BD012962 A method	BD012962 A method	C 624	11.2	43.1	45	6	CQ767583 Sequence
C 552	11.2	43.1	30	6	BD012962 Sequence	BD012962 Sequence	C 625	11.2	43.1	45	6	BD170183 Method Of
C 553	11.2	43.1	31	6	AR102872 Sequence	AR102872 Sequence	C 626	11.2	43.1	45	6	BD170184 Method Of
C 554	11.2	43.1	31	6	AR129416 Sequence	AR129416 Sequence	C 627	11.2	43.1	47	6	AR072106 Sequence
C 555	11.2	43.1	31	6	E37847 Process for	E37847 Process for	C 628	11.2	43.1	47	6	AR072107 Sequence
C 556	11.2	43.1	31	6	AR195819 Sequence	AR195819 Sequence	C 629	11.2	43.1	47	6	BD238344 Accelerat
C 557	11.2	43.1	32	6	AR104380 Sequence	AR104380 Sequence	C 630	11.2	43.1	47	6	AR288330 Sequence
C 558	11.2	43.1	32	6	BD249054 Centrifug	BD249054 Centrifug	C 631	11.2	43.1	47	6	AR289708 Sequence
C 559	11.2	43.1	32	6	BD187139 Saponin d	BD187139 Saponin d	C 632	11.2	43.1	48	6	AX224370 Sequence
C 560	11.2	43.1	34	6	AR9087 Sequence 95	AR9087 Sequence 95	C 633	11.2	43.1	48	9	HIVLCDR3H
C 561	11.2	43.1	34	6	AR195398 Sequence	AR195398 Sequence	C 634	11.2	43.1	50	6	AR055770 Sequence
C 562	11.2	43.1	34	6	AR220000 Sequence	AR220000 Sequence	C 635	11.2	43.1	50	6	CQ008815 Sequence
C 563	11.2	43.1	34	6	AR220717 Sequence	AR220717 Sequence	C 636	11.2	43.1	50	6	AR355902 Sequence
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C 567	11.2	43.1	35	6	A64752 Sequence 12	A64752 Sequence 12	C 640	11.2	43.1	50	10	AF071693 Mus muscu
C 568	11.2	43.1	35	6	AR161649 Sequence	AR161649 Sequence	C 641	11	42.3	11	6	AX472204 Sequence
C 569	11.2	43.1	36	6	AR217661 Sequence	AR217661 Sequence	C 642	11	42.3	20	6	A58720 Sequence 39
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C 571	11.2	43.1	37	6	AX752552 Sequence	AX752552 Sequence	C 644	11	42.3	20	6	AR2566412 Sequence
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C 576	11.2	43.1	38	6	AR043822 Sequence	AR043822 Sequence	C 649	11	42.3	20	6	BD023651 Process f
C 577	11.2	43.1	38	6	AR043823 Sequence	AR043823 Sequence	C 650	11	42.3	21	6	AR138429 Sequence
C 578	11.2	43.1	38	6	AR072134 Sequence	AR072134 Sequence	C 651	11	42.3	21	6	CQ814750 Sequence
C 579	11.2	43.1	38	6	AR072135 Sequence	AR072135 Sequence	C 652	11	42.3	21	6	I17685 Sequence 2
C 580	11.2	43.1	38	6	AR095988 Sequence	AR095988 Sequence	C 653	11	42.3	21	6	AR217298 Sequence
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C 585	11.2	43.1	38	6	AR157184 Sequence	AR157184 Sequence	C 658	11	42.3	23	6	AX752033 Sequence
C 586	11.2	43.1	38	6	AR164132 Sequence	AR164132 Sequence	C 659	11	42.3	24	6	A35263 Synthetic o
C 587	11.2	43.1	38	6	AR164133 Sequence	AR164133 Sequence	C 660	11	42.3	24	6	AR012296 Sequence
C 588	11.2	43.1	38	6	BD226339 Method of	BD226339 Method of	C 661	11	42.3	24	6	I14994 Sequence 80
C 589	11.2	43.1	38	6	BD234606 Thymidine	BD234606 Thymidine	C 662	11	42.3	24	6	I73714 Sequence 80
C 590	11.2	43.1	38	6	I05098 Sequence 2	I05098 Sequence 2	C 663	11	42.3	24	6	AX097392 Sequence
C 591	11.2	43.1	38	6	I32818 Sequence 14	I32818 Sequence 14	C 664	11	42.3	24	6	AX112094 Sequence
C 592	11.2	43.1	38	6	I59632 Sequence 15	I59632 Sequence 15	C 665	11	42.3	24	6	AX288381 Sequence
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C 597	11.2	43.1	38	6	AX800787 Sequence	AX800787 Sequence	C 670	11	42.3	24	6	AX444478 Sequence
C 598	11.2	43.1	39	6	A94044 Sequence 31	A94044 Sequence 31	C 671	11	42.3	24	6	AX446359 Sequence
C 599	11.2	43.1	39	6	AR232110 Sequence	AR232110 Sequence	C 672	11	42.3	24	6	AX446561 Sequence
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C 602	11.2	43.1	40	6	AR053631 Sequence	AR053631 Sequence	C 675	11	42.3	24	6	AX704985 Sequence
C 603	11.2	43.1	40	6			C 676	11	42.3	25	6	BD225574 Assay for

C 677	11	42.3	25	6	AR271709 Sequence	AR271709 Sequence	C 750	11	42.3	36	6	AR103024 Sequence	AR103024 Sequence
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C 700	11	42.3	29	6	BD235512 Desaturas	BD235512 Desaturas	C 773	11	42.3	40	6	BD227214	BD227214
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C 836	10.8	41.5	17	6	AX762178	Sequence	AX762178	Sequence	C 909	10.8	41.5	27	6	AR214260	Sequence
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ALIGNMENTS

BD181369 26 bp DNA linear PAT 15-MAY-2003  
A method for determination of a nucleic acid using a control.

BD181369  
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JP 2002335981-A/8.  
synthetic construct  
synthetic construct  
artificial sequences.  
1 (bases 1 to 26)  
Jaeger,S.  
A method for determination of a nucleic acid using a control  
F HOFFMANN LA ROCHE AG  
OS Artificial Sequence  
PN JP 2002335981-A/8  
PD 26-NOV-2002  
PF 04-MAR-2002 JP 2002057515  
PR 02-MAR-2001 EP 01105172.9  
PI STEPHAN JAEGER  
PC C12N15/09, C12Q1/68, G01N33/50, G01N33/53, G01N33/566, G01N33/58,  
C12N15/00  
CC Description of Artificial Sequence: ST280pc Primer parallel-  
complementary  
CC to ST280  
CC Key Location/Qualifiers  
FH Key 1..26  
FT source /organism='Artificial Sequence'.  
FT Location/Qualifiers  
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/mol\_type='genomic DNA'  
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FEATURES  
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Query Match 100.0%; Score 26; DB 6; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCTTTTCGACATCGGTACCTCAAT 26  
DB 1 CGTCTTTTCGACATCGGTACCTCAAT 26

RESULT 2  
AX523949 26 bp DNA linear PAT 21-NOV-2002  
LOCUS Sequence 8 from Patent EP1236804.  
ACCESSION AX523949  
VERSION AX523949.1 GI:25168880  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1  
AUTHORS Jaeger,S.  
TITLE A method for determination of a nucleic acid using a control  
JOURNAL Patent: EP 1236804-A 8 04-SEP-2002;  
Roche Diagnostics GmbH (DE) ; F. Hoffmann-La Roche AG (CH)  
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/note='ST280pc Primer parallel-complementary to ST280'

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Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCTTTTCGACATCGGTACCTCAAT 26  
DB 1 CGTCTTTTCGACATCGGTACCTCAAT 26

RESULT 3  
AX524847 26 bp DNA linear PAT 21-NOV-2002  
LOCUS Sequence 8 from Patent EP1236805.  
ACCESSION AX524847  
VERSION AX524847.1 GI:25169941  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1  
AUTHORS Jaeger,S.  
TITLE A method for the determination of a nucleic acid using a control  
JOURNAL Patent: EP 1236805-A 8 04-SEP-2002;  
Roche Diagnostics GmbH (DE) ; F. Hoffmann-La Roche AG (CH)  
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/note='ST280pc Primer parallel-complementary to ST280'

ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
LOCUS I38537 44 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 5 from patent US 5614398.
ACCESSION I38537
VERSION I38537.1 GI:2084591
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 44)
AUTHORS O'Brochta,D., Warren,W. and Atkinson,P.
TITLE Gene transfer system for insects
JOURNAL Patent: US 5614398-A 5 25-MAR-1997;
FEATURES
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Best Local Similarity 85.0%; Pred. NO. 9.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 6 TTCGAGATCGGTACCTCAA 25
Db 26 TTCACAGTTCGGTACCTGAA 7

RESULT 5
LOCUS AR053999/c 41 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 4 from patent US 5834306.
ACCESSION AR053999
VERSION AR053999.1 GI:5978861
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 41)
AUTHORS Webster,K.A. and Bishopric,N.H.
TITLE Tissue specific hypoxia regulated therapeutic constructs
JOURNAL Patent: US 5834306-A 4 10-NOV-1998;
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Best Local Similarity 81.0%; Pred. NO. 2.1e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 2 GTCCTTCGACATCGGTACCT 22
Db 30 GTCCTTTCCCTATCGGTACCT 10

RESULT 6
LOCUS AR146175/c 41 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 4 from patent US 6218179.
ACCESSION AR146175
VERSION AR146175.1 GI:15109364
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 41)
AUTHORS Webster,K.A., Bishopric,N.H., Murphy,B., Laderoute,K.R. and
Green,C.J.
TITLE Tissue specific hypoxia regulated constructs
JOURNAL Patent: US 6218179-A 4 17-APR-2001;

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Best Local Similarity 75.0%; Pred. NO. 2.7e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 3 TCCTTCGACATCGGTACCTCAAT 26
Db 37 TTTTCCAAGATAGGTACTTCCAT 14

RESULT 7
LOCUS BD263605/c 40 bp DNA linear PAT 17-JUL-2003
DEFINITION Novel streptococcus antigens.
ACCESSION BD263605
VERSION BD263605.1 GI:33073373
KEYWORDS JP 2002533123-A/22.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 40)
AUTHORS Hamel,J., Brodeur,B.R., Pineau,I., Martin,D., Rioux,C. and
Charland,N.
TITLE Novel streptococcus antigens
JOURNAL Patent: JP 2002533123-A 22 08-OCT-2002;
SHIRE BIOCHEM INC
COMMENT PN JP 2002533123-A/22
PD 08-OCT-2002
PF 20-DEC-1999 JP 2000591190
PR 23-DEC-1998 US 60/113800
PI JOSEF HAMEL, BERNARD R BRODEUR, ISABELLE PINEAU, DENIS MARTIN, PI
CLEMENT RIOUX,
PI NATHALIE CHARLAND
PC C12N15/09,A61K39/00,A61K39/39,A61P11/00,A61P25/00,
A61P27/16,
PC A61P31/04,C07K14/315,C07K19/00,C12N1/15,C12N1/19,C12N1/21, PC
C12N5/10,
PC C12P21/02,C12N15/00,C12N5/00
CC PCR oligonucleotide primer
FH Key Location/Qualifiers
FT source 1..40
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Query Match 55.4%; Score 14.4; DB 6; Length 40;
Best Local Similarity 75.0%; Pred. NO. 2.7e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 3 TCCTTCGACATCGGTACCTCAAT 26
Db 37 TTTTCCAAGATAGGTACTTCCAT 14

RESULT 8
LOCUS AX343106/c 40 bp DNA linear PAT 12-JAN-2002
DEFINITION Sequence 37 from Patent WO0198334.
ACCESSION AX343106
VERSION AX343106.1 GI:18152286
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
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unclassified.
1
REFERENCE
AUTHORS Hamel,J., Ouellet,C., Charland,N., Martin,D. and Brodeur,B.
TITLE Streptococcus antigens
JOURNAL Patent: WO 0198334-A 37 27-DEC-2001;
SHIRE BIOCHEM INC. (CA)
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Location/Qualifiers
/organism="unidentified"
/mol_type="unassigned DNA"
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/note="HAMJ 281"

ORIGIN
Query Match 55.4%; Score 14.4; DB 6; Length 40;
Best Local Similarity 75.0%; Pred. No. 2.7e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 TCTTTCGACATCGGTACTCAAT 26
Db 37 TTTTTCACAGATAGGTACTTCCAT 14

RESULT 9
LOCUS AX454034/c 30 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 10 from Patent WO0198539.
ACCESSION AX454034
VERSION AX454034.1 GI:21713674
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Mitsuhashi,M., Kambara,H., Matsunaga,H. and Kawamura,M.
TITLE Gene markers for lung cancer
JOURNAL Patent: WO 0198539-A 10 27-DEC-2001;
Hitachi Chemical Co., Ltd. (JP); HITACHI CHEMICAL RESEARCH CENTER,
INC. (US); Hitachi, Ltd. (JP)
FEATURES
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Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="7013 Primer P10."

ORIGIN
Query Match 54.6%; Score 14.2; DB 6; Length 30;
Best Local Similarity 84.2%; Pred. No. 3.4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 CGCAGATCGGTACTCAAT 26
Db 30 CGCAGATGGGAACCTTAAT 12

RESULT 10
LOCUS MLMLTRB1 48 bp ss-RNA linear VRL 05-AUG-2004
DEFINITION M-MuLV unintegrated circular retroviral DNA, partial LTR.
ACCESSION M10582
VERSION M10582.1 GI:331953
KEYWORDS
SEGMENT 1 of 2
SOURCE Moloney murine leukemia virus
ORGANISM Moloney murine leukemia virus
REFERENCE 1 (bases 1 to 48)
AUTHORS Shoemaker,C., Goff,S., Gilboa,E., Paskind,M., Mitra,S.W. and Baltimore,D.
TITLE Structure of cloned retroviral circular DNAs: implications for virus integration
JOURNAL Cold Spring Harb. Symp. Quant. Biol. 45 Pt 2, 711-717 (1981)

unclassified.
MEDLINE 81259596
PUBMED 6266763
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Location/Qualifiers
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/organism="Moloney murine leukemia virus"
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/note="long terminal repeat"

LTR

ORIGIN
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Best Local Similarity 77.3%; Pred. No. 4.4e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 GTCTTTCGACATCGGTACTC 23
Db 17 GTCTTTCACACTGATACGTTCTC 38

RESULT 11
LOCUS AX445171/c 24 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 1626 from Patent WO0216649.
ACCESSION AX445171
VERSION AX445171.1 GI:21692449
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Gunderson,K.
TITLE Probes and decoder oligonucleotides
JOURNAL Patent: WO 0216649-A 1626 28-FEB-2002;
Illumina, Inc. (US)
FEATURES
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Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Computer Generated Probe Sequence."

ORIGIN
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Best Local Similarity 88.2%; Pred. No. 5.5e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CAGATCGGTACTCAAT 26
Db 22 CAGATCCGTACCCCAAT 6

RESULT 12
LOCUS AR182869 34 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 41 from patent US 6339068.
ACCESSION AR182869
VERSION AR182869.1 GI:20226076
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 34)
AUTHORS Krieg,A.M., Davis,H.L., Wu,T. and Schorr,J.
TITLE Vectors and methods for immunization or therapeutic protocols
JOURNAL Patent: US 6339068-A 41 15-JAN-2002;
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Query Match 52.3%; Score 13.6; DB 6; Length 34;
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Best Local Similarity 80.0%; Pred. No. 7.2e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 TCGCAGATCGGTACCTCAAT 26
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Db 10 TCGCAGATCGATACCGAT 29

RESULT 13
LOCUS BD190521 40 bp DNA linear PAT 17-JUL-2003
DEFINITION NOVEL ESSENTIAL BACTERIAL GENES AND THEIR PROTEINS.
ACCESSION BD190521
VERSION BD190521.1 GI:33000260
KEYWORDS JP 2002541819-A/14.
SOURCE Escherichia coli
ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
REFERENCE 1 (bases 1 to 40)
AUTHORS Rabisinski,H., Brettu,H., Ehrat,K., Frykberg,C., Spaltmann,F. and
TITLE NOVEL ESSENTIAL BACTERIAL GENES AND THEIR PROTEINS
JOURNAL Patent: JP 2002541819-A 14 10-DEC-2002;
COMMENT Bayer AG
OS Escherichia coli
PN JP 2002541819-A/14
PD 10-DEC-2002
PF 28-MAR-2000 JP 2000611714
PR 10-APR-1999 DE 199 16 176.3
PI harald rabisinski,heike brettu,kersten ehrat,christoph PI
    frykberg,
    CC frank spaltmann,bernd berand
    CC Primer YGBP2A
FH Key Location/Qualifiers
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ORIGIN
Query Match 52.3%; Score 13.6; DB 6; Length 40;
Best Local Similarity 80.0%; Pred. No. 7.2e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 TTTCGACATCGGTACCTCA 24
    |||||
Db 9 TTTAGTGGATCGGTACCTCA 28

RESULT 14
LOCUS AX038843 40 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 22 from Patent WO0061792.
ACCESSION AX038843
VERSION AX038843.1 GI:11228168
KEYWORDS Escherichia coli
SOURCE Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
ORGANISM Enterobacteriaceae; Escherichia.
REFERENCE 1
AUTHORS Labischinski,H., Wieland,B., Broetz,H., Ehler,K., Freiberg,C. and
    Spaltmann,F.
TITLE Novel essential bacterial genes and their proteins
JOURNAL Patent: WO 0061792-A 22 19-OCT-2000;
    LABISCHINSKI HARALD (DE) ; WIELAND BERND (DE) ; BAYER AG (DE) ;
    BROETZ HEIKE (DE) ; EHLERT KERSTIN (DE) ; FREIBERG CHRISTOPH (DE) ;
    SPALTWMANN FRANK (US)
FEATURES
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Best Local Similarity 80.0%; Pred. No. 7.2e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 TCGCAGATCGGTACCTCAAT 26
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Db 10 TCGCAGATCGATACCGAT 29

RESULT 13
LOCUS BD190521 40 bp DNA linear PAT 17-JUL-2003
DEFINITION NOVEL ESSENTIAL BACTERIAL GENES AND THEIR PROTEINS.
ACCESSION BD190521
VERSION BD190521.1 GI:33000260
KEYWORDS JP 2002541819-A/14.
SOURCE Escherichia coli
ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
REFERENCE 1 (bases 1 to 40)
AUTHORS Rabisinski,H., Brettu,H., Ehrat,K., Frykberg,C., Spaltmann,F. and
TITLE NOVEL ESSENTIAL BACTERIAL GENES AND THEIR PROTEINS
JOURNAL Patent: JP 2002541819-A 14 10-DEC-2002;
COMMENT Bayer AG
OS Escherichia coli
PN JP 2002541819-A/14
PD 10-DEC-2002
PF 28-MAR-2000 JP 2000611714
PR 10-APR-1999 DE 199 16 176.3
PI harald rabisinski,heike brettu,kersten ehrat,christoph PI
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FH Key Location/Qualifiers
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ORIGIN
Query Match 52.3%; Score 13.6; DB 6; Length 40;
Best Local Similarity 80.0%; Pred. No. 7.2e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 TTTCGACATCGGTACCTCA 24
    |||||
Db 9 TTTAGTGGATCGGTACCTCA 28

RESULT 14
LOCUS AX038843 40 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 22 from Patent WO0061792.
ACCESSION AX038843
VERSION AX038843.1 GI:11228168
KEYWORDS Escherichia coli
SOURCE Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
ORGANISM Enterobacteriaceae; Escherichia.
REFERENCE 1
AUTHORS Labischinski,H., Wieland,B., Broetz,H., Ehler,K., Freiberg,C. and
    Spaltmann,F.
TITLE Novel essential bacterial genes and their proteins
JOURNAL Patent: WO 0061792-A 22 19-OCT-2000;
    LABISCHINSKI HARALD (DE) ; WIELAND BERND (DE) ; BAYER AG (DE) ;
    BROETZ HEIKE (DE) ; EHLERT KERSTIN (DE) ; FREIBERG CHRISTOPH (DE) ;
    SPALTWMANN FRANK (US)
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Best Local Similarity 80.0%; Pred. No. 7.2e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 TCGCAGATCGGTACCTCAAT 26
    |||||
Db 10 TCGCAGATCGATACCGAT 29

RESULT 13
LOCUS BD190521 40 bp DNA linear PAT 17-JUL-2003
DEFINITION NOVEL ESSENTIAL BACTERIAL GENES AND THEIR PROTEINS.
ACCESSION BD190521
VERSION BD190521.1 GI:33000260
KEYWORDS JP 2002541819-A/14.
SOURCE Escherichia coli
ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
REFERENCE 1 (bases 1 to 40)
AUTHORS Rabisinski,H., Brettu,H., Ehrat,K., Frykberg,C., Spaltmann,F. and
TITLE NOVEL ESSENTIAL BACTERIAL GENES AND THEIR PROTEINS
JOURNAL Patent: JP 2002541819-A 14 10-DEC-2002;
COMMENT Bayer AG
OS Escherichia coli
PN JP 2002541819-A/14
PD 10-DEC-2002
PF 28-MAR-2000 JP 2000611714
PR 10-APR-1999 DE 199 16 176.3
PI harald rabisinski,heike brettu,kersten ehrat,christoph PI
    frykberg,
    CC frank spaltmann,bernd berand
    CC Primer YGBP2A
FH Key Location/Qualifiers
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    /mol_type="genomic DNA"
    /db_xref="taxon:562"

ORIGIN
Query Match 52.3%; Score 13.6; DB 6; Length 40;
Best Local Similarity 80.0%; Pred. No. 7.2e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 TTTCGACATCGGTACCTCA 24
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Db 9 TTTAGTGGATCGGTACCTCA 28

RESULT 15
LOCUS CQ824393 24 bp DNA linear PAT 21-JUN-2004
DEFINITION Sequence 7 from Patent WO2004047866.
ACCESSION CQ824393
VERSION CQ824393.1 GI:49021418
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Margioris,A.N. and Gravanis,A.
TITLE Use of the crh (corticotropin releasing hormone) - ucn (urocortin)
    system in the treatment of inflammatory diseases
JOURNAL Patent: WO 2004047866-A 7 10-JUN-2004;
    Bionature E.A. Limited (Cy)
FEATURES
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    /note="Oligonucleotide, PCR Primer"

ORIGIN
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Best Local Similarity 73.9%; Pred. No. 9.1e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 GTCCTTTCGACATCGGTACCTCA 24
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Db 23 GTCCTTTCGACAGAGAACTTCA 1
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RESULT 16
LOCUS AR448717 25 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 3 from patent US 6673605.
ACCESSION AR448717
VERSION AR448717.1 GI:42677328
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Sawada,M.
TITLE Established cell line of microglia
JOURNAL Patent: US 6673605-A 3 06-JAN-2004;
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ORIGIN
Query Match 51.5%; Score 13.4; DB 6; Length 25;
Best Local Similarity 73.9%; Pred. No. 9.1e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 GTCCTTTCGACATCGGTACCTCA 24
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Db      24  GTCCTTCGAGAGGAAGCACTTCA 2
RESULT 17
LOCUS   AR101054          31 bp    DNA          linear          PAT 14-FEB-2001
DEFINITION
Sequence 24 from patent US 6083694.
ACCESSION AR101054
VERSION   AR101054.1  GI:12811852
KEYWORDS
SOURCE   Unknown.
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 31)
AUTHORS Hardy, J. and Goate, A.M.
TITLE    Method for elucidation and detection of polymorphisms, splice
variants, and proximal coding mutations using intronic sequences of
the alzheimer's S182 gene
JOURNAL  Patent: US 6083694-A 24 04-JUL-2000;
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ORIGIN
Query Match 51.5%; Score 13.4; DB 6; Length 31;
Best Local Similarity 93.3%; Pred. No. 9.2e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      3  TCTTTCGAGATCGGTACTCTCAA 25
|||||
Db      7  TCTTTCCTTTTCAGAACTCTCAA 29

RESULT 18
AR099751/c
LOCUS   AR099751          39 bp    DNA          linear          PAT 14-FEB-2001
DEFINITION
Sequence 22 from patent US 6077949.
ACCESSION AR099751
VERSION   AR099751.1  GI:12809517
KEYWORDS
SOURCE   Unknown.
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 39)
AUTHORS Munroe, D.G., Gupta, A.K., Vyas, T.B., McCallum, K. and Fan, E.
TITLE    Cloned glucagon-like peptide 2 receptors
JOURNAL  Patent: US 6077949-A 22 20-JUN-2000;
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source   Location/Qualifiers
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/mol_type="unassigned DNA"

ORIGIN
Query Match 51.5%; Score 13.4; DB 6; Length 39;
Best Local Similarity 93.3%; Pred. No. 9.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      11 AGATCGGTACTCTCAA 25
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Db      22 AGATCGGTACTCTCGA 8

RESULT 19
BD064614/c
LOCUS   BD064614          39 bp    DNA          linear          PAT 27-AUG-2002
DEFINITION
Cloned glucagon-like peptide-2 receptors.
ACCESSION BD064614
VERSION   BD064614.1  GI:22610217
KEYWORDS JP 2001507571-A/19
SOURCE   synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE
1 (bases 1 to 39)
AUTHORS Munroe, D.G., Gupta, A.K., Vyas, T.B., McCallum, K. and Fan, E.
TITLE    Cloned glucagon-like peptide-2 receptors
JOURNAL  Patent: US 6077949-A 22 20-JUN-2000;
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source   Location/Qualifiers
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/note="Aptamer"

ORIGIN
Query Match 51.5%; Score 13.4; DB 6; Length 48;
Best Local Similarity 73.9%; Pred. No. 9.3e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      4  CTTTCGAGATCGGTACTCTCAAT 26
|||||
Db      6  CTAGCCACATCGGTACTCTAT 28

RESULT 21
AY124654S3
LOCUS   AY124654S3          50 bp    DNA          linear          MAM 11-FEB-2003
DEFINITION
Equus caballus beta-2-microglobulin precursor (b-2-m) gene, exon 3
and complete cds.
ACCESSION AY124656
VERSION   AY124656.1  GI:28315892
KEYWORDS

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REFERENCE
1 (bases 1 to 39)
Munroe, D.G., Gupta, A.K., Vyas, T.B., McCallum, K. and Fan, E.
TITLE    Cloned glucagon-like peptide-2 receptors
JOURNAL  Patent: JP 2001507571-A 19 12-JUN-2001;
COMMENT  ALLELIX BIOPHARMACEUTICALS INC
PN       JP 2001507571-A/19
PD       12-JUN-2001
PF       15-DEC-1997 JP 1998526050
PR       13-DEC-1996 US 08/767224, 24-JAN-1997 US 08/787721 PR
24-APR-1997 US 08/845546
PI       DONALD G MUNROE, ASHWANI K GUPTA, TEJAL B VYAS, KIRK MCCALLUM, PI
ERMEI FAN
PC       C12N15/12, C07K14/705, C12N5/10, C12N15/62, C07K16/28, C12Q1/68, PC
G01N33/50
CC       Strandedness: Single;
CC       Topology: Linear;
FH       Key Location/Qualifiers
FEATURES
source   Location/Qualifiers
1..39
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 51.5%; Score 13.4; DB 6; Length 39;
Best Local Similarity 93.3%; Pred. No. 9.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      11 AGATCGGTACTCTCAA 25
|||||
Db      22 AGATCGGTACTCTCGA 8

RESULT 20
AX305162
LOCUS   AX305162          48 bp    RNA          linear          PAT 11-DEC-2001
DEFINITION
Sequence 10 from Patent WO0188123.
ACCESSION AX305162
VERSION   AX305162.1  GI:17644792
KEYWORDS
SOURCE   synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
James, W.S.
Ligands specific for an isoform of the prion protein
TITLE    Patent: WO 0188123-A 10 22-NOV-2001;
JOURNAL  Isis Innovation Limited (GB)
FEATURES
source   Location/Qualifiers
1..48
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Aptamer"

ORIGIN
Query Match 51.5%; Score 13.4; DB 6; Length 48;
Best Local Similarity 73.9%; Pred. No. 9.3e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      4  CTTTCGAGATCGGTACTCTCAAT 26
|||||
Db      6  CTAGCCACATCGGTACTCTAT 28

RESULT 21
AY124654S3
LOCUS   AY124654S3          50 bp    DNA          linear          MAM 11-FEB-2003
DEFINITION
Equus caballus beta-2-microglobulin precursor (b-2-m) gene, exon 3
and complete cds.
ACCESSION AY124656
VERSION   AY124656.1  GI:28315892
KEYWORDS

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SEGMENT 3 of 3
SOURCE  Equus caballus (horse)
ORGANISM  Equus caballus
REFERENCE  Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS  Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
TITLE  1 (bases 1 to 50)
JOURNAL  Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,
MEDLINE  Carpenter,S.L. and Antczak,D.F.
PUBMED  Characterization of the beta(2)-microglobulin gene of the horse
22444330 Immunogenetics 54 (10), 725-733 (2003)
REFERENCE  2 (bases 1 to 50)
AUTHORS  Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,
TITLE  Carpenter,S.L. and Antczak,D.F.
JOURNAL  Characterization of the beta(2)-microglobulin gene of the horse
22444330 Immunogenetics 54 (10), 725-733 (2003)
PUBMED  12557059
REFERENCE  2 (bases 1 to 50)
AUTHORS  Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,
TITLE  Carpenter,S.L. and Antczak,D.F.
JOURNAL  Direct Submission
PUBMED  Submitted (20-JUN-2002) James A. Baker Institute for Animal Health,
22444330 College of Veterinary Medicine, Cornell University, Hungerford Hill
Immunogenetics 54 (10), 725-733 (2003)
PUBMED  Rd., Ithaca, NY 14850, USA
FEATURES
source
Location/Qualifiers
1..50
/organism="Equus caballus"
/mol_type="genomic DNA"
/db_xref="taxon:9796"
/chromosome="1"
/notes="breed: Arabian"
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join(AY124654.1:<1..67,AY124655.1:1..276,20..>50)
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/CDS
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/protein_id="AA077009.1"
/db_xref="GI:28315893"
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CYVSGFHPPEIEIDLKNGERKVDRLSFKDWSFYLLVHTDFTPNGVDEYSCRQV
HSTLKDPLIVKWRDL"
mat_peptide
join(AY124654.1:61..67,AY124655.1:1..276,20..>30)
/exon
/gene="b-2-m"
number=3
3'UTR
34..>50
/gene="b-2-m"
ORIGIN
Query Match 51.5%; Score 13.4; DB 4; Length 50;
Best Local Similarity 73.9%; Pred. No. 9.3e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 3 TCTTTCCGAGATCGGTACTCAA 25
Db 10 TTTTTCATAGATCGAGACCTCTA 32
RESULT 22
AY124657S3
LOCUS 50 bp DNA linear MAM 11-FEB-2003
DEFINITION Equus caballus beta-2-microglobulin precursor (b-2-m) gene, exon 3
and complete cds.
ACCESSION AY124659.1 GI:28315897
VERSION 3 of 3
KEYWORDS Equus caballus (horse)
SOURCE Equus caballus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
REFERENCE 1 (bases 1 to 50)
AUTHORS Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,
TITLE Carpenter,S.L. and Antczak,D.F.
JOURNAL Characterization of the beta(2)-microglobulin gene of the horse
22444330 Immunogenetics 54 (10), 725-733 (2003)
PUBMED 12557059
REFERENCE 1 (bases 1 to 50)
AUTHORS Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,
TITLE Carpenter,S.L. and Antczak,D.F.
JOURNAL Characterization of the beta(2)-microglobulin gene of the horse
22444330 Immunogenetics 54 (10), 725-733 (2003)
PUBMED 12557059

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REFERENCE 2 (bases 1 to 50)  
 AUTHORS Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,  
 Carpenter,S.L. and Antczak,D.F.  
 TITLE Direct Submission  
 JOURNAL Submitted (20-JUN-2002) James A. Baker Institute for Animal Health,  
 College of Veterinary Medicine, Cornell University, Hungerford Hill  
 Rd., Ithaca, NY 14850, USA

FEATURES  
 source Location/Qualifiers  
 1..50  
 /organism="Equus caballus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9796"  
 /chromosome="1"  
 /note="breed: Miniature Horse"  
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 /gene="b-2-m"  
 join(AY124660.1:<1..67,AY124661.1:1..276,20..>50)  
 /gene="b-2-m"  
 /product="beta-2-microglobulin precursor"  
 join(AY124660.1:1..67,AY124661.1:1..276,20..33)  
 /gene="b-2-m"  
 /codon\_start=1  
 /product="beta-2-microglobulin precursor"  
 /protein\_id="AAM77011.1"  
 /db\_xref="GI:28315903"  
 /translation="MARVVALVLLGLSLTGLEAVRPVKQVYGRHPAENGKPNFLN  
 CVVSGFHPPEIEIDLKNGEKVKDRSDFSFKDWSFYLLVHTDFTPNGVDYSCRVO  
 HSTLKDPLIVKWRDL"  
 mat\_peptide join(AY124660.1:61..67,AY124661.1:1..276,20..30)  
 /gene="b-2-m"  
 /product="beta-2-microglobulin"  
 20..>50  
 /gene="b-2-m"  
 /number=3  
 34..>50  
 /gene="b-2-m"  
 exon  
 3'UTR  
 ORIGIN  
 Query Match 51.5%; Score 13.4; DB 4; Length 50;  
 Best Local Similarity 73.9%; Pred. No. 9.3e+04;  
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 Oy 3 TCTTTCCGACATCGGTACCTCAA 25  
 | ||||| ||||| ||||| |||||  
 Db 10 TTTTTCATAGATCGAGACCTCTA 32

RESULT 24  
 AY124663S3 50 bp DNA linear MAM 11-FEB-2003  
 LOCUS Equus caballus beta-2-microglobulin precursor (b-2-m) gene, exon 3  
 DEFINITION and complete cds.  
 ACCESSION AY124665  
 VERSION AY124665.1 GI:28315907  
 KEYWORDS  
 SEGMENT 3 of 3  
 SOURCE Equus caballus (horse)  
 ORGANISM Equus caballus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 REFERENCE 1 (bases 1 to 50)  
 AUTHORS Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,  
 Carpenter,S.L. and Antczak,D.F.  
 TITLE Characterization of the beta(2)-microglobulin gene of the horse  
 JOURNAL Immunogenetics 54 (10), 725-733 (2003)  
 MEDLINE 22444330  
 PUBMED 12557059  
 REFERENCE 2 (bases 1 to 50)  
 AUTHORS Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,  
 Carpenter,S.L. and Antczak,D.F.  
 TITLE Direct Submission  
 JOURNAL Submitted (20-JUN-2002) James A. Baker Institute for Animal Health,  
 College of Veterinary Medicine, Cornell University, Hungerford Hill  
 Rd., Ithaca, NY 14850, USA

Rd., Ithaca, NY 14850, USA

FEATURES  
 source Location/Qualifiers  
 1..50  
 /organism="Equus caballus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9796"  
 /chromosome="1"  
 /note="breed: Standardbred"  
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 /gene="b-2-m"  
 join(AY124663.1:<1..67,AY124664.1:1..276,20..>50)  
 /gene="b-2-m"  
 /product="beta-2-microglobulin precursor"  
 join(AY124663.1:1..67,AY124664.1:1..276,20..33)  
 /gene="b-2-m"  
 /codon\_start=1  
 /product="beta-2-microglobulin precursor"  
 /protein\_id="AAM77012.1"  
 /db\_xref="GI:28315908"  
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 CVVSGFHPPEIEIDLKNGEKVKDRSDFSFKDWSFYLLVHTDFTPNGVDYSCRVO  
 HSTLKDPLIVKWRDL"  
 mat\_peptide join(AY124663.1:61..67,AY124664.1:1..276,20..30)  
 /gene="b-2-m"  
 /product="beta-2-microglobulin"  
 20..>50  
 /gene="b-2-m"  
 /number=3  
 34..>50  
 /gene="b-2-m"  
 exon  
 3'UTR  
 ORIGIN  
 Query Match 51.5%; Score 13.4; DB 4; Length 50;  
 Best Local Similarity 73.9%; Pred. No. 9.3e+04;  
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 Oy 3 TCTTTCCGACATCGGTACCTCAA 25  
 | ||||| ||||| ||||| |||||  
 Db 10 TTTTTCATAGATCGAGACCTCTA 32

RESULT 25  
 AY124666S3 50 bp DNA linear MAM 11-FEB-2003  
 LOCUS Equus caballus beta-2-microglobulin precursor (b-2-m) gene, exon 3  
 DEFINITION and complete cds.  
 ACCESSION AY124668  
 VERSION AY124668.1 GI:28315912  
 KEYWORDS  
 SEGMENT 3 of 3  
 SOURCE Equus caballus (horse)  
 ORGANISM Equus caballus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 REFERENCE 1 (bases 1 to 50)  
 AUTHORS Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,  
 Carpenter,S.L. and Antczak,D.F.  
 TITLE Characterization of the beta(2)-microglobulin gene of the horse  
 JOURNAL Immunogenetics 54 (10), 725-733 (2003)  
 MEDLINE 22444330  
 PUBMED 12557059  
 REFERENCE 2 (bases 1 to 50)  
 AUTHORS Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,  
 Carpenter,S.L. and Antczak,D.F.  
 TITLE Direct Submission  
 JOURNAL Submitted (20-JUN-2002) James A. Baker Institute for Animal Health,  
 College of Veterinary Medicine, Cornell University, Hungerford Hill  
 Rd., Ithaca, NY 14850, USA

FEATURES  
 source Location/Qualifiers  
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 /organism="Equus caballus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9796"



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/chromosome="1"
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product="beta-2-microglobulin precursor"
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/translation="MARVALVLGLSLTGLEAVPRVPKQVYSRHPAENGKPNFLN
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/protein_id="AAW77013.1"
/db_xref="GI:28315913"
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CYVSGFHPPEIIDLKNGEKMKVDRSDLSFKDMSFYLLVHTDFTPNGVDEYSCRQV
HSTLKDPLIVKWRDL"
join (AY124666.1:1..67,AY124667.1:1..276,20..>50)
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product="beta-2-microglobulin"
20..>50
/gene="b-2-m"
/number=3
34..>50
/gene="b-2-m"

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/gene="b-2-m"
product="beta-2-microglobulin"
20..>50
/gene="b-2-m"
/number=3
34..>50
/gene="b-2-m"

exon
20..>50
/gene="b-2-m"
/number=3
34..>50
/gene="b-2-m"

3'UTR
20..>50
/gene="b-2-m"

ORIGIN
Query Match 51.5%; Score 13.4; DB 4; Length 50;
Best Local Similarity 73.9%; Pred. No. 9.3e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 TCTTTCCGAGATCGGTACTCAA 25
| |||| |||| |||| ||||
Db 10 TTTTTCATAGATCGAGACTCTA 32

RESULT 26
AY124669S3
LOCUS AY124669S3 50 bp DNA linear MAM 11-FEB-2003
DEFINITION Equus asinus isolate 1 beta-2-microglobulin precursor (b-2-m) gene, exon 3 and complete cds.
ACCESSION AY124671
VERSION AY124671.1 GI:28315917
KEYWORDS 3 of 3
SEGMENT Equus przewalskii
SOURCE Equus przewalskii
ORGANISM Equus przewalskii
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
REFERENCE 1 (bases 1 to 50)
AUTHORS Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,
Carpenter,S.L. and Antczak,D.F.
TITLE Characterization of the beta(2)-microglobulin gene of the horse
JOURNAL Immunogenetics 54 (10), 725-733 (2003)
MEDLINE 22444330
PUBMED 12557059
REFERENCE 2 (bases 1 to 50)
AUTHORS Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,
Carpenter,S.L. and Antczak,D.F.
TITLE Direct Submission
JOURNAL Submitted (20-JUN-2002) James A. Baker Institute for Animal Health,
College of Veterinary Medicine, Cornell University, Hungerford Hill
Rd., Ithaca, NY 14850, USA
FEATURES
source
1..50
/organism="Equus przewalskii"
/mol_type="genomic DNA"
/db_xref="taxon:9798"
/note="breed: Przewalski's Horse"
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/gene="b-2-m"
join (AY124669.1:1..67,AY124670.1:1..276,20..>50)
/gene="b-2-m"
product="beta-2-microglobulin precursor"

Qy 3 TCTTTCCGAGATCGGTACTCAA 25
| |||| |||| |||| ||||
Db 10 TTTTTCATAGATCGAGACTCTA 32

RESULT 27
AY124672S3
LOCUS AY124672S3 50 bp DNA linear MAM 11-FEB-2003
DEFINITION Equus asinus isolate 1 beta-2-microglobulin precursor (b-2-m) gene, exon 3 and complete cds.
ACCESSION AY124674
VERSION AY124674.1 GI:28315922
KEYWORDS 3 of 3
SEGMENT Equus asinus (ass)
SOURCE Equus asinus
ORGANISM Equus asinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
REFERENCE 1 (bases 1 to 50)
AUTHORS Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,
Carpenter,S.L. and Antczak,D.F.
TITLE Direct Submission
JOURNAL Submitted (20-JUN-2002) James A. Baker Institute for Animal Health,
College of Veterinary Medicine, Cornell University, Hungerford Hill
Rd., Ithaca, NY 14850, USA
FEATURES
source
1..50
/organism="Equus asinus"
/mol_type="genomic DNA"
/isolate="1"
/db_xref="taxon:9793"
/order (AY124672.1:1..67,AY124673.1:1..276,1..>50)
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product="beta-2-microglobulin precursor"
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/protein_id="AAW77015.1"
/db_xref="GI:28315923"
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 20. .>50  
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 /number=3  
 34. .>50  
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 3'UTR  
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 Query Match 51.5%; Score 13.4; DB 4; Length 50;  
 Best Local Similarity 73.9%; Pred. No. 9.3e+04;  
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 3 TCTTTCGAGATCGGTACTCTAA 25  
 ||||| ||||| |||||  
 Db 10 TTTTTCATAGATCGAGACCTCTA 32  
 ||||| ||||| |||||  
 RESULT 28  
 AY124675S3 50 bp DNA linear MAM 11-FEB-2003  
 LOCUS  
 DEFINITION Equus asinus isolate 2 beta-2-microglobulin precursor (b-2-m) gene,  
 exon 3 and complete cds.  
 ACCESSION AY124677.1 GI:28315927  
 VERSION  
 KEYWORDS  
 SEGMENT  
 SOURCE  
 ORGANISM  
 Equus asinus (ass)  
 Equus asinus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 REFERENCE  
 AUTHORS  
 Tallmadge, R.L., Lear, T.L., Johnson, A.K., Guerin, G., Millon, L.V.,  
 Carpenter, S.L. and Antczak, D.F.  
 Characterization of the beta(2)-microglobulin gene of the horse  
 Immunogenetics 54 (10), 725-733 (2003)  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 22444330  
 REFERENCE  
 AUTHORS  
 Tallmadge, R.L., Lear, T.L., Johnson, A.K., Guerin, G., Millon, L.V.,  
 Carpenter, S.L. and Antczak, D.F.  
 Direct Submission  
 Submitted (20-JUN-2002) James A. Baker Institute for Animal Health,  
 College of Veterinary Medicine, Cornell University, Hungerford Hill  
 Rd., Ithaca, NY 14850, USA  
 FEATURES  
 source  
 1. 50  
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 /mol\_type="genomic DNA"  
 /isolate="2"  
 /db\_xref="taxon:9793"  
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 /gene="b-2-m"  
 join (AY124675.1<1. .67,AY124676.1:1. .276,20. .>50)  
 /product="beta-2-microglobulin precursor"  
 join (AY124675.1:1. .67,AY124676.1:1. .276,20. .33)  
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 /codon\_start=1  
 /product="beta-2-microglobulin precursor"  
 /protein\_id="AAM77016.1"  
 /db\_xref="GI:28315928"  
 /translation="MARVVALVLLGLSLTGLEAVQRIKPVQVYSRHPAENGKFNFLN  
 CYSGFHPPEIEIDLLKNGEKMKVDRSDLSFSKDSFYLVLVHTDFTFNGVDEYSCRQ  
 HSTLKEPLIVKWRDL"  
 mat\_peptide  
 join (AY124675.1:61. .67,AY124676.1:1. .276,20. .30)  
 /gene="b-2-m"  
 /product="beta-2-microglobulin"  
 20. .>50  
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 exon

/number=3  
 34. .>50  
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 3'UTR  
 ORIGIN  
 Query Match 51.5%; Score 13.4; DB 4; Length 50;  
 Best Local Similarity 73.9%; Pred. No. 9.3e+04;  
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 3 TCTTTCGAGATCGGTACTCTAA 25  
 ||||| ||||| |||||  
 Db 10 TTTTTCATAGATCGAGACCTCTA 32  
 ||||| ||||| |||||  
 RESULT 29  
 AY124678S3 50 bp DNA linear MAM 11-FEB-2003  
 LOCUS  
 DEFINITION Equus asinus isolate 3 beta-2-microglobulin precursor (b-2-m) gene,  
 exon 3 and complete cds.  
 ACCESSION AY124680.1 GI:28315932  
 VERSION  
 KEYWORDS  
 SEGMENT  
 SOURCE  
 ORGANISM  
 Equus asinus (ass)  
 Equus asinus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 REFERENCE  
 AUTHORS  
 Tallmadge, R.L., Lear, T.L., Johnson, A.K., Guerin, G., Millon, L.V.,  
 Carpenter, S.L. and Antczak, D.F.  
 Characterization of the beta(2)-microglobulin gene of the horse  
 Immunogenetics 54 (10), 725-733 (2003)  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 22444330  
 REFERENCE  
 AUTHORS  
 Tallmadge, R.L., Lear, T.L., Johnson, A.K., Guerin, G., Millon, L.V.,  
 Carpenter, S.L. and Antczak, D.F.  
 Direct Submission  
 Submitted (20-JUN-2002) James A. Baker Institute for Animal Health,  
 College of Veterinary Medicine, Cornell University, Hungerford Hill  
 Rd., Ithaca, NY 14850, USA  
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 HSTLKEPLIVKWRDL"  
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 Best Local Similarity 73.9%; Pred. No. 9.3e+04;  
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 TCTTTCCGAGATCGGTACCTCAA 25
Db 10 TTTTTCATAGATCGAGACTCTA 32

RESULT 30
AY124681S3
LOCUS      50 bp      DNA      linear      MAM 11-FEB-2003
DEFINITION Equus asinus isolate 4 beta-2-microglobulin precursor (b-2-m) gene,
            exon 3 and complete cds.
ACCESSION  AY124683
VERSION     AY124683.1  GI:28315937
KEYWORDS   3 of 3
SEGMENT    Equus asinus (asn)
SOURCE     Equus asinus
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
REFERENCE  1 (bases 1 to 50)
AUTHORS   Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,
            Carpenter,S.L. and Antczak,D.F.
TITLE     Characterization of the beta(2)-microglobulin gene of the horse
JOURNAL   Immunogenetics 54 (10), 725-733 (2003)
MEDLINE   22444330
PUBMED    12557059
REFERENCE  2 (bases 1 to 50)
AUTHORS   Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,
            Carpenter,S.L. and Antczak,D.F.
TITLE     Direct Submission
JOURNAL   Submitted (20-JUN-2002) James A. Baker Institute for Animal Health,
            College of Veterinary Medicine, Cornell University, Hungerford Hill
            Rd., Ithaca, NY 14850, USA
FEATURES   Location/Qualifiers
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            /protein_id="AAM77018.1"
            /db_xref="GI:28315938"
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Query Match      51.5%; Score 13.4; DB 4; Length 50;
Best Local Similarity 73.9%; Pred.No. 9.3e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 TCTTTCCGAGATCGGTACCTCAA 25
Db 10 TTTTTCATAGATCGAGACTCTA 32

RESULT 31
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LOCUS      50 bp      DNA      linear      MAM 11-FEB-2003
DEFINITION Equus asinus isolate 5 beta-2-microglobulin precursor (b-2-m) gene,
            exon 3 and complete cds.
ACCESSION  AY124686
VERSION     AY124686.1  GI:28315942
KEYWORDS   3 of 3
SEGMENT    Equus asinus (asn)
SOURCE     Equus asinus
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
REFERENCE  1 (bases 1 to 50)
AUTHORS   Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,
            Carpenter,S.L. and Antczak,D.F.
TITLE     Characterization of the beta(2)-microglobulin gene of the horse
JOURNAL   Immunogenetics 54 (10), 725-733 (2003)
MEDLINE   22444330
PUBMED    12557059
REFERENCE  2 (bases 1 to 50)
AUTHORS   Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,
            Carpenter,S.L. and Antczak,D.F.
TITLE     Direct Submission
JOURNAL   Submitted (20-JUN-2002) James A. Baker Institute for Animal Health,
            College of Veterinary Medicine, Cornell University, Hungerford Hill
            Rd., Ithaca, NY 14850, USA
FEATURES   Location/Qualifiers
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Query Match      51.5%; Score 13.4; DB 4; Length 50;
Best Local Similarity 73.9%; Pred.No. 9.3e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 TCTTTCCGAGATCGGTACCTCAA 25
Db 10 TTTTTCATAGATCGAGACTCTA 32

RESULT 32
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LOCUS      50 bp      DNA      linear      MAM 11-FEB-2003
DEFINITION Equus burchellii chapmani beta-2-microglobulin precursor (b-2-m)
            gene, exon 3 and complete cds.
ACCESSION  AY124689
VERSION     AY124689.1  GI:28315947
KEYWORDS   3 of 3
SEGMENT    Equus asinus (asn)
SOURCE     Equus asinus
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
REFERENCE  1 (bases 1 to 50)
AUTHORS   Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,
            Carpenter,S.L. and Antczak,D.F.
TITLE     Characterization of the beta(2)-microglobulin gene of the horse
JOURNAL   Immunogenetics 54 (10), 725-733 (2003)
MEDLINE   22444330
PUBMED    12557059
REFERENCE  2 (bases 1 to 50)
AUTHORS   Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,
            Carpenter,S.L. and Antczak,D.F.
TITLE     Direct Submission
JOURNAL   Submitted (20-JUN-2002) James A. Baker Institute for Animal Health,
            College of Veterinary Medicine, Cornell University, Hungerford Hill
            Rd., Ithaca, NY 14850, USA
FEATURES   Location/Qualifiers
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Query Match      51.5%; Score 13.4; DB 4; Length 50;
Best Local Similarity 73.9%; Pred.No. 9.3e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 TCTTTCCGAGATCGGTACCTCAA 25
Db 10 TTTTTCATAGATCGAGACTCTA 32

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Wed Nov 24 08:46:09 2004

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KEYWORDS  
SEGMENT 3 of 3  
SOURCE Equus burchellii chapmani (Chapman's Zebra)  
ORGANISM Equus burchellii chapmani  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

REFERENCE  
AUTHORS 1 (bases 1 to 50)  
Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,  
Carpenter,S.L. and Antczak,D.F.  
Characterization of the beta(2)-microglobulin gene of the horse  
Immunogenetics 54 (10), 725-733 (2003)  
22444330

TITLE  
JOURNAL  
MEDLINE  
PUBMED

REFERENCE  
AUTHORS 2 (bases 1 to 50)  
Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,  
Carpenter,S.L. and Antczak,D.F.  
Direct Submission  
Submitted (20-JUN-2002) James A. Baker Institute for Animal Health,  
College of Veterinary Medicine, Cornell University, Hungerford Hill  
Rd., Ithaca, NY 14850, USA  
22444330

TITLE  
JOURNAL  
MEDLINE  
PUBMED

REFERENCE  
AUTHORS 2 (bases 1 to 50)  
Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,  
Carpenter,S.L. and Antczak,D.F.  
Direct Submission  
Submitted (20-JUN-2002) James A. Baker Institute for Animal Health,  
College of Veterinary Medicine, Cornell University, Hungerford Hill  
Rd., Ithaca, NY 14850, USA  
22444330

TITLE  
JOURNAL  
MEDLINE  
PUBMED

FEATURES  
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Best Local Similarity 73.9%; Pred. No. 9.3e+04;  
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 3 TCTTTCCGAGATCGTACTCAA 25  
Db 10 TTTTTCATAGATCGAGACTCTA 32  
RESULT 33  
LOCUS AY124690S3 50 bp DNA linear MAM 11-FEB-2003  
DEFINITION Equus burchellii antiquorum beta-2-microglobulin precursor (b-2-m)  
gene, exon 3 and complete cds.  
ACCESSION AY124692  
VERSION AY124692.1 GI:28315952  
KEYWORDS  
SEGMENT 3 of 3  
SOURCE Equus burchellii antiquorum (Damara's Zebra)  
ORGANISM Equus burchellii antiquorum  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

REFERENCE  
AUTHORS 1 (bases 1 to 50)  
Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,  
Carpenter,S.L. and Antczak,D.F.  
Characterization of the beta(2)-microglobulin gene of the horse  
Immunogenetics 54 (10), 725-733 (2003)  
22444330

TITLE  
JOURNAL  
MEDLINE  
PUBMED

REFERENCE  
AUTHORS 2 (bases 1 to 50)  
Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,  
Carpenter,S.L. and Antczak,D.F.  
Direct Submission  
Submitted (20-JUN-2002) James A. Baker Institute for Animal Health,  
College of Veterinary Medicine, Cornell University, Hungerford Hill  
Rd., Ithaca, NY 14850, USA  
22444330

TITLE  
JOURNAL  
MEDLINE  
PUBMED

FEATURES  
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Query Match 51.5%; Score 13.4; DB 4; Length 50;  
Best Local Similarity 73.9%; Pred. No. 9.3e+04;  
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 3 TCTTTCCGAGATCGTACTCAA 25  
Db 10 TTTTTCATAGATCGAGACTCTA 32  
RESULT 34  
LOCUS AY124693S3 50 bp DNA linear MAM 11-FEB-2003  
DEFINITION Equus burchellii boehmi beta-2-microglobulin precursor (b-2-m)  
gene, exon 3 and complete cds.  
ACCESSION AY124695  
VERSION AY124695.1 GI:28315957  
KEYWORDS  
SEGMENT 3 of 3  
SOURCE Equus burchellii boehmi (Grant's Zebra)  
ORGANISM Equus burchellii boehmi  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
REFERENCE 1 (bases 1 to 50)  
Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,  
Carpenter,S.L. and Antczak,D.F.  
Characterization of the beta(2)-microglobulin gene of the horse  
Immunogenetics 54 (10), 725-733 (2003)  
22444330

12557059 .  
 2 (bases 1 to 50)  
 Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,  
 Carpenter,S.L. and Antczak,D.F.  
 Direct Submission  
 Submitted (20-JUN-2002) James A. Baker Institute for Animal Health,  
 College of Veterinary Medicine, Cornell University, Hungerford Hill  
 Rd., Ithaca, NY 14850, USA

FEATURES  
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 34. .>50  
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 Query Match 51.5%; Score 13.4; DB 4; Length 50;  
 Best Local Similarity 73.9%; Pred.No.9.3e+04;  
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 TCTTTCGAGATCGGTACCTCAA 25  
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 Db 10 TTTTTCATAGATCGAGACTCTA 32

RESULT 35  
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 LOCUS  
 DEFINITION  
 Equus grevyi beta-2-microglobulin precursor (b-2-m) gene, exon 3  
 and complete cds.  
 AY124698  
 AY124698.1 GI:28315962  
 3 of 3  
 Equus grevyi (Grevy's Zebra)  
 ORGANISM  
 Equus grevyi  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 1 (bases 1 to 50)  
 Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,  
 Carpenter,S.L. and Antczak,D.F.  
 Characterization of the beta(2)-microglobulin gene of the horse  
 Immunogenetics 54 (10), 725-733 (2003)  
 22444330  
 PUBMED  
 12557059  
 2 (bases 1 to 50)  
 Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,  
 Carpenter,S.L. and Antczak,D.F.  
 Direct Submission  
 Submitted (20-JUN-2002) James A. Baker Institute for Animal Health,

College of Veterinary Medicine, Cornell University, Hungerford Hill Rd., Ithaca, NY 14850, USA

FEATURES  
 source 1. .50  
 /organism="Equus grevyi"  
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 HSTLKPLIVKWRDL"  
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 20. .>50  
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ORIGIN  
 Query Match 51.5%; Score 13.4; DB 4; Length 50;  
 Best Local Similarity 73.9%; Pred. No. 9.3e+04;  
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 TCTTTCGACGATCGGTACCTCAA 25  
 10 TTTTTCATAGATCGAGACCTCTA 32

Db

RESULT 36  
 AY124699S3  
 LOCUS  
 DEFINITION Equus zebra hartmannae beta-2-microglobulin precursor (b-2-m) gene,  
 exon 3 and complete cds.  
 ACCESSION AY124701  
 VERSION AY124701.1 GI:28315967  
 KEYWORDS  
 SEGMENT  
 SOURCE 3 of 3  
 ORGANISM Equus zebra hartmannae (Hartmann's Zebra)  
 Equus zebra hartmannae  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 1 (bases 1 to 50)  
 Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,  
 Carpenter,S.L. and Antczak,D.F.  
 Characterization of the beta(2)-microglobulin gene of the horse  
 Immunogenetics 54 (10), 725-733 (2003)  
 22444330  
 PUBLISHED 12557059  
 REFERENCE 2 (bases 1 to 50)  
 AUTHORS Tallmadge,R.L., Lear,T.L., Johnson,A.K., Guerin,G., Millon,L.V.,  
 Carpenter,S.L. and Antczak,D.F.  
 Direct Submission  
 TITLE Submitted (20-JUN-2002) James A. Baker Institute for Animal Health,  
 College of Veterinary Medicine, Cornell University, Hungerford Hill  
 Rd., Ithaca, NY 14850, USA  
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LOCUS Method of constructing transgenic plant having improved amino acid
DEFINITION composition and yield.
ACCESSION BD189528.1 GI:32999267
VERSION WO 0300041-A/13.
KEYWORDS synthetic construct
SOURCE artificial construct
ORGANISM 1 (bases 1 to 30)
REFERENCE Kisaka,H. and Kida,T.
AUTHORS Method of constructing transgenic plant having improved amino acid
TITLE composition and yield
JOURNAL Patent: WO 0300041-A 13 03-JAN-2003;
COMMENT AJINOMOTO CO INC,HIROAKI KISAKA,TAKAO KIDA
OS Artificial Sequence
PN WO 0300041-A/13
PD 03-JAN-2003
PF 14-JUN-2001 WO 2001JP005077
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CC sequence for chloroplast transit peptide
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VERSION JP 2001238556-A/13.
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REFERENCE Kisaka,H. and Kida,T.
AUTHORS Method for making transgenic plants having improved amino acid
TITLE composition
JOURNAL Patent: JP 2001238556-A 13 04-SEP-2001;
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PF 18-DEC-2000 JP 20000404322

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DEFINITION composition and yield.
ACCESSION BD189534
VERSION BD189534.1 GI:32999273
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SOURCE synthetic construct
ORGANISM 1 (bases 1 to 30)
REFERENCE Kisaka,H. and Kida,T.
AUTHORS Method of constructing transgenic plant having improved amino acid
TITLE composition and yield
JOURNAL Patent: WO 0300041-A 19 03-JAN-2003;
COMMENT AJINOMOTO CO INC,HIROAKI KISAKA,TAKAO KIDA
OS Artificial Sequence
PN WO 0300041-A/19
PD 03-JAN-2003
PF 14-JUN-2001 WO 2001JP005077
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PC AOH5/00,CL2N15/53,CL2N15/83
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CC transit peptide-GDH coding sequence
CC key Location/Qualifiers
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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 3 GCAGATGGCTTCTCAAT 20

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LOCUS Method for making transgenic plants having improved amino acid
DEFINITION composition.
ACCESSION BD189534
VERSION BD189534.1 GI:22558806
KEYWORDS JP 2001238556-A/13.
SOURCE synthetic construct
ORGANISM 1 (bases 1 to 30)
REFERENCE Kisaka,H. and Kida,T.
AUTHORS Method for making transgenic plants having improved amino acid
TITLE composition
JOURNAL Patent: JP 2001238556-A 13 04-SEP-2001;
COMMENT AJINOMOTO CO INC
OS Artificial Sequence
PN JP 2001238556-A/13
PD 04-SEP-2001
PF 18-DEC-2000 JP 20000404322

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PI HIROAKI KISAKA,TAKAO KIDA  
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CC sequence for chloroplast transit peptide

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1..30

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LOCUS

DEFINITION

Method for making transgenic plants having improved amino acid

composition.

ACCESSION

BD017636

VERSION

BD017636.1 GI:22558812

KEYWORDS

JP 2001238556-A/19.

SOURCE

synthetic construct

ORGANISM

artificial sequences.

REFERENCE

1 (bases 1 to 30)

AUTHORS

Kisaka,H. and Kida,T.

TITLE

Method for making transgenic plants having improved amino acid

composition

JOURNAL

Patent: JP 2001238556-A 19 04-SEP-2001;

AJINOMOTO CO INC

COMMENT

OS Artificial Sequence

PN JP 2001238556-A/19

PD 04-SEP-2001

PF 18-DEC-2000 JP 2000404322

PI HIROAKI KISAKA,TAKAO KIDA

PC A01H5/00,C12N5/10,C12N9/06,C12N15/09,C12N5/00,C12N15/00 CC

Description of Artificial Sequence:PCR primer for producing CC

chloroplast

CC transit peptide-GDH coding sequence

FT Key Location/Qualifiers

FT source 1..30

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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 3 GCAGATGGCTTCCTCAAT 20

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Total number of hits satisfying chosen parameters: 3992700

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Post-processing: Minimum Match 0%  
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Listing first 1000 summaries

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10: geneseqn2003cs:\*  
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12: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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C 27	13.8	53.1	32	10	ADF42313 Arabidops
C 28	13.8	53.1	50	6	ABZ01654 Human leu
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C 30	13.6	52.3	34	2	AAV74227 Cpg-N mot
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C 108	12.8	49.2	38	8	ACA94739	ACA94739	Class B T
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12	ADMG64393	Hbv enzy
12	ADMG64392	Hbv enzy
12	ADMG64391	Hbv enzy
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12	ADMG64389	Hbv enzy
12	ADMG64388	Hbv enzy
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12	ADMG64319	Hbv enzy
12	ADMG64318	Hbv enzy
12	ADMG64317	Hbv enzy
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12	ADMG64301	Hbv enzy
12	ADMG64300	Hbv enzy
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12	ADMG64298	Hbv enzy
12	ADMG64297	Hbv enzy
12	ADMG64296	Hbv enzy
12	ADMG64295	Hbv en

241	12	46.2	20	12	ADH77273	Adh77273 Human PAZ
C 242	12	46.2	21	2	AQ071151	AQ071151 Merlin ex
243	12	46.2	21	2	AD001317	Ad001317 Selectabl
244	12	46.2	21	3	AA014510	AA014510 Primer us
245	12	46.2	21	4	AD018412	Ad018412 Genetidin
246	12	46.2	21	4	AAI66711	AAI66711 A. gossyp
247	12	46.2	21	4	ABK16409	ABK16409 Ashbya go
248	12	46.2	21	9	ACF05776	ACF05776 Genetidin
249	12	46.2	21	10	ABQ80476	ABQ80476 P. infest
250	12	46.2	21	10	ADF75123	ADF75123 PCR prime
251	12	46.2	24	6	ABQ06320	ABQ06320 Oligonuc1
252	12	46.2	24	6	ABQ06361	ABQ06361 Oligonuc1
253	12	46.2	24	6	ABQ01200	ABQ01200 Oligonuc1
254	12	46.2	25	6	ABQ12951	ABQ12951 Oligonuc1
C 255	12	46.2	25	8	AD001832	Ad001832 Human MDZ
C 256	12	46.2	25	8	AD001837	Ad001837 Human MDZ
C 257	12	46.2	25	8	AD001835	Ad001835 Human MDZ
C 258	12	46.2	25	8	AD001836	Ad001836 Human MDZ
C 259	12	46.2	25	8	AD001833	Ad001833 Human MDZ
C 260	12	46.2	25	8	AD001834	Ad001834 Human MDZ
261	12	46.2	25	9	ACI85237	ACI85237 Human mic
262	12	46.2	25	9	ACI79051	ACI79051 Human mic
263	12	46.2	25	9	ACI13107	ACI13107 Human mic
264	12	46.2	25	9	ACK13561	ACK13561 Human mic
265	12	46.2	25	9	ACK30128	ACK30128 Human mic
266	12	46.2	25	9	ACK30764	ACK30764 Human mic
C 267	12	46.2	26	12	ADM82860	ADM82860 Human dip
268	12	46.2	27	6	ABK15329	ABK15329 PCR prime
269	12	46.2	28	2	AA078219	AA078219 Melon MEE
C 270	12	46.2	30	3	AA091690	AA091690 Saccharom
C 271	12	46.2	30	10	ADC15686	ADC15686 E. intest
C 272	12	46.2	30	11	ADO20556	ADO20556 Hansenula
C 273	12	46.2	30	12	ADN43250	ADN43250 Brassica
C 274	12	46.2	31	2	AA039096	AA039096 Human gen
275	12	46.2	32	3	AA094038	AA094038 Stereose
276	12	46.2	33	8	ABZ23954	ABZ23954 A. radiob
C 277	12	46.2	33	12	ADO24653	ADO24653 Primer pK
C 278	12	46.2	34	12	ADG31153	ADG31153 PCR prime
C 279	12	46.2	35	3	AA072692	AA072692 PCR prime
C 280	12	46.2	35	8	ACC45320	ACC45320 Coryneb
C 281	12	46.2	36	2	AA092225	AA092225 MonKey/hu
282	12	46.2	36	2	AA0762897	AA0762897 Human or
283	12	46.2	36	2	AA095150	AA095150 Human/mon
284	12	46.2	36	2	AA095678	AA095678 Human/mon
285	12	46.2	36	2	AA023788	AA023788 Primer fo
286	12	46.2	36	2	AA031410	AA031410 Human or
287	12	46.2	36	8	ABX76665	ABX76665 Immunoglo
288	12	46.2	36	10	ADE31620	ADE31620 Immunoglo
C 289	12	46.2	38	2	AA074239	AA074239 Plasmid V
C 290	12	46.2	38	2	AA0701161	AA0701161 Kanamycin
C 291	12	46.2	38	2	AA015482	AA015482 5' primer
292	12	46.2	38	2	AA040765	AA040765 Primer to
C 293	12	46.2	38	2	AA029803	AA029803 Primer #1
C 294	12	46.2	38	2	AA085547	AA085547 VIR vecto
C 295	12	46.2	38	2	AA021774	AA021774 VIR vacci
C 296	12	46.2	38	2	AA058410	AA058410 Primer fo
C 297	12	46.2	38	2	AA031783	AA031783 Nucleotid
C 298	12	46.2	38	3	AA046125	AA046125 PCR prime
C 299	12	46.2	38	4	AA009619	AA009619 Vaccine v
C 300	12	46.2	38	4	AA009433	AA009433 Vector VI
C 301	12	46.2	38	12	AD058168	AD058168 Human inf
302	12	46.2	39	9	AA055522	AA055522 LINE retr
303	12	46.2	41	4	AA081873	AA081873 HBV gene
304	12	46.2	41	6	ABZ46317	ABZ46317 Human ald
305	12	46.2	41	6	ABZ48829	ABZ48829 Human ald
306	12	46.2	41	12	ADP07504	ADP07504 PCR prime
C 307	12	46.2	42	6	ABT12767	ABT12767 Thermomyc
C 308	12	46.2	42	6	ABT12768	ABT12768 Thermomyc
C 309	12	46.2	43	2	AA039128	AA039128 Reporter
310	12	46.2	43	2	AA097605	AA097605 Shigella
C 311	12	46.2	46	6	ABK10302	ABK10302 Directed
C 312	12	46.2	48	6	AA020445	AA020445 Prion pro
C 313	12	46.2	48	6	AA020440	AA020440 Prion pro

C 314	12	46.2	48	10	ADB48220	ADB48220 Primer of
C 315	12	46.2	50	6	ABZ02849	ABZ02849 Human leu
C 316	12	46.2	50	6	ABZ05415	ABZ05415 Human leu
317	12	46.2	50	8	ACA15212	ACA15212 Prokaryot
318	11.8	45.4	15	12	ADM53673	ADM53673 Nucleic a
319	11.8	45.4	17	8	ACD55947	ACD55947 HBV amber
320	11.8	45.4	17	8	ACD54912	ACD54912 HBV DNaz
321	11.8	45.4	17	10	ADF62130	ADF62130 Human PCC
322	11.8	45.4	17	12	ADM60370	ADM60370 Hepatitis
323	11.8	45.4	17	12	ADM60039	ADM60039 Hepatitis
C 324	11.8	45.4	18	4	AA016132	AA016132 Black pan
C 325	11.8	45.4	18	10	ADB54040	ADB54040 Oligonuc1
C 326	11.8	45.4	19	4	AA029775	AA029775 Presenili
327	11.8	45.4	20	3	AA023818	AA023818 Human amy
328	11.8	45.4	20	10	ADG33689	ADG33689 Human PCR
C 329	11.8	45.4	20	12	ADH18431	ADH18431 2'-MOE ga
C 330	11.8	45.4	20	12	ADO32972	ADO32972 Antisense
331	11.8	45.4	22	3	AA088417	AA088417 Sequencin
332	11.8	45.4	22	4	AA012578	AA012578 Primer SR
333	11.8	45.4	22	4	AA042476	AA042476 Schizophr
334	11.8	45.4	22	4	AA043072	AA043072 EST AAS26
335	11.8	45.4	22	5	AA023819	AA023819 Schizophr
336	11.8	45.4	22	12	ADO79053	ADO79053 Schizophr
337	11.8	45.4	22	12	ADO79045	ADO79045 Schizophr
C 338	11.8	45.4	23	12	ADK97986	ADK97986 Primer Of
C 339	11.8	45.4	24	3	AA061467	AA061467 PCR prime
340	11.8	45.4	24	6	ABA98776	ABA98776 Neuroplli
C 341	11.8	45.4	24	6	AA040792	AA040792 Magnaport
C 342	11.8	45.4	25	2	AA053692	AA053692 Nucleotid
C 343	11.8	45.4	25	2	AA099464	AA099464 Complemen
344	11.8	45.4	25	2	AA0169860	AA0169860 Transcrip
345	11.8	45.4	25	9	ACI70511	ACI70511 Human mic
346	11.8	45.4	25	9	ACI54752	ACI54752 Human mic
347	11.8	45.4	25	9	ACI27369	ACI27369 Human mic
C 348	11.8	45.4	25	9	ACI199063	ACI199063 Human mic
C 349	11.8	45.4	25	9	ACK04428	ACK04428 Human mic
C 350	11.8	45.4	25	9	ACK02646	ACK02646 Human mic
351	11.8	45.4	25	9	ACK17527	ACK17527 Human mic
352	11.8	45.4	25	9	ACI70510	ACI70510 Human mic
C 353	11.8	45.4	25	9	ACI80465	ACI80465 Human mic
C 354	11.8	45.4	25	9	ACK26653	ACK26653 Human mic
C 355	11.8	45.4	25	9	ACI07850	ACI07850 Human mic
C 356	11.8	45.4	25	9	ACI61953	ACI61953 Human mic
C 357	11.8	45.4	25	9	ACI67194	ACI67194 Human mic
358	11.8	45.4	25	9	ACI62614	ACI62614 Human mic
C 359	11.8	45.4	25	9	ACI22409	ACI22409 Human mic
C 360	11.8	45.4	25	9	ACI76474	ACI76474 Human mic
361	11.8	45.4	25	9	ACI54753	ACI54753 Human mic
C 362	11.8	45.4	25	9	ACI61952	ACI61952 Human mic
C 363	11.8	45.4	25	9	ACH58006	ACH58006 DNA targe
C 364	11.8	45.4	25	9	ACH59181	ACH59181 DNA targe
C 365	11.8	45.4	25	10	ACF58012	ACF58012 Mouse rpf
366	11.8	45.4	25	10	ADF62881	ADF62881 Human PCC
C 367	11.8	45.4	25	12	ADL71224	ADL71224 PCR prime
368	11.8	45.4	27	4	AAF84932	AAF84932 PCR prime
369	11.8	45.4	27	6	AA038888	AA038888 Alfalfa n
370	11.8	45.4	28	2	AA090648	AA090648 Primer De
C 371	11.8	45.4	28	6	AA040714	AA040714 Rat VEGF
C 372	11.8	45.4	29	8	AA047236	AA047236 RACE PCR
C 373	11.8	45.4	30	2	AA076778	AA076778 Mycobacte
C 374	11.8	45.4	30	6	AB058865	AB058865 Helicobac
C 375	11.8	45.4	31	2	AA062542	AA062542 Granule b
C 376	11.8	45.4	31	6	AB041150	AB041150 Plasmid p
377	11.8	45.4	32	3	AA072463	AA072463 Soybean i
378	11.8	45.4	32	8	AA051365	AA051365 Soybean i
C 379	11.8	45.4	32	10	ADC85151	ADC85151 Ion trans
C 380	11.8	45.4	33	4	AA0168366	AA0168366 Human imm
381	11.8	45.4	33	4	AA091257	AA091257 Human inf
382	11.8	45.4	33	12	ADM93361	ADM93361 Chimeric
C 383	11.8	45.4	34	2	AA062792	AA062792 PCR prime
C 384	11.8	45.4	34	2	AA081643	AA081643 Oligonuc1
C 385	11.8	45.4	35	2	AA044106	AA044106 Human G-P
C 386	11.8	45.4	36	2	AA0606085	AA0606085 Junction

36	2	Aat316574	Thermococ	460	11.6	44.6	20	2	AAV62485	MAP kinas
36	2	Aaz11699	H. influe	c 461	11.6	44.6	20	2	Aax38391	E. coli K
36	2	Aat211699	H. influe	c 461	11.6	44.6	20	2	Aax38391	E. coli K
36	6	Ab188047	Aquifex a	c 462	11.6	44.6	20	2	Aax3574	PCR prime
36	6	Ab188047	Aquifex a	c 462	11.6	44.6	20	4	Aah78289	Nucleotid
36	6	Aal14134	DNA regio	c 463	11.6	44.6	20	4	Aah78289	Nucleotid
37	3	Aaa96063	Oligonucl	c 464	11.6	44.6	20	6	Ab194421	Capture o
37	3	Aaa96063	Oligonucl	c 464	11.6	44.6	20	6	Ab194421	Capture o
37	3	Ad13055	Human ubi	c 465	11.6	44.6	20	12	Adh44532	Human ext
37	12	Adj46078	Primer fo	c 466	11.6	44.6	20	12	Adh44509	Extracell
38	2	Aat14566	Recombina	c 467	11.6	44.6	20	12	Adj32675	Human ERK
38	2	Aat14566	Recombina	c 467	11.6	44.6	20	12	Adj32675	Human ERK
38	2	Aav62791	PCR prime	c 468	11.6	44.6	20	12	Adj32652	Human ERK
38	2	Aav62791	PCR prime	c 468	11.6	44.6	20	12	Adj32652	Human ERK
38	2	Aav81642	Oligonucl	c 469	11.6	44.6	20	12	Ado85065	Human adi
39	4	Aaf62140	Primer fo	c 470	11.6	44.6	20	12	Ado85100	Human adi
39	10	Adc38577	Transloca	c 471	11.6	44.6	21	10	Adc42607	Human PAN
40	2	Aax08534	Oligonucl	c 472	11.6	44.6	23	4	Adc42607	Human PAN
40	2	Aax08534	Oligonucl	c 472	11.6	44.6	23	4	Adc42607	Human PAN
40	2	Aax08534	Oligonucl	c 473	11.6	44.6	23	6	Aab10800	rabbit ha
40	2	Aax08534	Oligonucl	c 473	11.6	44.6	23	6	Aab10800	rabbit ha
40	6	Aah22855	Nucleotid	c 474	11.6	44.6	24	6	Aaq05781	pol prime
40	6	Aah22855	Nucleotid	c 474	11.6	44.6	24	6	Aaq05781	pol prime
40	6	Ab188042	Aquifex a	c 475	11.6	44.6	24	6	Abi85412	Capture o
40	6	Ab188042	Aquifex a	c 475	11.6	44.6	24	6	Abi85412	Capture o
40	6	Abz44032	Human NDU	c 476	11.6	44.6	24	6	Abi85413	Capture o
40	6	Abz44032	Human NDU	c 476	11.6	44.6	24	6	Abi85413	Capture o
40	6	Abz44032	Human NDU	c 477	11.6	44.6	24	8	Abi85413	Capture o
40	6	Abz44032	Human NDU	c 477	11.6	44.6	24	8	Abi85413	Capture o
40	6	Abz44032	Human NDU	c 478	11.6	44.6	24	8	Abi85413	Capture o
40	6	Abz44032	Human NDU	c 478	11.6	44.6	24	8	Abi85413	Capture o
40	6	Abz44032	Human NDU	c 479	11.6	44.6	24	12	Adn02052	Escherich
40	6	Abz44032	Human NDU	c 479	11.6	44.6	24	12	Adn02052	Escherich
40	6	Abz44032	Human NDU	c 480	11.6	44.6	25	3	Aaa68255	Bacteriop
40	6	Abz44032	Human NDU	c 480	11.6	44.6	25	3	Aaa68255	Bacteriop
40	6	Abz44032	Human NDU	c 481	11.6	44.6	25	3	Aaa68255	Bacteriop
40	6	Abz44032	Human NDU	c 481	11.6	44.6	25	3	Aaa68255	Bacteriop
40	6	Abz44032	Human NDU	c 482	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 482	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 483	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 483	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 484	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 484	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 485	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 485	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 486	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 486	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 487	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 487	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 488	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 488	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 489	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 489	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 490	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 490	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 491	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 491	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 492	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 492	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 493	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 493	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 494	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 494	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 495	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 495	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 496	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 496	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 497	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 497	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 498	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 498	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 499	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 499	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 500	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 500	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 501	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 501	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 502	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 502	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 503	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 503	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 504	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 504	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 505	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 505	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 506	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 506	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 507	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 507	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 508	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 508	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 509	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 509	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 510	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 510	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 511	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 511	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 512	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 512	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 513	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 513	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 514	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 514	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 515	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 515	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 516	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 516	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 517	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 517	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 518	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 518	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 519	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 519	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 520	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 520	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 521	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 521	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 522	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 522	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 523	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 523	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 524	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 524	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 525	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 525	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 526	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 526	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 527	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 527	11.6	44.6	25	8	Aaa68335	Bacteriop
40	6	Abz44032	Human NDU	c 528	11.6	44.6	25	8	Aaa68335	Bacteriop

533	11.6	44.6	35	3	AAX290495	Aax290495 Sequence	c 606	11.4	43.8	25	9	ACI98089	AcI98089 Human mic
534	11.6	44.6	35	8	ABX15633	Abx15633 Tnos PCR	c 607	11.4	43.8	25	9	ACI49917	AcI49917 Human mic
535	11.6	44.6	36	6	ABX70346	Abx70346 Novel Hel	c 608	11.4	43.8	25	9	ACI30979	AcI30979 Human mic
536	11.6	44.6	37	3	AAV66669	Aav66669 Human Fas	c 609	11.4	43.8	25	9	ACI72528	AcI72528 Human mic
537	11.6	44.6	37	3	AAV78368	Aav78368 Fas antiq	c 610	11.4	43.8	25	9	ACI52935	AcI52935 Human mic
538	11.6	44.6	37	6	ABK59397	Abk59397 Human CLC	c 611	11.4	43.8	25	9	ACK28857	AcK28857 Human mic
539	11.6	44.6	37	6	ACN19291	Acn19291 WNV Zinzv	c 612	11.4	43.8	25	9	ACK07439	AcK07439 Human mic
540	11.6	44.6	37	6	ACN19753	Acn19753 WNV Zinzv	c 613	11.4	43.8	25	9	ACI39623	AcI39623 Human mic
541	11.6	44.6	37	6	ACN19000	Acn19000 WNV Zinzv	c 614	11.4	43.8	25	9	ACI98088	AcI98088 Human mic
542	11.6	44.6	37	6	ACN19455	Acn19455 WNV Zinzv	c 615	11.4	43.8	25	9	ACI49161	AcI49161 Human mic
543	11.6	44.6	37	6	ACN19555	Acn19555 WNV Zinzv	c 616	11.4	43.8	25	9	ACI85897	AcI85897 Human mic
544	11.6	44.6	37	6	ACN31203	Acn31203 WNV minus	c 617	11.4	43.8	25	9	ACI35967	AcI35967 Human mic
545	11.6	44.6	37	8	ACA08036	AcA08036 Necrosis	c 618	11.4	43.8	25	9	ACI97203	AcI97203 Human mic
546	11.6	44.6	39	2	AAV30724	Aav30724 Telomeras	c 619	11.4	43.8	25	9	ACI86858	AcI86858 Human mic
547	11.6	44.6	39	2	AAV30728	Aav30728 Telomeras	c 620	11.4	43.8	25	9	ACK19084	AcK19084 Human mic
548	11.6	44.6	39	2	AAV30722	Aav30722 Telomeras	c 621	11.4	43.8	25	9	ACK31020	AcK31020 Human mic
549	11.6	44.6	39	2	AAV30726	Aav30726 Telomeras	c 622	11.4	43.8	25	9	ACK112246	AcK112246 Human mic
550	11.6	44.6	39	6	ABS61143	AbS61143 Human pol	c 623	11.4	43.8	25	9	ACI93626	AcI93626 Human mic
551	11.6	44.6	39	6	ABS61155	AbS61155 Human pol	c 624	11.4	43.8	25	9	ACK13413	AcK13413 Human mic
552	11.6	44.6	39	10	ADG78919	Adg78919 Schizophr	c 625	11.4	43.8	25	9	ACI50282	AcI50282 Human mic
553	11.6	44.6	39	12	ADI82353	Adi82353 Amorpho-4	c 626	11.4	43.8	25	9	ACI50666	AcI50666 Human mic
554	11.6	44.6	40	4	ACA91706	AcA91706 Mouse fat	c 627	11.4	43.8	25	9	ACK26538	AcK26538 Human mic
555	11.6	44.6	41	2	AAX89736	Aax89736 CLQ502 SY	c 628	11.4	43.8	25	9	ACI27383	AcI27383 Human mic
556	11.6	44.6	41	6	ABA99841	AbA99841 Human TGF	c 629	11.4	43.8	25	9	ACI66176	AcI66176 Human mic
557	11.6	44.6	42	3	AAZ47004	Aaz47004 Primer TA	c 630	11.4	43.8	25	9	ACI26227	AcI26227 Human mic
558	11.6	44.6	43	12	ADP97045	Adp97045 C. albica	c 631	11.4	43.8	25	9	ACI90735	AcI90735 Human mic
559	11.6	44.6	44	2	AAT01107	Aat01107 V1J-SIV M	c 632	11.4	43.8	25	9	ACK23318	AcK23318 Human mic
560	11.6	44.6	44	2	AAQ85223	Aaq85223 Ureaplas	c 633	11.4	43.8	25	9	ACI77433	AcI77433 Human mic
561	11.6	44.6	44	2	AAQ85171	Aaq85171 Ureaplas	c 634	11.4	43.8	25	9	ACI10182	AcI10182 Human mic
562	11.6	44.6	44	2	AAQ85225	Aaq85225 Ureaplas	c 635	11.4	43.8	25	9	ACI38924	AcI38924 Human mic
563	11.6	44.6	44	2	AAQ85224	Aaq85224 Ureaplas	c 636	11.4	43.8	25	9	ACK15053	AcK15053 Human mic
564	11.6	44.6	46	2	AAQ69267	Aaq69267 Human ara	c 637	11.4	43.8	25	9	ACH63928	AcH63928 DNA targe
565	11.6	44.6	46	2	AAT63729	Aat63729 Human ara	c 638	11.4	43.8	25	9	ACC84715	AcC84715 Interleuk
566	11.6	44.6	46	2	AAT79510	Aat79510 Primer St	c 639	11.4	43.8	25	12	ADP15866	Adp15866 Renal cel
567	11.6	44.6	46	2	AAX17017	Aax17017 Test sequ	c 640	11.4	43.8	25	12	ADP15284	Adp15284 Renal cel
568	11.6	44.6	46	6	ABK82508	AbK82508 DNA bindi	c 641	11.4	43.8	26	5	AAF17327	Aaf17327 Informati
569	11.6	44.6	46	10	ADL07701	Adl07701 Group II	c 642	11.4	43.8	26	5	AAH68490	Aah68490 C glutami
570	11.6	44.6	46	10	ADL07699	Adl07699 Group II	c 643	11.4	43.8	26	6	ABK99870	AbK99870 Babesia c
571	11.6	44.6	46	12	ADE80047	Ade80047 Duplex ol	c 644	11.4	43.8	27	2	AAV94096	Aav94096 Human II-
572	11.6	44.6	47	3	AZ67096	Aaz67096 Human map	c 645	11.4	43.8	27	3	AAV58532	Aav58532 Human PRO
573	11.6	44.6	47	12	ADG83281	Adg83281 Primer sp	c 646	11.4	43.8	28	2	AAV81576	Aav81576 Oligonuel
574	11.6	44.6	50	2	AAK88053	Aak88053 Ku protei	c 647	11.4	43.8	28	2	AAV81575	Aav81575 Oligonuel
575	11.6	44.6	50	4	AAAL30002	Aal30002 Human SNP	c 648	11.4	43.8	28	3	AAZ88942	Aaz88942 Human bol
576	11.6	44.6	50	6	ABZ17038	Abz17038 Arabidops	c 649	11.4	43.8	28	3	AAF86148	Aaf86148 RACE prim
577	11.6	44.6	50	6	ABZ06478	Abz06478 Human leu	c 650	11.4	43.8	28	4	AAH47085	Aah47085 Human MUC
578	11.6	44.6	50	6	ABZ06931	Abz06931 Human leu	c 651	11.4	43.8	29	4	AAAD03038	Aad03038 ROX from
579	11.6	44.6	50	6	ABZ07204	Abz07204 Human leu	c 652	11.4	43.8	29	4	AAH47085	Aah47085 ROX legu
580	11.6	44.6	50	6	ABZ06541	Abz06541 Human leu	c 653	11.4	43.8	30	3	AAH47085	Aah47085 Barley th
581	11.6	44.6	50	6	ABZ06868	Abz06868 Human leu	c 654	11.4	43.8	30	3	AAH47085	Aah47085 Barley NA
582	11.6	44.6	50	12	ADQ94817	Adq94817 Generic b	c 655	11.4	43.8	30	4	AAH48460	Aah48460 Bacterial
583	11.6	44.6	50	12	ADQ94816	Adq94816 Generic b	c 656	11.4	43.8	30	4	AAH45706	Aah45706 Human ace
584	11.4	43.8	17	10	ADF62125	Adf62125 Human PCC	c 657	11.4	43.8	30	5	AAAS00601	Aas00601 Human MUC
585	11.4	43.8	18	4	AAF26868	Aaf26868 SR alpha	c 658	11.4	43.8	30	6	ABK69882	AbK69882 Novel Hel
586	11.4	43.8	20	2	AAK94016	Aak94016 PCR prime	c 659	11.4	43.8	30	6	ABK53800	AbK53800 DMS-accept
587	11.4	43.8	20	4	AAF26867	Aaf26867 SR alpha	c 660	11.4	43.8	31	2	AAQ99845	Aaq99845 Haematopo
588	11.4	43.8	20	8	ABX94761	Abx94761 Human gam	c 661	11.4	43.8	31	2	AAQ26721	Aaq26721 PCR prime
589	11.4	43.8	20	10	ADC26014	Adc26014 Sense PCR	c 662	11.4	43.8	31	3	AAZ37461	Aaz37461 PCR prime
590	11.4	43.8	20	12	ADI32597	Adi32597 Ovine GDF	c 663	11.4	43.8	31	3	AAZ13344	Aaz13344 PCR prime
591	11.4	43.8	21	2	AAQ41247	Aaq41247 env/U3 pr	c 664	11.4	43.8	31	4	AAAD10910	Aad10910 B. derami
592	11.4	43.8	21	3	AAQ60710	Aaq60710 Rice cyto	c 665	11.4	43.8	31	4	AAF86142	Aaf86142 Degenerat
593	11.4	43.8	21	3	ADE80904	AdE80904 Streptoco	c 666	11.4	43.8	31	6	AAAD27923	Aad27923 Human hae
594	11.4	43.8	21	10	ADD31208	AdD31208 RT-PCR pr	c 667	11.4	43.8	31	6	ACN22068	AcN22068 WNV DNazv
595	11.4	43.8	21	10	ACF79836	Adf79836 siRNA to	c 668	11.4	43.8	31	8	ABX16162	AbX16162 Human hae
596	11.4	43.8	23	2	AAT01519	Aat01519 Human her	c 669	11.4	43.8	32	2	AAAT75945	Aat75945 DEN-2 clo
597	11.4	43.8	23	2	AAV17059	Aav17059 Wound ind	c 670	11.4	43.8	32	2	AAAT75946	Aat75946 DEN-2 clo
598	11.4	43.8	23	2	AAV12236	Aav12236 Varicella	c 671	11.4	43.8	32	6	ABSS52870	AbS52870 Plasmid P
599	11.4	43.8	23	2	AAK91454	Aak91454 T. gondii	c 672	11.4	43.8	32	12	ADI38951	Adi38951 Glucose-6
600	11.4	43.8	23	2	AAK58942	Aak58942 Tomato TI	c 673	11.4	43.8	33	2	AAQ29504	Aaq29504 neoI3-567
601	11.4	43.8	23	4	AAK42777	Aak42777 T. gondii	c 674	11.4	43.8	33	2	AAQ46748	Aaq46748 HIV captu
602	11.4	43.8	23	6	ABA93038	AbA93038 Gancorma	c 675	11.4	43.8	33	2	AAQ89524	Aaq89524 Human imm
603	11.4	43.8	23	10	ADG17384	Adg17384 T. gondii	c 676	11.4	43.8	33	2	AAAT63540	Aat63540 Killer to
604	11.4	43.8	25	9	ACI95953	AcI95953 HLA HLA-B	c 677	11.4	43.8	33	2	AAAT63542	Aat63542 Killer to
605	11.4	43.8	25	9	ACI60782	AcI60782 Human mic	c 678	11.4	43.8	33	6	ABA04379	AbA04379 AtERF3 PC

679	11.4	43.8	34	6	ABL88053	Thermotog	C 752	11.2	43.1	20	10	AAL55537	Aal55537 qSH-1 gen
680	11.4	43.8	34	6	AAS21189	Transmiss	C 753	11.2	43.1	20	12	ADH18782	Adh18782 Human apo
681	11.4	43.8	34	12	ADH10208	npt gene	754	11.2	43.1	20	12	ADH18461	Adh18461 2'-MOS ga
C 682	11.4	43.8	35	2	AAT86112	Human sol	755	11.2	43.1	20	12	ADO33002	Ado33002 Antisense
C 683	11.4	43.8	35	2	AAT89119	Synthetic	C 756	11.2	43.1	20	12	ADO33323	Ado33323 Human apo
C 684	11.4	43.8	35	2	AAT99119	PCR prime	C 757	11.2	43.1	21	3	AAAI4887	Aaai4887 PCR prime
C 685	11.4	43.8	35	2	AAZ11244	Human sol	C 758	11.2	43.1	21	6	AAD38205	Aad38205 Human PAP
C 686	11.4	43.8	35	2	AAZ11244	TGMV-a mi	C 759	11.2	43.1	21	8	AAL59895	Aal59895 Forward P
C 687	11.4	43.8	35	6	ABL88050	Thermotog	C 760	11.2	43.1	22	10	ACC59547	Acc59547 Chlamydia
C 688	11.4	43.8	35	12	ADL65354	Comamonas	761	11.2	43.1	22	12	ADN97998	Adn97998 Human pho
C 689	11.4	43.8	36	12	ACG64551	Herpesvir	762	11.2	43.1	22	12	ADN98000	Adn98000 Human pho
C 690	11.4	43.8	37	2	AAT75490	Primer E	C 763	11.2	43.1	23	12	ADO10863	Ado10863 Single mu
C 691	11.4	43.8	37	2	AAT75490	B steartot	764	11.2	43.1	24	6	ABQ03283	Abq03283 Oligonucle
C 692	11.4	43.8	37	2	AAT75490	Reverse p	765	11.2	43.1	24	8	ACQ03283	Acq03283 Chloramph
C 693	11.4	43.8	38	4	AAT75490	Human Chk	766	11.2	43.1	24	10	ADK48903	Adk48903 F. hepari
C 694	11.4	43.8	38	4	AAT75490	Intracell	767	11.2	43.1	24	12	ADK48903	Adk48903 Sequence
C 695	11.4	43.8	39	2	AAT75490	3'-primer	768	11.2	43.1	25	2	AAQ67981	Aaq67981 Human Pho
C 696	11.4	43.8	40	2	AAZ46174	PCR prime	769	11.2	43.1	25	6	ABT03743	Abt03743 Candida a
C 697	11.4	43.8	40	2	AAZ46174	Animal fe	770	11.2	43.1	25	6	ABT03743	Abt03743 Human mic
C 698	11.4	43.8	40	12	ADK98514	Antisense	C 771	11.2	43.1	25	6	ABT03743	Abt03743 Human mic
C 699	11.4	43.8	40	12	ADK98514	Brassica	C 772	11.2	43.1	25	6	ABT03743	Abt03743 Human mic
C 700	11.4	43.8	41	2	AAV50566	Human map	C 773	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 701	11.4	43.8	41	6	ABZ48053	Human ATP	774	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 702	11.4	43.8	41	6	ABZ48053	Human pur	775	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 703	11.4	43.8	42	11	ADU95848	Rotavirus	776	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 704	11.4	43.8	42	11	ADU95848	PCR prime	777	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 705	11.4	43.8	42	11	ADU95848	Novel rec	778	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 706	11.4	43.8	43	2	AAV12249	Varicella	C 779	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 707	11.4	43.8	43	2	AAV12249	Novel rec	C 780	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 708	11.4	43.8	44	6	AAZ22228	Human ret	781	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 709	11.4	43.8	44	6	AAZ22228	Novel rec	782	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 710	11.4	43.8	45	12	ADH73687	Novel rec	C 783	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 711	11.4	43.8	45	12	ADH73687	Novel rec	784	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 712	11.4	43.8	46	10	ACA92292	PCR prime	C 785	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 713	11.4	43.8	46	12	ADN43281	Nucleotid	786	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 714	11.4	43.8	47	3	AAZ66809	Human map	787	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 715	11.4	43.8	47	3	AAZ66809	Human map	788	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 716	11.4	43.8	47	4	AAZ66809	Human map	C 789	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 717	11.4	43.8	47	4	AAZ66809	Human map	790	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 718	11.4	43.8	47	5	AAZ66809	Human map	791	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 719	11.4	43.8	49	3	AAZ66809	Human map	C 792	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 720	11.4	43.8	50	3	AAZ66809	Human map	793	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 721	11.4	43.8	50	3	AAZ66809	Human map	C 794	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 722	11.4	43.8	50	6	AAZ66809	Human map	795	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 723	11.4	43.8	50	6	AAZ66809	Human map	796	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 724	11.4	43.8	50	6	AAZ66809	Human map	797	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 725	11.4	43.8	50	6	AAZ66809	Human map	C 798	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 726	11.4	43.8	50	6	AAZ66809	Human map	C 799	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 727	11.4	43.8	50	6	AAZ66809	Human map	800	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 728	11.4	43.8	50	6	AAZ66809	Human map	801	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 729	11.4	43.8	50	6	AAZ66809	Human map	C 802	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 730	11.4	43.8	50	6	AAZ66809	Human map	803	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 731	11.4	43.8	50	6	AAZ66809	Human map	C 804	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 732	11.4	43.8	50	6	AAZ66809	Human map	805	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 733	11.4	43.8	50	12	ADP12673	50-mer ol	C 806	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 734	11.4	43.8	17	8	ADB00334	Human MD2	C 807	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 735	11.4	43.8	17	8	ADB00334	Human MD2	C 808	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 736	11.4	43.8	18	3	AAZ47716	Human CD4	C 809	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 737	11.4	43.8	18	3	AAZ47716	Human CD4	C 810	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 738	11.4	43.8	19	3	AAZ47716	Human CD4	811	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 739	11.4	43.8	19	3	AAZ47716	Human CD4	812	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 740	11.4	43.8	19	5	AAZ47716	Human CD4	C 813	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 741	11.4	43.8	19	5	AAZ47716	Human CD4	814	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 742	11.4	43.8	20	2	AAZ47716	Human CD4	C 815	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 743	11.4	43.8	20	2	AAZ47716	Human CD4	C 816	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 744	11.4	43.8	20	2	AAZ47716	Human CD4	C 817	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 745	11.4	43.8	20	2	AAZ47716	Human CD4	C 818	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 746	11.4	43.8	20	2	AAZ47716	Human CD4	C 819	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 747	11.4	43.8	20	3	AAZ47716	Human CD4	C 820	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 748	11.4	43.8	20	3	AAZ47716	Human CD4	C 821	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 749	11.4	43.8	20	3	AAZ47716	Human CD4	822	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 750	11.4	43.8	20	8	AAZ47716	Human CD4	823	11.2	43.1	25	9	ACK16719	Ack16719 Human mic
C 751	11.4	43.8	20	10	ADD20233	Oreochrom	824	11.2	43.1	25	9	ACK16719	Ack16719 Human mic

825	11.2	43.1	28	2	AAT97359	Construct	Aat97359	11.2	43.1	38	2	AAT48478	Class B T
826	11.2	43.1	28	2	AAT220499	PCR prime	Aax20499	11.2	43.1	38	2	AAV60086	Class D t
827	11.2	43.1	28	2	AAV68127	Oligonucle	Aav68127	11.2	43.1	38	2	AAV60087	Class E t
828	11.2	43.1	28	2	AAV99477	PCR prime	Aav99477	11.2	43.1	38	2	Aaz06714	Primer fo
829	11.2	43.1	28	2	AAT220489	PCR prime	Aaz20489	11.2	43.1	38	2	Aax57632	Mutagenic
830	11.2	43.1	28	3	AZ555040	Neisseria	Aaz55040	11.2	43.1	38	2	AAX60053	Class E t
831	11.2	43.1	28	3	AAK63096	Antisense	AAK63096	11.2	43.1	38	2	AAX60052	Class D t
832	11.2	43.1	28	3	AAK49268	Antisense	AAK49268	11.2	43.1	38	2	AAX15361	Mutagenic
833	11.2	43.1	28	3	AAK49268	CDK4 gene	AAK49268	11.2	43.1	38	2	AAX15361	Mutagenic
834	11.2	43.1	28	3	AAK49268	Nucleotid	Aaf67615	11.2	43.1	38	3	AAZ56134	Class E t
835	11.2	43.1	28	5	AAK49268	Oligonucle	Aaf67615	11.2	43.1	38	3	AAZ56133	Class D t
836	11.2	43.1	28	5	AAK49268	Fragment	Aaf67621	11.2	43.1	38	3	AAZ292035	PCR prime
837	11.2	43.1	28	5	AAK49268	Fragment	Aaf67622	11.2	43.1	38	3	AAZ292035	PCR prime
838	11.2	43.1	28	5	AAK49268	Neisseria	Aas44081	11.2	43.1	38	3	AAAS58633	Nucleotid
839	11.2	43.1	28	6	AAQ78248	Human igG	Aas17782	11.2	43.1	38	3	AAAS58635	Nucleotid
840	11.2	43.1	28	6	AAQ78248	Primer us	Abq78248	11.2	43.1	38	4	AAC61973	Nucleotid
841	11.2	43.1	28	6	ABK67061	Human gen	ABK67061	11.2	43.1	38	4	AAC61974	Nucleotid
842	11.2	43.1	28	6	ABK64363	Retrovira	ABK64363	11.2	43.1	38	4	AAH47639	Nucleotid
843	11.2	43.1	28	8	ABX10455	Human non	ABX10455	11.2	43.1	38	4	AAH47638	Nucleotid
844	11.2	43.1	28	10	ABSS57859	Rat G-pro	ABSS57859	11.2	43.1	38	5	AAH25579	Nucleotid
845	11.2	43.1	28	12	ADE84735	Lymphocyt	Ade84735	11.2	43.1	38	5	AAH25580	Nucleotid
846	11.2	43.1	28	12	ADO24644	Primer 13	Ado24644	11.2	43.1	38	6	ABK98650	Transposo
847	11.2	43.1	29	2	AAV81779	Human ALK	Aav81779	11.2	43.1	38	8	ACA94741	Class E T
848	11.2	43.1	29	2	AZ000019	Anti sens	Aaz00019	11.2	43.1	38	8	ABX16494	Tet opera
849	11.2	43.1	29	2	AAK88115	Antifreez	Aax88115	11.2	43.1	38	8	ABX16495	Tet opera
850	11.2	43.1	29	2	AAK76793	PCR prime	Aax76793	11.2	43.1	38	8	ABX04774	Thymidine
851	11.2	43.1	29	8	ACC80932	Primer #2	Acc80932	11.2	43.1	38	9	ACD13901	Tetracycl
852	11.2	43.1	30	4	AAK75877	Oligonuc	Aaf75877	11.2	43.1	38	9	ACC84798	Nucleotid
853	11.2	43.1	30	6	ABSS5788	Streptoco	ABSS5788	11.2	43.1	38	10	ADBS23398	Tet opera
854	11.2	43.1	31	3	AAK54005	Granule b	Aax54005	11.2	43.1	38	10	ADBS23397	Tet opera
855	11.2	43.1	31	3	AAK60717	PCR prime	Aax60717	11.2	43.1	38	10	ADBS23397	Tet opera
856	11.2	43.1	31	3	AAK73690	Primer is	Aax73690	11.2	43.1	38	10	ADBS23397	Tet opera
857	11.2	43.1	31	4	AAK58793	Avian E c	Aaf58793	11.2	43.1	38	9	ACD13901	Tetracycl
858	11.2	43.1	31	6	ADH76359	E. coli i	Adh76359	11.2	43.1	40	2	AAK88877	Circular
859	11.2	43.1	32	12	ADJ92431	Human cys	Adi92431	11.2	43.1	40	2	AAK88877	Circular
860	11.2	43.1	32	2	AAT10320	PCR prime	Aat10320	11.2	43.1	40	3	AAAS8639	Nucleotid
861	11.2	43.1	32	3	AAK58637	Nucleotid	Aas58637	11.2	43.1	40	3	AAAS8639	Nucleotid
862	11.2	43.1	32	8	ACA61036	Cytochrom	ACA61036	11.2	43.1	40	6	ABA98152	Oligonuc
863	11.2	43.1	32	9	ADA67749	K. pneumo	Ada67749	11.2	43.1	40	6	ABA98103	Synthetic
864	11.2	43.1	33	6	ABK50695	PCR prime	Abk50695	11.2	43.1	40	8	ABT17495	Selection
865	11.2	43.1	33	8	AAK52142	Fungus-or	Aal52142	11.2	43.1	41	3	AAK71003	Molecular
866	11.2	43.1	33	9	ACC84745	E. coli p	Acc84745	11.2	43.1	41	3	AAK71007	Molecular
867	11.2	43.1	34	2	AAK08626	Primer us	Aax08626	11.2	43.1	41	6	ABZ43442	Human NQO
868	11.2	43.1	34	2	AAK08618	Primer us	Aax08618	11.2	43.1	41	6	ABZ43442	Human NQO
869	11.2	43.1	34	2	AAK08622	Primer us	Aax08622	11.2	43.1	41	6	ABZ43442	Human NQO
870	11.2	43.1	34	2	AAK01640	Triabody	Aax01640	11.2	43.1	41	8	ACC00164	Probe #2
871	11.2	43.1	34	2	AAK01634	Anti-B7.1	Aax01634	11.2	43.1	41	10	ADD05343	DNA methy
872	11.2	43.1	34	3	AAK56734	Beta-lact	Aax56734	11.2	43.1	42	3	AAZ64546	Hairpin r
873	11.2	43.1	34	11	ADQ96818	Novel zin	Adq96818	11.2	43.1	42	3	AAZ64546	Hairpin r
874	11.2	43.1	34	12	ADI28634	Mycoplasma	Adi28634	11.2	43.1	42	3	AAZ64546	Hairpin r
875	11.2	43.1	34	12	ADI28635	Mycoplasma	Adi28635	11.2	43.1	42	3	AAZ64546	Hairpin r
876	11.2	43.1	35	2	AAT94502	PCR prime	Aat94502	11.2	43.1	42	10	ABS56914	Rat high
877	11.2	43.1	35	10	ADC36233	Weed cont	Adc36233	11.2	43.1	42	12	ADP88463	Antibody
878	11.2	43.1	35	12	ADH10520	S. enteri	Adh10520	11.2	43.1	42	12	ADP88463	Antibody
879	11.2	43.1	36	3	AAK58638	Nucleotid	Aas58638	11.2	43.1	42	12	ADQ90881	Rat high
880	11.2	43.1	36	3	AAK58630	Nucleotid	Aas58630	11.2	43.1	42	12	ADQ90881	Rat high
881	11.2	43.1	36	3	AAK58641	Nucleotid	Aas58641	11.2	43.1	43	2	AAQ23173	HPV probe
882	11.2	43.1	36	3	AAK58642	Nucleotid	Aas58642	11.2	43.1	43	2	AAQ23173	HPV probe
883	11.2	43.1	36	3	AAK58643	Nucleotid	Aas58643	11.2	43.1	43	2	AAQ23173	HPV probe
884	11.2	43.1	36	3	AAK58634	Nucleotid	Aas58634	11.2	43.1	43	2	AAQ23173	HPV probe
885	11.2	43.1	36	6	ADK45167	Flea chit	Adk45167	11.2	43.1	43	2	AAQ23173	HPV probe
886	11.2	43.1	36	10	ADK45167	Bacillus	Adk45167	11.2	43.1	43	2	AAQ23173	HPV probe
887	11.2	43.1	36	12	ADL15684	Murine im	Adl15684	11.2	43.1	43	2	AAQ23173	HPV probe
888	11.2	43.1	37	4	AAK90262	Primer #1	Aac90262	11.2	43.1	43	12	ADP97154	C. albica
889	11.2	43.1	37	6	ACN19955	WNV Zinz	Acn19955	11.2	43.1	44	3	AAAS8640	Nucleotid
890	11.2	43.1	37	10	ADC98725	PCR prime	Adc98725	11.2	43.1	44	10	ACC59552	Chlamydia
891	11.2	43.1	37	10	ADK71442	Drug-tole	Adk71442	11.2	43.1	44	10	ACC59552	Chlamydia
892	11.2	43.1	38	2	AAQ90044	B. amyloli	Aaq90044	11.2	43.1	45	2	AAZ33934	Human PRO
893	11.2	43.1	38	2	AAQ90044	Class D t	Aat11363	11.2	43.1	45	3	AAK78631	Human PRO
894	11.2	43.1	38	2	AAQ90044	Class E t	Aat11364	11.2	43.1	45	3	AAK78631	Human PRO
895	11.2	43.1	38	2	AAQ90044	Class E t	Aat11364	11.2	43.1	45	3	AAK78631	Human PRO
896	11.2	43.1	38	2	AAQ90044	Class D T	Aat45714	11.2	43.1	45	9	ADA24589	Secreted
897	11.2	43.1	38	2	AAQ90044	Class E T	Aat45715	11.2	43.1	45	9	ADA24589	Secreted
898	11.2	43.1	38	2	AAQ90044	Class E T	Aat45715	11.2	43.1	45	9	ADA24589	Secreted
899	11.2	43.1	38	2	AAQ90044	Class E T	Aat45715	11.2	43.1	45	9	ADA24589	Secreted
900	11.2	43.1	38	2	AAQ90044	Class E T	Aat45715	11.2	43.1	45	9	ADA24589	Secreted
901	11.2	43.1	38	2	AAQ90044	Class E T	Aat45715	11.2	43.1	45	9	ADA24589	Secreted
902	11.2	43.1	38	2	AAQ90044	Class E T	Aat45715	11.2	43.1	45	9	ADA24589	Secreted
903	11.2	43.1	38	2	AAQ90044	Class E T	Aat45715	11.2	43.1	45	9	ADA24589	Secreted
904	11.2	43.1	38	2	AAQ90044	Class E T	Aat45715	11.2	43.1	45	9	ADA24589	Secreted
905	11.2	43.1	38	2	AAQ90044	Class E T	Aat45715	11.2	43.1	45	9	ADA24589	Secreted
906	11.2	43.1	38	2	AAQ90044	Class E T	Aat45715	11.2	43.1	45	9	ADA24589	Secreted
907	11.2	43.1	38	2	AAQ90044	Class E T	Aat45715	11.2	43.1	45	9	ADA24589	Secreted
908	11.2	43.1	38	2	AAQ90044	Class E T	Aat45715	11.2	43.1	45	9	ADA24589	Secreted
909	11.2	43.1	38	2	AAQ90044	Class E T	Aat45715	11.2	43.1	45	9	ADA24589	Secreted
910	11.2	43.1	38	2	AAQ90044	Class E T	Aat45715	11.2	43.1	45	9	ADA24589	Secreted
911	11.2	43.1	38	2	AAQ90044	Class E T	Aat45715	11.2	43.1	45	9	ADA24589	Secreted
912	11.2	43.1	38	2	AAQ90044	Class E T	Aat45715	11.2	43.1	45	9	ADA24589	Secreted
913	11.2	43.1	38	2	AAQ90044	Class E T	Aat45715	11.2	43.1	45	9	ADA24589	Secreted
914	11.2	43.1	38	2	AAQ90044	Class E T	Aat45715	11.2	43.1	45	9	ADA24589	Secreted
915	11.2	43.1	38	2	AAQ90044	Class E T	Aat45715	11.2	43.1	45	9	ADA24589	Secreted
916	11.2	43.1	38	2	AAQ90044	Class E T	Aat45715	11.2	43.1	45	9	ADA24589	Secreted
917	11.2	43.1	38	2	AAQ90044	Class E T	Aat45715	11.2	43.1	45	9	ADA24589	Secreted
918	11.2	43.1	38	2	AAQ90044	Class E T	Aat45715	11.2	43.1	45	9	ADA24589	Secreted
919	11.2	43.1	38	2	AAQ90044	Class E T	Aat45715	11.2	43.1	45	9	ADA24589	Secreted
920	11.2	43.1	38	2	AAQ90044	Class E T	Aat45715	11.2	43.1	45	9	ADA24589	Secreted
921	11.2	43.1	38	2	AAQ90044	Class E T	Aat45715	11.2	43.1	45	9	ADA24589	Secreted
922	11.2	43.1	38	2	AAQ90044	Class E T	Aat45715						



Acdd29063 Novel hum  
 Adb73556 Human PRO  
 Adb76272 Human PRO  
 Adc43698 Human PRO  
 Adc61458 Human PRO  
 Adc63422 Human PRO  
 Adc66522 Human PRO  
 Adc68646 Human PRO  
 Adc62706 Human PRO  
 Adc67771 Human PRO  
 Adc41091 Human PRO  
 Adc67146 Human PRO  
 Adc62082 Human PRO  
 Adc41715 Human PRO  
 Adc49084 Human PRO  
 Ade35138 Human PRO  
 Ade16252 Human PRO  
 Adc72867 Human PRO  
 Adc72225 Human PRO  
 Ade16876 Human PRO  
 Adf46890 Human PRO  
 Adg52647 Human PRO  
 Adg59967 Human PRO  
 Adf60727 Human PRO  
 Adc42467 Novel hum  
 Ade48384 Human PRO  
 Ade89485 Human PRO  
 Adf61125 Human PRO  
 Adf39817 Human PRO  
 Adf45613 Human PRO

XX Amplification of a target nucleic acid region using a specific control  
 PT sequence.  
 PT  
 PS Example 2; Fig 3; 28pp; English.  
 XX  
 CC The invention relates to a method for amplification of a target nucleic  
 CC acid region in a sample using a specific control sequence. The invention  
 CC is also directed to a method of determination of a target nucleic acid  
 CC using a special control nucleic acid. Nucleic acids of the invention are  
 CC used as a control in a reaction for amplifying target nucleic acids and  
 CC as a control in a hybridisation reaction for determination of target  
 CC nucleic acids. The present sequence is HCV (Hepatitis C virus) type I DNA  
 CC amplifying PCR primer. This primer is used to illustrate the methods of  
 CC the invention. Note: This sequence is stated to be same as that shown as  
 CC SEQ ID NO:8 in sequence listing. However this sequence has additional T  
 CC at its 3' end  
 XX  
 SQ Sequence 27 BP; 5 A; 8 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 100.0%; Score 26; DB 6; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 0.004;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTCTTCGAGATCGGTACCTCAAT 26  
 Db 1 CGTCTTCGAGATCGGTACCTCAAT 26

RESULT 2  
 AAD43741  
 ID AAD43741 standard; DNA; 27 BP.

# ALIGNMENTS

XX AAD43289  
 ID AAD43289 standard; DNA; 27 BP.  
 XX  
 AC AAD43289;  
 XX  
 DT 14-NOV-2002 (first entry)  
 XX  
 DE HCV DNA amplifying PCR primer, ST280pc.  
 XX  
 KW Amplification; target nucleic acid; PCR; primer; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 FH Key Location/Qualifiers  
 FT stem\_loop 1..16  
 FT misc\_binding 1..5  
 FT misc\_binding 11..16  
 FT misc\_binding 11..16  
 FT /tag= a  
 FT /tag= b  
 FT /bound\_moiety= "Nucleotides 16-11"  
 FT /tag= c  
 FT /bound\_moiety= "Nucleotides 5-1"  
 XX  
 PN EP1236805-A1.  
 XX  
 PD 04-SEP-2002.  
 XX  
 PF 27-FEB-2002; 2002EP-00004483.  
 XX  
 PR 02-MAR-2001; 2001EP-00105172.  
 XX  
 PA (HOFF ) ROCHE DIAGNOSTICS GMBH.  
 PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
 XX  
 FI Jaeger S;  
 XX  
 DR WPI; 2002-610695/66.  
 XX  
 PS

EP1236804-A1.  
 04-SEP-2002.  
 02-MAR-2001; 2001EP-00105172.  
 02-MAR-2001; 2001EP-00105172.  
 (HOFF ) ROCHE DIAGNOSTICS GMBH.  
 (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
 Jaeger S;  
 WPI; 2002-610694/66.  
 Amplification of a target nucleic acid region using control sequences.  
 Example 2; Fig 3; 29pp; English.



XX The invention relates to a method for amplification of a target nucleic  
 CC acid region. The method is useful for amplification of a nucleic acid  
 CC molecule using control nucleic acid sequences. The control nucleic acid  
 CC sequences are at least in part parallel-complementary to the sequence of  
 CC the target nucleic acid. The present sequence is HCV DNA amplifying PCR  
 CC primer. Note: This sequence is stated to be same as that shown as SEQ ID  
 CC NO:8 in sequence listing. However this sequence has additional A at its  
 CC 3' end. (Updated on 07-AUG-2003 to correct OS field.)  
 XX

SQ Sequence 27 BP; 5 A; 8 C; 5 G; 9 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 26; DB 6; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 0.004;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGTCTTTCGCAGATCGGTACCTCAAT 26  
 |||||  
 DB 1 CGTCTTTCGCAGATCGGTACCTCAAT 26

RESULT 3  
 AC153779/c  
 ID AC153779 standard; DNA; 25 BP.  
 XX  
 AC AC153779;  
 XX  
 DT 13-OCT-2003 (first entry)  
 XX  
 DE Human microarray DNA oligonucleotide SEQ ID NO 53770.  
 XX  
 KW EST; ss; probe; expressed sequence tag; microarray; gene expression;  
 KW genetic variation; biallelic marker; polymorphism; human;  
 KW cross-species comparison.  
 XX  
 OS Homo sapiens.  
 XX  
 FN US2003104410-A1.  
 XX  
 PD 05-JUN-2003.  
 XX  
 PF 15-MAR-2002; 2002US-00098263.  
 XX  
 PR 16-MAR-2001; 2001US-0276759P.  
 XX  
 PA (AFFY-) AFFYMETRIX INC.  
 XX  
 PI Mittmann MP;  
 XX  
 DR WPI; 2003-567953/53.  
 XX  
 PT New array of nucleic acid probes, useful for in situ hybridization, in  
 PT Southern, Northern or dot-blot hybridization to identify or detect the  
 PT sequence or specific mutations of any gene.  
 XX  
 PS Claim 1; SEQ ID NO 53770; 9pp; English.  
 XX

The invention discloses a microarray comprising a plurality of nucleic  
 CC acid probes including one of 2,018,500 fully defined sequences, or its  
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
 CC Also disclosed is a method of gene expression analysis. The array is used  
 CC in monitoring gene expression levels by hybridisation to a DNA library,  
 CC in analysis of genetic variation or in hybridisation of tag-labelled  
 CC compounds. The nucleic acid probes are specifically designed for analysis  
 CC of at least one target sequence. The method of analysis comprises  
 CC hybridising at least one or more nucleic acids to at least two or more  
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
 CC probes are attached to a solid support. The analysis comprises monitoring  
 CC gene expression levels, identifying biallelic markers or polymorphisms,  
 CC or family members of a gene and a cross-species comparison. Each of the  
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
 CC probes is useful in in situ hybridisation, in Southern, Northern or dot-  
 CC blot hybridisation to identify or detect the sequence or specific

CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
 CC primer extensions or in screening cDNA or genomic libraries or subclones  
 CC for additional subclones containing segments of DNA that have been  
 CC isolated and previously sequenced. The sequence presented is one of the  
 CC nucleic acid probes incorporated in the microarray. Note: The sequence  
 CC data for this patent can also be obtained in electronic format directly  
 CC from USPIO at seqdata.uspto.gov/sequence.html  
 XX

SQ Sequence 25 BP; 8 A; 5 C; 7 G; 5 T; 0 U; 0 Other;  
 Query Match 65.4%; Score 17; DB 9; Length 25;  
 Best Local Similarity 80.0%; Pred. No. 1.4e+02;  
 Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 GTCTTTTCGCAGATCGGTACCTCAAT 26  
 |||||  
 DB 25 GTACTTCGCGATAGGTACCTCTAT 1

RESULT 4  
 ACH57122/c  
 ID ACH57122 standard; DNA; 25 BP.  
 XX  
 AC ACH57122;  
 XX  
 DT 16-OCT-2003 (first entry)  
 XX  
 DE DNA target sequence #6258 useful in array for genetic analyses.  
 XX  
 KW Gene expression analysis; array; hybridisation; genetic variation;  
 KW tag-labelled compound; gene family; in situ hybridisation;  
 KW library screening; Southern hybridisation; northern hybridisation;  
 KW dot-blot hybridisation; gene sequence; mutation detection;  
 KW target sequence; probe; PCR; primer; ss.  
 XX  
 OS Unidentified.  
 XX  
 FN US2003082596-A1.  
 XX  
 PD 01-MAY-2003.  
 XX  
 PF 08-AUG-2002; 2002US-00215112.  
 XX  
 PR 08-AUG-2001; 2001US-0311040P.  
 XX  
 PA (MITT/) MITTMANN M.  
 XX  
 PI Mittmann M;  
 XX  
 DR WPI; 2003-576608/54.  
 XX  
 PT New probe array useful e.g. for monitoring gene expression levels, for  
 PT analysing genetic variations, or for hybridizing tag-labeled compounds,  
 PT comprises multiple nucleic acid probes.  
 XX  
 PS Claim 1; SEQ ID NO 6258; 9pp; English.  
 XX

The present invention relates to nucleic acid sequences that are  
 CC complementary to particular genes, and can be used as probes for a  
 CC variety of analyses such as gene expression analysis. Each probe  
 CC comprises 9 or more consecutive nucleotides from at least one of 14936  
 CC nucleotide sequences defined in the patent, or their perfect sense match,  
 CC sense mismatch, antisense match or antisense mismatch oligonucleotides.  
 CC The probes may be used in an array comprising at least 10 distinct  
 CC nucleic acid probes. The array is useful in monitoring gene expression  
 CC levels by hybridisation to a DNA library, in analysing genetic  
 CC variations, and in hybridising tag-labelled compounds. The probes are  
 CC useful for identifying family members of a gene. The probes are also  
 CC useful in in situ hybridisations, in screening cDNA or genomic libraries  
 CC (or derived subclones) for additional clones containing segments of DNA  
 CC that have been previously isolated and sequenced, in Southern, northern,  
 CC or dot-blot hybridisation of genomic DNA to identify or detect the  
 CC sequence of any gene or detect specific mutations in any gene, and in

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CC for additional subclones containing segments of DNA that have been  
 CC isolated and previously sequenced. The sequence presented is one of the  
 CC nucleic acid probes incorporated in the microarray. Note: The sequence  
 CC data for this patent can also be obtained in electronic format directly  
 CC from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)  
 CC  
 CC Sequence 25 BP; 7 A; 5 C; 7 G; 6 T; 0 U; 0 Other;  
 CC

Query Match 59.2%; Score 15.4; DB 9; Length 25;  
 Best Local Similarity 76.0%; Pred. No. 8.9e+02;  
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 GCTTTGCGAGATCGGTACCTCAAT 26  
 Db 25 GTATTTCGAGGACCGGTACCTCGA 1

RESULT 6  
 ACH57668/c  
 ID ACH57668 standard; DNA; 25 BP.  
 XX  
 AC ACH57668;  
 XX  
 DT 16-OCT-2003 (first entry)  
 XX  
 DE DNA target sequence #6804 useful in array for genetic analyses.  
 XX  
 KW Gene expression analysis; array; hybridisation; genetic variation;  
 KW tag-labelled compound; gene family; in situ hybridisation;  
 KW library screening; Southern hybridisation; northern hybridisation;  
 KW dot-blot hybridisation; gene sequence; mutation detection;  
 KW target sequence; probe; PCR; primer; ss.  
 XX  
 OS Unidentified.  
 XX  
 XX US2003082596-A1.  
 XX  
 PD 01-MAY-2003.  
 XX  
 PF 08-AUG-2002; 2002US-00215112.  
 XX  
 PR 08-AUG-2001; 2001US-0311040P.  
 XX  
 PA (MITT/) MITTMANN M.  
 XX  
 PI Mittmann M;  
 XX  
 DR WPI; 2003-576608/54.  
 XX  
 PT New probe array useful e.g. for monitoring gene expression levels, for  
 PT analyzing genetic variations, or for hybridizing tag-labeled compounds,  
 PT comprises multiple nucleic acid probes.  
 XX  
 PS Claim 1; SEQ ID NO 6804; 9pp; English.  
 XX

CC The present invention relates to nucleic acid sequences that are  
 CC complementary to particular genes, and can be used as probes for a  
 CC variety of analyses such as gene expression analysis. Each probe  
 CC comprises 9 or more consecutive nucleotides from at least one of 14936  
 CC nucleotide sequences defined in the patent, or their perfect sense match,  
 CC sense mismatch, antisense match or antisense mismatch oligonucleotides.  
 CC The probes may be used in an array comprising at least 10 distinct  
 CC nucleic acid probes. The array is useful in monitoring gene expression  
 CC levels by hybridisation to a DNA library, in analysing genetic  
 CC variations, and in hybridising tag-labelled compounds. The probes are  
 CC useful for identifying family members of a gene. The probes are also  
 CC useful in situ hybridisations, in screening cDNA or genomic libraries  
 CC (or derived subclones) for additional clones containing segments of DNA  
 CC that have been previously isolated and sequenced, in Southern, northern,  
 CC or dot-blot hybridisation of genomic DNA to identify or detect the  
 CC sequence of any gene or detect specific mutations in any gene, and in  
 CC mapping the 5' termini of mRNA molecules by primer extensions. The  
 CC nucleic acid sequences of the invention are also useful as PCR primers.

CC mapping the 5' termini of mRNA molecules by primer extensions. The  
 CC nucleic acid sequences of the invention are also useful as PCR primers.  
 CC The invention provides a large collection of nucleic acid sequences  
 CC complementary to particular genes with a wide range of analytical uses.  
 CC ACH50865-ACH65260 represent the target sequences of the invention. Note:  
 CC The sequence data for this patent was obtained in electronic format  
 CC directly from the USPTO web site at [seqdata.uspto.gov/psipdIDEntry.html](http://seqdata.uspto.gov/psipdIDEntry.html)  
 CC  
 CC Sequence 25 BP; 5 A; 8 C; 7 G; 5 T; 0 U; 0 Other;  
 CC

Query Match 61.5%; Score 16; DB 9; Length 25;  
 Best Local Similarity 79.2%; Pred. No. 4.4e+02;  
 Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 GCTTTGCGAGATCGGTACCTCAA 25  
 Db 24 GTCAATTCGAGGACCGGTACCTCGA 1

RESULT 5  
 ACI53778/c  
 ID ACI53778 standard; DNA; 25 BP.  
 XX  
 AC ACI53778;  
 XX  
 DT 13-OCT-2003 (first entry)  
 XX  
 DE Human microarray DNA oligonucleotide SEQ ID NO 53769.  
 XX  
 KW EST; ss; probe; expressed sequence tag; microarray; gene expression;  
 KW genetic variation; biallelic marker; polymorphism; human;  
 KW cross-species comparison.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2003104410-A1.  
 XX  
 PD 05-JUN-2003.  
 XX  
 PF 15-MAR-2002; 2002US-00098263.  
 XX  
 PR 16-MAR-2001; 2001US-0276759P.  
 XX  
 PA (AFFY-) AFFYMETRIX INC.  
 XX  
 PI Mittmann MP;  
 XX  
 DR WPI; 2003-567953/53.  
 XX  
 PT New array of nucleic acid probes, useful for in situ hybridization, in  
 PT Southern, Northern or dot-blot hybridization to identify or detect the  
 PT sequence or specific mutations of any gene.  
 XX  
 PS Claim 1; SEQ ID NO 53769; 9pp; English.  
 XX

CC The invention discloses a microarray comprising a plurality of nucleic  
 CC acid probes including one of 2,018,500 fully defined sequences, or its  
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
 CC Also disclosed is a method of gene expression analysis. The array is used  
 CC in monitoring gene expression levels by hybridisation to a DNA library,  
 CC in analysis of genetic variation or in hybridisation of tag-labelled  
 CC compounds. The nucleic acid probes are specifically designed for analysis  
 CC of at least one target sequence. The method of analysis comprises  
 CC hybridising at least one or more nucleic acids to at least two or more  
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
 CC probes are attached to a solid support. The analysis comprises monitoring  
 CC gene expression levels, identifying biallelic markers or polymorphisms,  
 CC or family members of a gene and a cross-species comparison. Each of the  
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-  
 CC blot hybridisation to identify or detect the sequence or specific  
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
 CC primer extensions or in screening cDNA or genomic libraries or subclones

CC The invention provides a large collection of nucleic acid sequences  
 CC complementary to particular genes with a wide range of analytical uses.  
 CC ACH50865-ACH65260 represent the target sequences of the invention. Note:  
 CC The sequence data for this patent was obtained in electronic format  
 CC directly from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html  
 XX  
 XX Sequence 25 BP; 5 A; 5 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 58.5%; Score 15.2; DB 9; Length 25;  
 Best Local Similarity 85.0%; Pred. No. 1.1e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 TCGCAGATCGGTACTCTCAAT 26  
 |||||  
 Db 21 TCACAGACAGGTACTCTCAAT 2

RESULT 7  
 ACH57794/c  
 ID ACH57794 standard; DNA; 25 BP.

XX ACH57794;

XX 16-OCT-2003 (first entry)

XX DNA target sequence #6930 useful in array for genetic analyses.

XX Gene expression analysis; array; hybridisation; genetic variation;  
 KW tag-labelled compound; gene family; in situ hybridisation;  
 KW library screening; Southern hybridisation; northern hybridisation;  
 KW dot-blot hybridisation; gene sequence; mutation detection;  
 KW target sequence; probe; PCR; primer; ss.

XX Unidentified.

XX US2003082596-A1.

XX 01-MAY-2003.

XX 08-AUG-2002; 2002US-00215112.

XX 08-AUG-2001; 2001US-0311040P.

XX (MITT/) MITTMANN M.

XX Mittmann M;

XX WPI; 2003-576608/54.

XX New probe array useful e.g. for monitoring gene expression levels, for  
 PT analyzing genetic variations, or for hybridizing tag-labeled compounds,  
 PT comprises multiple nucleic acid probes.

XX Claim 1; SEQ ID NO 6930; 9pp; English.

XX The present invention relates to nucleic acid sequences that are  
 CC complementary to particular genes, and can be used as probes for a  
 CC variety of analyses such as gene expression analysis. Each probe  
 CC comprises 9 or more consecutive nucleotides from at least one of 14936  
 CC nucleotide sequences defined in the patent, or their perfect sense match,  
 CC sense mismatch, antisense match or antisense mismatch oligonucleotides.  
 CC The probes may be used in an array comprising at least 10 distinct  
 CC nucleic acid probes. The array is useful in monitoring gene expression  
 CC levels by hybridisation to a DNA library, in analysing genetic  
 CC variations, and in hybridising tag-labelled compounds. The probes are  
 CC useful for identifying family members of a gene. The probes are also  
 CC useful in situ hybridisations, in screening cDNA or genomic libraries  
 CC (or derived subclones) for additional clones containing segments of DNA  
 CC that have been previously isolated and sequenced, in Southern, northern,  
 CC or dot-blot hybridisation of genomic DNA to identify or detect the  
 CC sequence of any gene or detect specific mutations in any gene, and in  
 CC mapping the 5' termini of mRNA molecules by primer extensions. The  
 CC nucleic acid sequences of the invention are also useful as PCR primers.

CC The invention provides a large collection of nucleic acid sequences  
 CC complementary to particular genes with a wide range of analytical uses.  
 CC ACH50865-ACH65260 represent the target sequences of the invention. Note:  
 CC The sequence data for this patent was obtained in electronic format  
 CC directly from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html  
 XX  
 XX Sequence 25 BP; 6 A; 5 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 58.5%; Score 15.2; DB 9; Length 25;  
 Best Local Similarity 85.0%; Pred. No. 1.1e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 TCGCAGATCGGTACTCTCAAT 26  
 |||||  
 Db 21 TCACAGACAGGTACTCTCAAT 2

RESULT 8  
 ACH54380/c  
 ID ACH54380 standard; DNA; 25 BP.

XX ACH54380;

XX 16-OCT-2003 (first entry)

XX DNA target sequence #3516 useful in array for genetic analyses.

XX Gene expression analysis; array; hybridisation; genetic variation;  
 KW tag-labelled compound; gene family; in situ hybridisation;  
 KW library screening; Southern hybridisation; northern hybridisation;  
 KW dot-blot hybridisation; gene sequence; mutation detection;  
 KW target sequence; probe; PCR; primer; ss.

XX Unidentified.

XX US2003082596-A1.

XX 01-MAY-2003.

XX 08-AUG-2002; 2002US-00215112.

XX 08-AUG-2001; 2001US-0311040P.

XX (MITT/) MITTMANN M.

XX Mittmann M;

XX WPI; 2003-576608/54.

XX New probe array useful e.g. for monitoring gene expression levels, for  
 PT analyzing genetic variations, or for hybridizing tag-labeled compounds,  
 PT comprises multiple nucleic acid probes.

XX Claim 1; SEQ ID NO 3516; 9pp; English.

XX The present invention relates to nucleic acid sequences that are  
 CC complementary to particular genes, and can be used as probes for a  
 CC variety of analyses such as gene expression analysis. Each probe  
 CC comprises 9 or more consecutive nucleotides from at least one of 14936  
 CC nucleotide sequences defined in the patent, or their perfect sense match,  
 CC sense mismatch, antisense match or antisense mismatch oligonucleotides.  
 CC The probes may be used in an array comprising at least 10 distinct  
 CC nucleic acid probes. The array is useful in monitoring gene expression  
 CC levels by hybridisation to a DNA library, in analysing genetic  
 CC variations, and in hybridising tag-labelled compounds. The probes are  
 CC useful for identifying family members of a gene. The probes are also  
 CC useful in situ hybridisations, in screening cDNA or genomic libraries  
 CC (or derived subclones) for additional clones containing segments of DNA  
 CC that have been previously isolated and sequenced, in Southern, northern,  
 CC or dot-blot hybridisation of genomic DNA to identify or detect the  
 CC sequence of any gene or detect specific mutations in any gene, and in  
 CC mapping the 5' termini of mRNA molecules by primer extensions. The  
 CC nucleic acid sequences of the invention are also useful as PCR primers.

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can be amplified in the same reaction by targeting multiple sequences with (EP). Simultaneous amplification and detection is facilitated using detection probes associated with a substrate. Multiplex detection can be facilitated by an array of detection probes with different detection probes at different locations of a substrate. The present sequence is a primer used in the TEX method to detect/amplify HCV (Hepatitis C virus) target sequences.

Sequence 18 BP; 2 A; 5 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 57.7%; Score 15; DB 12; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03; Indels 0; Gaps 0;  
Matches 15; Conservative 0; Mismatches 0;

1 CGCTCTTCGAGATC 15  
4 CGCTCTTCGAGATC 18

RESULT 10  
AC127637/c  
ID AC127637 standard; DNA; 25 BP.  
XX AC127637;  
XX AC127637;  
DT 13-OCT-2003 (first entry)  
DE Human microarray DNA oligonucleotide SEQ ID NO 27628.  
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;  
KW genetic variation; biallelic marker; polymorphism; human;  
KW cross-species comparison.  
XX Homo sapiens.  
XX US2003104410-A1.  
XX 05-JUN-2003.  
XX 15-MAR-2002; 2002US-00098263.  
XX 16-MAR-2001; 2001US-0276759P.  
XX (AFY-) APFYMETRIX INC.  
XX Mittmann MP;  
XX WPI; 2003-567953/53.  
XX New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.  
XX Claim 1; SEQ ID NO 27628; 9pp; English.  
XX The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones

The invention provides a large collection of nucleic acid sequences complementary to particular genes with a wide range of analytical uses. ACH50865-ACH65260 represent the target sequences of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at [seqdata.uspto.gov/psipdIDentry.html](http://seqdata.uspto.gov/psipdIDentry.html)

Sequence 25 BP; 6 A; 4 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 58.5%; Score 15.2; DB 9; Length 25;  
Best Local Similarity 85.0%; Pred. No. 1.1e+03; Indels 0; Gaps 0;  
Matches 17; Conservative 0; Mismatches 3;

7 TCGCAGATCGGTACTCAAT 26  
22 TCACAGACAGGTACTCAAT 3

RESULT 9  
ADP87820  
ID ADP87820 standard; DNA; 18 BP.  
XX ADP87820;  
XX ADP87820;  
DT 09-SEP-2004 (first entry)  
DE Primer for TEX detection of Hepatitis C virus T1.  
XX TEX; thermodynamic equilibrium extension of primers; HCV; ss; primer.  
KW Hepatitis C virus.  
OS US2004115643-A1.  
XX 17-JUN-2004.  
XX 12-DEC-2002; 2002US-00318416.  
XX 12-DEC-2002; 2002US-00318416.  
XX (LIZA/) LIZARDI P M.  
XX (GRIB/) GRIBANOV O G.  
XX Lizardi PM, Gribanov OG;  
XX WPI; 2004-468050/44.  
XX Amplifying nucleic acid for detecting nucleic acid, by extension of one or more primers using target templates having replication terminating feature, dissociation of primer from templates to produce multiple extended primers.  
XX Disclosure; Fig 8; 75pp; English.  
XX The invention relates to amplifying (M1) a nucleic acid, involving contacting one or more extension primers (EP) and target templates and incubating under conditions to promote interaction of (EP) and templates, extension of (EP) using the interacting (TT), and dissociation of the extended (EP) from (TT), to produce multiple extended (EP) from at least one (TT), where each (TT) comprise a replication terminating feature. In (M1), (EP) and target templates are incubated under isothermal conditions or single set of conditions. The target templates are nucleic acid sequences of interest. Each of (EP) comprises or are nucleic acid sequences of interest, preferably nucleotides, where the nucleotides consist of the target complement portion. Each (EP) consists of a target complement portion, preferably nucleotides, where the nucleotides consist of the target complement portion. The method is useful for amplifying nucleic acid and for detecting nucleic acid sequences which involves performing (M1), and detecting one or more of the extended (EP). In (M1), only those sequences targeted by (EP) are amplified, thus allowing specific sequences to be targeted for amplification. Flexibility in the location of replication terminating feature allows flexibility in targeting sequences. If a targeted sequence is not present, the sequence will not be amplified. Multiple sequences

CC for additional subclones containing segments of DNA that have been  
 CC isolated and previously sequenced. The sequence presented is one of the  
 CC nucleic acid probes incorporated in the microarray. Note: The sequence  
 CC data for this patent can also be obtained in electronic format directly  
 CC from USPTO at seqdata.uspto.gov/sequence.html

XX Sequence 25 BP; 6 A; 7 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 56.2%; Score 14.6; DB 9; Length 25;

Best Local Similarity 81.0%; Pred. No. 2.3e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TCTTTCGAGATCGGTACCTC 23

Db 23 TCCTTCGGGGATCGGTACCCAC 3

RESULT 11

AAT31021/c

ID AAT31022 standard; DNA; 41 BP.

XX AAT31022;

AC AAT31022;

DT 26-SEP-1996 (first entry)

DE Human endothelin-1 gene promoter PCR primer F.

XX Gene therapy; hypoxia related enhancer element; HREE; ischaemia;  
 KW reperfusion; promoter; endothelin-1; endothelium; PCR; primer;  
 KW polymerase chain reaction; ss.

XX Synthetic.

XX WO9620276-A1.

XX 04-JUL-1996.

XX 13-NOV-1995; 95WO-IB000996.

XX 23-DEC-1994; 94US-00365486.

XX (STRI ) SRI INT.

XX Webster KA, Bishopric NH, Murphy B, Laderoute KR, Green CJ;  
 FI WPI; 1996-321849/32.

XX Chimeric gene contg. therapeutic gene linked to HREE - partic. for  
 PT expressing SOD etc. in hypoxic tissue to reduce tissue injury caused by  
 PT ischaemia or reperfusion.

XX Example 1; Page 46; 118pp; English.

CC A DNA fragment (AAT31013) contg. 700 bp of the human endothelin (ET-1)  
 CC gene promoter was created by PCR using HeLa genomic DNA as template. ET-1  
 CC specific primers were based on the ET-1 gene promoter sequence. The  
 CC forward primer (AAT31022) contained PstI and KpnI sites, and the reverse  
 CC primer (AAT31023) contained HindIII and XbaI sites. The PCR product was  
 CC cloned into pGL2BV. The promoter can be used to target hypoxia-regulated  
 CC genes specifically to cells of the vascular endothelium, since it  
 CC contains elements conferring tissue specificity as well as hypoxia  
 CC response enhancer elements able to up-regulate transcription of a  
 CC (therapeutic) gene under hypoxic conditions

XX Sequence 41 BP; 12 A; 8 C; 12 G; 9 T; 0 U; 0 Other;

Query Match 56.2%; Score 14.6; DB 2; Length 41;

Best Local Similarity 81.0%; Pred. No. 2.4e+03;  
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GTCCTTCGAGATCGGTACCT 22

Db 30 GTCCTTCCTTCGATCGGTACCT 10

RESULT 12

ABS97227

ID ABS97227 standard; DNA; 21 BP.

XX ABS97227;

AC ABS97227;

XX 23-DEC-2002 (first entry)

XX Human CYP4502E1 promoter polymorphism #13.

XX Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;  
 KW cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;  
 KW adrenergic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRP3; NR112;  
 KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;  
 KW cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;  
 KW epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;  
 KW glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;  
 KW HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;  
 KW NADPH quinone oxidoreductase 2; NQO2; sulfotransferase thermolabile; STM;  
 KW UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;  
 KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;  
 KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;  
 KW multidrug resistance associated protein 3; cancer; prostate;  
 KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;  
 KW altered drug metabolism; cardiovascular function; colorectal tumour;  
 KW central nervous system; pulmonary; immunological; SNF;  
 KW single nucleotide polymorphism.

XX Homo sapiens.

XX WO200257410-A2.

XX 25-JUL-2002.

XX 28-NOV-2001; 2001WO-US044838.

XX 28-NOV-2000; 2000US-00724389.

XX (DNAS-) DNA SCI LAB INC.

XX Guida M, Hall J;

XX WPI; 2002-698522/75.

XX Isolated nucleic acid molecules having polymorphisms in known human genes  
 e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers  
 for locating, identifying and characterizing the genes responsible for  
 disorder-related traits.

XX Example 3; Page 104; 714pp; English.

XX This invention relates to the sequence of an isolated nucleic acid  
 molecule comprising at least one base variation from that of a known  
 human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),  
 cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),  
 aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator  
 (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding  
 inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating  
 protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl  
 transferase (HNMT), (kallikrein 2) KLK2, nicotinamide -N-methyl  
 sulfotransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4  
 (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl  
 transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1  
 (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3  
 (MRP3), orphan nuclear receptor (NR112), or acetylcholine muscarinic  
 receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.  
 CC The polymorphisms in the human genes cited in the invention are useful as  
 CC genetic linkage markers for locating and characterising the genes that  
 CC are responsible for specific traits within the genome and eventually  
 CC identifying the genes responsible for a variety of disorder-related

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CC traits as a result of their e.g., overexpression, constitutive  
 CC expression, mutation or underexpression, which may be used in diagnosing  
 CC and/or treating the disorders. The nucleic acid molecules comprising the  
 CC polymorphic sequences contained in CYP4501A1, CYP4501A2, CYP4502E1,  
 CC ARNT, BPHX2, GST12, NNMT, NQO2, NR112, STM, UGT2B4, UGT2B15, AHR,  
 CC MDRI and/or MDR3 are useful for screening individuals for altered drug  
 CC metabolism. The polymorphic sequences contained in CYP4501A1, CYP4501A2,  
 CC AHR, MDRI and/or MDR3 may also be used to screen individuals for  
 CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are  
 CC used to screen for altered cardiovascular function, in COX2 for altered  
 CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central  
 CC nervous system function, in FLAP and HNMT for altered serine  
 CC immunological or haematological function, in KLK2 for altered serine  
 CC protease activity in the prostate, in LTF for altered immunological or  
 CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and  
 CC peripheral nervous system function. The present sequence represents a  
 CC polymorphic DNA sequence of the invention

XX Sequence 21 BP; 6 A; 5 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 55.4%; Score 14.4; DB 6; Length 21;  
 Best Local Similarity 93.8%; Pred. No. 2.8e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 GCAGATCGGTACTCTCA 24  
 |||||  
 DB 6 GCAGTTCGTACTCTCA 21

RESULT 13  
 AAT88375  
 ID AAT88375 standard; DNA; 23 BP.

XX AAT88375;

XX 28-JAN-1998 (first entry)

DE Primer for T. peptonophilus thermostable DNA polymerase cDNA.

XX Thermotable; DNA polymerase; nucleic acid sequence amplification;  
 KW primer; PCR; ss.

XX Synthetic.

OS Thermococcus peptonophilus.

XX Key Location/Qualifiers

FT modified\_base 3 /tag= a  
 FT /mod\_base= i

FT modified\_base 9 /tag= b

FT /mod\_base= i

FT modified\_base 15 /tag= c

FT /mod\_base= i

XX JF09252776-A.

XX 30-SRP-1997.

XX 19-MAR-1996; 96JP-00063112.

XX 19-MAR-1996; 96JP-00063112.

XX (TOYM ) TOYBO KK.

XX WPI; 1997-530149/49.

XX Thermococcus peptonophilus thermostable DNA polymerase - useful for

XX nucleic acid sequence amplification, e.g. polymerase chain reaction.

XX Example 1; Page 24; 27pp; Japanese.

XX

CC The present primer was used in the preparation of a Thermococcus  
 CC peptonophilus derived thermostable DNA polymerase cDNA. The enzyme can be  
 CC used for nucleic acid sequence amplification, e.g. PCR

XX Sequence 23 BP; 4 A; 7 C; 3 G; 5 T; 0 U; 4 Other;

Query Match 55.4%; Score 14.4; DB 2; Length 23;  
 Best Local Similarity 71.4%; Pred. No. 2.8e+03;  
 Matches 15; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 CTTTCGACATCGGTACTCTCA 24  
 |||||  
 DB 2 CTTTCGACATCGGTACTCTCA 22

RESULT 14

ACI61181  
 ID ACI61181 standard; DNA; 25 BP.

XX ACI61181;

XX 13-OCT-2003 (first entry)

DE Human microarray DNA oligonucleotide SEQ ID NO 61172.

XX EST; ss; probe; expressed sequence tag; microarray; gene expression;  
 KW genetic variation; biallelic marker; polymorphism; human;  
 KW cross-species comparison.

XX Homo sapiens.

XX US2003104410-A1.

XX 05-JUN-2003.

XX 15-MAR-2002; 2002US-00098263.

XX 16-MAR-2001; 2001US-0276759P.

XX (AFFY-) AFFYMETRIX INC.

XX Mittmann MP;

XX WPI; 2003-567953/53.

XX New array of nucleic acid probes, useful for in situ hybridization, in  
 PT Southern, Northern or dot-blot hybridization to identify or detect the  
 PT sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 61172; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic  
 CC acid probes including one of 2,018,500 fully defined sequences, or its  
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
 CC Also disclosed is a method of gene expression analysis. The array is used  
 CC in monitoring gene expression levels by hybridisation to a DNA library,  
 CC in analysis of genetic variation or in hybridisation of tag-labelled  
 CC compounds. The nucleic acid probes are specifically designed for analysis  
 CC of at least one target sequence. The method of analysis comprises  
 CC hybridising at least one or more nucleic acids to at least two or more  
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
 CC probes are attached to a solid support. The analysis comprises monitoring  
 CC gene expression levels, identifying biallelic markers or polymorphisms,  
 CC or family members of a gene and a cross-species comparison. Each of the  
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-  
 CC blot hybridisation to identify or detect the sequence or specific  
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
 CC primer extensions or in screening cDNA or genomic libraries or subclones  
 CC for additional subclones containing segments of DNA that have been  
 CC isolated and previously sequenced. The sequence presented is one of the  
 CC nucleic acid probes incorporated in the microarray. Note: The sequence  
 CC data for this patent can also be obtained in electronic format directly

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CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 7 A; 4 C; 8 G; 6 T; 0 U; 0 Other;

Query Match      55.4%; Score 14.4; DB 9; Length 25;
Best Local Similarity 93.8%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 TCGCAGATCGGTACCT 22
Db 1 TCGTAGATCGGTACCT 16

RESULT 15
ACH57248/c
ID ACH57248 standard; DNA; 25 BP.
XX
AC ACH57248;
XX
DT 16-OCT-2003 (first entry)
XX
DE DNA target sequence #6384 useful in array for genetic analyses.
XX
KW Gene expression analysis; array; hybridisation; genetic variation;
KW tag-labelled compound; gene family; in situ hybridisation;
KW library screening; Southern hybridisation; northern hybridisation;
KW dot-blot hybridisation; gene sequence; mutation detection;
KW target sequence; probe; PCR; primer; ss.
XX
OS Unidentified.
XX
FN US2003082596-A1.
XX
PD 01-MAY-2003.
XX
PF 08-AUG-2002; 2002US-00215112.
XX
PR 08-AUG-2001; 2001US-0311040P.
XX
PA (MITT/) MITTMANN M.
XX
PI Mittmann M;
XX
WPI; 2003-576608/54.

New probe array useful e.g. for monitoring gene expression levels, for
analyzing genetic variations, or for hybridizing tag-labeled compounds,
comprises multiple nucleic acid probes.

Claim 1; SEQ ID NO 6384; 9pp; English.

The present invention relates to nucleic acid sequences that are
complementary to particular genes, and can be used as probes for a
variety of analyses such as gene expression analysis. Each probe
comprises 9 or more consecutive nucleotides from at least one of 14936
nucleotide sequences defined in the patent, or their perfect sense match,
sense mismatch, antisense match or antisense mismatch oligonucleotides.
The probes may be used in an array comprising at least 10 distinct
nucleic acid probes. The array is useful in monitoring gene expression
levels by hybridisation to a DNA library, in analysing genetic
variations, and in hybridising tag-labelled compounds. The probes are
useful for identifying family members of a gene. The probes are also
useful in situ hybridisations, in screening cDNA or genomic libraries
(or derived subclones) for additional clones containing segments of DNA
that have been previously isolated and sequenced, in Southern, northern,
or dot-blot hybridisation of genomic DNA to identify or detect the
sequence of any gene or detect specific mutations in any gene, and in
mapping the 5' termini of mRNA molecules by primer extensions. The
nucleic acid sequences of the invention are also useful as PCR primers.
The invention provides a large collection of nucleic acid sequences
complementary to particular genes with a wide range of analytical uses.
ACH50865-ACH5260 represent the target sequences of the invention. Note:
The sequence data for this patent was obtained in electronic format
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CC directly from the USPTO web site at seqdata.uspto.gov/psipdsIDEntry.html
XX
SQ Sequence 25 BP; 6 A; 8 C; 7 G; 4 T; 0 U; 0 Other;

Query Match      55.4%; Score 14.4; DB 9; Length 25;
Best Local Similarity 75.0%; Pred. No. 2.9e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 GTCTTTCGACAGTCGGTACCTCA 25
Db 24 GTCATTCGAGTCGGTACCTCGA 1

RESULT 16
AAA65754/c
ID AAA65754 standard; DNA; 40 BP.
XX
AC AAA65754;
XX
DT 21-NOV-2000 (first entry)
XX
DE Streptococcus pneumoniae BVH-3 PCR primer SEQ ID NO:29.
XX
KW Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;
KW prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
KW otitis media; pneumonia; immunisation; bactericidal; PCR primer; ss.
XX
OS Streptococcus pneumoniae.
XX
FN WO2000039299-A2.
XX
PD 06-JUL-2000.
XX
PF 20-DEC-1999; 99WO-CA001218.
XX
PR 23-DEC-1998; 98US-0113800P.
XX
PA (BIOC-) BIOCHEM PHARMA INC.
XX
PI Hamel J, Brodeur BR, Pineau I, Martin D, Rioux C, Charland N;
XX
WPI; 2000-452397/39.

Streptococcal antigens useful for vaccinating against e.g. meningitis,
otitis media, bacteraemia and/or pneumonia.

Example 8; Page 49; 106pp; English.

The present invention describes nucleic acids (I) encoding protein
antigens (II) from Streptococcus pneumoniae. The protein antigens have
bactericidal activity. The nucleic acids, encoding the protein antigens,
may be used for the recombinant production of the proteins they encode.
The protein antigens may then be used as vaccines for the prevention and
treatment of Streptococcal infections in mammals (especially humans)
which result in, e.g. meningitis, otitis media, bacteraemia and/or
pneumonia. The present sequence represents a PCR primer for a S.
pneumoniae GAS BVH-71 protein antigen, which is used in an example from
the present invention

Sequence 40 BP; 14 A; 6 C; 6 G; 14 T; 0 U; 0 Other;

Query Match      55.4%; Score 14.4; DB 3; Length 40;
Best Local Similarity 75.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 TCCTTTCGACAGTCGGTACCTCAAT 26
Db 37 TTTTCCAGATAGGTACTTCCAT 14

RESULT 17
ABK33676/c
ID ABK33676 standard; DNA; 40 BP.
```



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us-10-087-631b-8.max.rng

XX AC ABK33676;  
XX DT 08-MAY-2002 (first entry)  
XX DE S. pneumoniae BVH-3 gene, PCR primer HAM7 281.  
XX KW BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia; pneumonia;  
XX KW streptococcal bacterial infection; PCR; primer; ss.  
XX OS Streptococcus pneumoniae.  
XX PN W0200198334-A2.  
XX PD 27-DEC-2001.  
XX PF 19-JUN-2001; 2001WO-CA000908.  
XX PR 20-JUN-2000; 2000US-0212683P.  
XX PA (SHIR-) SHIRE BIOCHEM INC.  
XX PI Hamel J, Ouellet C, Charland N, Martin D, Brodeur B;  
XX DR WPI; 2002-122272/16.  
XX PT New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing  
XX PT polypeptides, useful as vaccine components for treating or preventing  
XX PT streptococcal infections such as otitis media, meningitis, and  
XX PT bacteremia.  
XX PS Example 1; Page 30; 113pp; English.  
XX CC The invention describes an isolated polypeptide (I) with 70-90% identity  
XX CC to Streptococcus pneumonia protein BVH-3, BVH-11, variants of BVH-3 or  
XX CC BVH-11, or chimeric sequences derived from them. A vaccine (II)  
XX CC comprising (I) is useful for therapeutic or prophylactic treatment of  
XX CC meningitis, otitis media, bacteraemia or pneumonia infection in an  
XX CC individual susceptible to these disorders. (II) is also useful for  
XX CC therapeutic or prophylactic treatment of any streptococcal bacterial  
XX CC infection (e.g., caused by Streptococcus pneumoniae, group A  
XX CC Streptococcus such as Streptococcus pyogenes, group B Streptococcus such  
XX CC as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. noxia or  
XX CC Streptococcus aureus) in an individual susceptible to the infection. A  
XX CC polynucleotide (III) encoding (I) is useful in DNA immunisation  
XX CC techniques. The Streptococcus polypeptides are useful in a diagnostic  
XX CC test for S. pneumoniae infection. (III) is useful for designing DNA  
XX CC probes for use in detecting the presence of Streptococcus in a biological  
XX CC sample suspected of containing the bacteria. The DNA probes may also be  
XX CC used for detecting circulating S. pneumonia nucleic acid in a sample for  
XX CC diagnosing streptococcal infections. This sequence represents a primer  
XX CC used for the isolation of S. pneumoniae genes from which the antigenic  
XX CC peptides of the invention are derived  
XX SQ Sequence 40 BP; 14 A; 6 C; 6 G; 14 T; 0 U; 0 Other;  
Query Match 55.4%; Score 14.4; DB 6; Length 40;  
Best Local Similarity 75.0%; Pred. No. 3e+03;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 3 TCTTTCCGACATCGGTACTCAAT 26  
Db 37 TTTTCCAGATAGGTACTTCCAT 14  
RESULT 18  
ACK29528/c  
ID ACK29528 standard; DNA; 25 BP.  
XX AC ACK29528;  
XX DT 14-OCT-2003 (first entry)  
XX

DE Human microarray DNA oligonucleotide SEQ ID NO 129509.  
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;  
KW Genetic variation; diallelic marker; polymorphism; human;  
KW cross-species comparison.  
XX OS Homo sapiens.  
XX US2003104410-A1.  
XX PN 05-JUN-2003.  
XX PD 15-MAR-2002; 2002US-00098263.  
XX PF 16-MAR-2001; 2001US-0276759P.  
XX PR (AFFY-) AFFYMETRIX INC.  
XX PA Mittmann MP;  
XX PI WPI; 2003-567953/53.  
XX DR New array of nucleic acid probes, useful for in situ hybridization, in  
XX PT Southern, Northern or dot-blot hybridization to identify or detect the  
XX PT sequence or specific mutations of any gene.  
XX PS Claim 1; SEQ ID NO 129509; 9pp; English.  
XX CC The invention discloses a microarray comprising a plurality of nucleic  
XX CC acid probes including one of 2,018,500 fully defined sequences, or its  
XX CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
XX CC Also disclosed is a method of gene expression analysis. The array is used  
XX CC in monitoring gene expression levels by hybridisation to a DNA library,  
XX CC in analysis of genetic variation or in hybridisation of tag-labelled  
XX CC compounds. The nucleic acid probes are specifically designed for analysis  
XX CC of at least one target sequence. The method of analysis comprises  
XX CC hybridising at least one or more nucleic acids to at least two or more  
XX CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
XX CC probes are attached to a solid support. The analysis comprises monitoring  
XX CC gene expression levels, identifying diallelic markers or polymorphisms,  
XX CC or family members of a gene and a cross-species comparison. Each of the  
XX CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
XX CC probes is useful in situ hybridisation, in Southern, Northern or dot-  
XX CC blot hybridisation to identify or detect the sequence or specific  
XX CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
XX CC primer extensions or in screening cDNA or genomic libraries or subclones  
XX CC for additional subclones containing segments of DNA that have been  
XX CC isolated and previously sequenced. The sequence presented is one of the  
XX CC nucleic acid probes incorporated in the microarray. Note: The sequence  
XX CC data for this patent can also be obtained in electronic format directly  
XX CC from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)  
XX SQ Sequence 25 BP; 5 A; 6 C; 6 G; 8 T; 0 U; 0 Other;  
Query Match 54.6%; Score 14.2; DB 9; Length 25;  
Best Local Similarity 84.2%; Pred. No. 3.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 7 TCCGACATCGGTACTCAAT 25  
Db 19 TCACAGACAGGACTCTCAA 1  
RESULT 19  
ACH56079/c  
ID ACH56079 standard; DNA; 25 BP.  
XX AC ACH56079;  
XX DT 16-OCT-2003 (first entry)  
XX DE DNA target sequence #5215 useful in array for genetic analyses.  
XX



Gene expression analysis; array; hybridisation; genetic variation; tag-labelled compound; gene family; in situ hybridisation; library screening; Southern hybridisation; northern hybridisation; dot-blot hybridisation; gene sequence; mutation detection; target sequence; probe; PCR; primer; ss.

Unidentified.

US2003082596-A1.

01-MAY-2003.

08-AUG-2002; 2002US-00215112.

08-AUG-2001; 2001US-0311040P.

(MITT/) MITTMANN M.

Mittmann M;

WPI; 2003-576608/54.

New probe array useful e.g. for monitoring gene expression levels, for analysing genetic variations, or for hybridizing tag-labeled compounds, comprises multiple nucleic acid probes.

Claim 1; SEQ ID NO 5215; 9pp; English.

The present invention relates to nucleic acid sequences that are complementary to particular genes, and can be used as probes for a variety of analyses such as gene expression analysis. Each probe comprises 9 or more consecutive nucleotides from at least one of 14936 nucleotide sequences defined in the patent, or their perfect sense match, sense mismatch, antisense match or antisense mismatch oligonucleotides. The probes may be used in an array comprising at least 10 distinct nucleic acid probes. The array is useful in monitoring gene expression levels by hybridisation to a DNA library, in analysing genetic variations, and in hybridising tag-labelled compounds. The probes are useful for identifying family members of a gene. The probes are also useful in situ hybridisations, in screening cDNA or genomic libraries (or derived subclones) for additional clones containing segments of DNA that have been previously isolated and sequenced, in Southern, northern, or dot-blot hybridisation of genomic DNA to identify or detect the sequence of any gene or detect specific mutations in any gene, and in mapping the 5' termini of mRNA molecules by primer extensions. The nucleic acid sequences of the invention are also useful as PCR primers. The invention provides a large collection of nucleic acid sequences complementary to particular genes with a wide range of analytical uses. ACH50865-ACH65260 represent the target sequences of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at [seqdata.uspto.gov/psipsIDEntry.html](http://seqdata.uspto.gov/psipsIDEntry.html)

Sequence 25 BP; 5 A; 6 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 54.6%; Score 14.2; DB 9; Length 25;  
Best Local Similarity 84.2%; Pred. No. 3.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 TCGCAGATCGGTACTCTCA 25

Db 19 TCACAGACAGGTACTCTCA 1

RESULT 20

AA172282/c

ID AA172282 standard; DNA; 30 BP.

XX

AC AA172282;

XX

DT 15-APR-2002 (first entry)

XX

DE 7013 marker primer P10.

XX

KW Lung; cancer; metastasis; solid tumour; blood; bone marrow; syndecan 1;  
KW collagen 1 alpha 2; 7013; 7018; amplification; mammal; human; dog; cat;  
KW bile duct; colon; breast; uterus; oesophagus; larynx; liver; brain; PCR;  
KW remission; relapse; polymerase chain reaction; primer; amplify; ss.  
XX  
OS Synthetic.

XX WO200198539-A2.

XX 27-DEC-2001.

XX 21-JUN-2001; 2001WO-US019980.

XX 21-JUN-2000; 2000US-0215727P.

XX 27-OCT-2000; 2000US-0243976P.

XX (HITB ) HITACHI CHEM CO LTD.

XX (HITB ) HITACHI CHEM RES CENT INC.

XX (HITA ) HITACHI LTD.

XX Mitsuhashi M, Kambara H, Matsunaga H, Kawamura M;

XX WPI; 2002-098233/13.

XX Identifying lung cancer/metastasis of solid tumor in patient by isolating blood or non-lung tissue, or bone marrow from patient and identifying presence of marker e.g. syndecan 1, collagen 1 alpha 2, 7013, or 7018.

XX Example 3; Page 9; 29pp; English.

XX The sequences given A172277-86 are primers which were used to identify markers in normal lung cells and lung cell lines. The primers amplify sequences which were identified using the method of the invention for identifying lung cancer or metastasis of a solid tumour. The method comprises isolating blood (or non-lung tissue in the case of identifying lung cancer, or bone marrow in case of identifying metastasis) from a patient, and identifying the presence of at least one marker (M) such as syndecan 1, collagen 1 alpha 2, 7013, or 7018. The method of the invention is useful for identifying lung cancer in a mammal e.g., human, dog or cat, and identifying metastasis of solid tumour in a patient, where the solid tumour is of bile duct, colon, breast, uterus, oesophagus or larynx. The method is useful for identifying presence of lung cancer cells in the blood or bone marrow, and also for identifying metastasis and thus for identifying lung cancer cells in an organ such as liver or brain. The method is useful to identify the presence of lung cancer cells at a very early stage in the disease, or after remission or to identify a relapse

XX Sequence 30 BP; 12 A; 5 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 54.6%; Score 14.2; DB 6; Length 30;  
Best Local Similarity 84.2%; Pred. No. 3.7e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 8 CGCAGATCGGTACTCTCAAT 26

Db 30 CGCAGATCGGAACCTTAAT 12

RESULT 21

AC142451/c

ID AC142451 standard; DNA; 25 BP.

XX

AC AC142451;

XX

DT 13-OCT-2003 (first entry)

XX

DE Human microarray DNA oligonucleotide SEQ ID NO 42442.

XX

XX EST; ss; probe; expressed sequence tag; microarray; gene expression;  
KW genetic variation; biallelic marker; polymorphism; human;  
KW cross-species comparison.

XX

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OS Homo sapiens.  
 PN US2003104410-A1.  
 XX  
 XX 05-JUN-2003.  
 XX  
 XX 15-MAR-2002; 2002US-00098263.  
 XX  
 XX 16-MAR-2001; 2001US-0276759P.  
 XX  
 XX (AFFY-) AFFYMETRIX INC.  
 XX  
 XX Mittmann MP;  
 XX  
 XX WPI; 2003-567953/53.  
 XX  
 XX New array of nucleic acid probes, useful for in situ hybridization, in  
 PT Southern, Northern or dot-blot hybridization to identify or detect the  
 PT sequence or specific mutations of any gene.  
 PT  
 PS Claim 1; SEQ ID NO 42442; 9pp; English.  
 XX  
 CC The invention discloses a microarray comprising a plurality of nucleic  
 CC acid probes including one of 2,018,500 fully defined sequences, or its  
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
 CC Also disclosed is a method of gene expression analysis. The array is used  
 CC in monitoring gene expression levels by hybridisation to a DNA library,  
 CC in analysis of genetic variation or in hybridisation of tag-labelled  
 CC compounds. The nucleic acid probes are specifically designed for analysis  
 CC of at least one target sequence. The method of analysis comprises  
 CC hybridising at least one or more nucleic acids to at least two or more  
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
 CC probes are attached to a solid support. The analysis comprises monitoring  
 CC gene expression levels, identifying biallelic markers or polymorphisms,  
 CC or family members of a gene and a cross-species comparison. Each of the  
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-  
 CC blot hybridisation to identify or detect the sequence or specific  
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
 CC primer extensions or in screening cDNA or genomic libraries or subclones  
 CC for additional subclones containing segments of DNA that have been  
 CC isolated and previously sequenced. The sequence presented is one of the  
 CC nucleic acid probes incorporated in the microarray. Note: The sequence  
 CC data for this patent can also be obtained in electronic format directly  
 CC from USPTO at seqdata.uspto.gov/sequence.html  
 XX  
 SQ Sequence 25 BP; 6 A; 8 C; 6 G; 5 T; 0 U; 0 Other;  
 XX  
 Query Match 53.8%; Score 14; DB 9; Length 25;  
 Best Local Similarity 77.3%; Pred. No. 4.5e+03;  
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 2 GTCTTTTCGACAGTCGGTACCTC 23  
 |||||  
 Db 22 GTCTTTTCACAGTCGGGAACCTC 1  
 |||||  
 RESULT 22  
 ACK26781/c  
 ID ACK26781 standard; DNA; 25 BP.  
 XX  
 AC ACK26781;  
 XX  
 XX 14-OCT-2003 (first entry)  
 XX  
 DE Human microarray DNA oligonucleotide SEQ ID NO 126762.  
 XX  
 DE EST; ss; probe; expressed sequence tag; microarray; gene expression;  
 KW genetic variation; biallelic marker; polymorphism; human;  
 KW cross-species comparison.  
 XX  
 XX Homo sapiens.  
 OS  
 XX

PN US2003104410-A1.  
 XX  
 XX 05-JUN-2003.  
 XX  
 XX 15-MAR-2002; 2002US-00098263.  
 XX  
 XX 16-MAR-2001; 2001US-0276759P.  
 XX  
 XX (AFFY-) AFFYMETRIX INC.  
 XX  
 XX Mittmann MP;  
 XX  
 XX WPI; 2003-567953/53.  
 XX  
 XX New array of nucleic acid probes, useful for in situ hybridization, in  
 PT Southern, Northern or dot-blot hybridization to identify or detect the  
 PT sequence or specific mutations of any gene.  
 PT  
 PS Claim 1; SEQ ID NO 126762; 9pp; English.  
 XX  
 CC The invention discloses a microarray comprising a plurality of nucleic  
 CC acid probes including one of 2,018,500 fully defined sequences, or its  
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
 CC Also disclosed is a method of gene expression analysis. The array is used  
 CC in monitoring gene expression levels by hybridisation to a DNA library,  
 CC in analysis of genetic variation or in hybridisation of tag-labelled  
 CC compounds. The nucleic acid probes are specifically designed for analysis  
 CC of at least one target sequence. The method of analysis comprises  
 CC hybridising at least one or more nucleic acids to at least two or more  
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
 CC probes are attached to a solid support. The analysis comprises monitoring  
 CC gene expression levels, identifying biallelic markers or polymorphisms,  
 CC or family members of a gene and a cross-species comparison. Each of the  
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-  
 CC blot hybridisation to identify or detect the sequence or specific  
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
 CC primer extensions or in screening cDNA or genomic libraries or subclones  
 CC for additional subclones containing segments of DNA that have been  
 CC isolated and previously sequenced. The sequence presented is one of the  
 CC nucleic acid probes incorporated in the microarray. Note: The sequence  
 CC data for this patent can also be obtained in electronic format directly  
 CC from USPTO at seqdata.uspto.gov/sequence.html  
 XX  
 SQ Sequence 25 BP; 11 A; 6 C; 5 G; 3 T; 0 U; 0 Other;  
 XX  
 Query Match 53.8%; Score 14; DB 9; Length 25;  
 Best Local Similarity 77.3%; Pred. No. 4.5e+03;  
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 CGTCTTTTCGACAGTCGGTACCT 22  
 |||||  
 Db 23 CGTCTTTTCGACAGTCGGTATCT 2  
 |||||  
 RESULT 23  
 ABQ07185/c  
 ID ABQ07185 standard; DNA; 24 BP.  
 XX  
 AC ABQ07185;  
 XX  
 XX 11-JUN-2002 (first entry)  
 XX  
 DE Oligonucleotide adapter/capture probe 7176.  
 XX  
 DE Oligonucleotide array; adapter sequence; probe; ss.  
 KW  
 XX  
 OS Synthetic.  
 XX  
 PN WO200216649-A2.  
 XX  
 XX 28-FEB-2002.  
 PD  
 XX





Db 26 TTCGACGCTCGTACCT 10

## RESULT 28

ABZ01654

ID ABZ01654 standard; DNA; 50 BP.

XX AC

XX ABZ01654;

XX

DT 09-JAN-2003 (first entry)

XX

DE Human leukocyte gene expression profiling probe SEQ ID NO 1645.

XX

KW T7; leukocyte; gene expression profiling; allograft rejection;  
KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;  
KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;  
KW ss.

XX

OS Homo sapiens.

XX

FN WO200257414-A2.

XX

PD 25-JUL-2002.

XX

PF 22-OCT-2001; 2001WO-US047856.

XX

XX 20-OCT-2000; 2000US-0241994P.

PR

PR 08-JUN-2001; 2001US-0296764P.

XX

FA (BIOC-) BIOTEC INC.

XX

XX Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;

PI Ly N, Woodward R, Quertermous T, Johnson F;

XX

XX WPI; 2002-636525/68.

XX

PT New system for leukocyte expression profiling, diagnosing a disease, or  
PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis  
PT or congestive heart failure, comprises diagnostic oligonucleotides.

XX

PS Claim 1; Page 378; Opp; English.

XX

CC The invention relates to a system for detecting gene expression, which  
CC comprises one or two isolated DNA molecules that detect expression of a  
CC gene, where the gene corresponds to any of 8143 oligonucleotides  
CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful  
CC for leukocyte expression profiling. It is particularly useful for  
CC diagnosing a disease, monitoring (rate of) progression of a disease,  
CC predicting therapeutic outcome, determining prognosis for a patient,  
CC predicting disease complications in an individual or monitoring response  
CC to treatment in an individual. The diseases include cardiac allograft  
CC rejection, kidney allograft rejection, liver allograft rejection,  
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,  
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection

XX

SQ Sequence 50 BP; 15 A; 12 C; 10 G; 13 T; 0 U; 0 Other;

## Query Match

Best Local Similarity 53.1%; Score 13.8; DB 6; Length 50;

Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 GTCTTTTCGACGATCGGTACCTCAAT 26

||||| | |||||

Db 4 GTCTCAAGGTATCGGTACCTCAAT 28

||||| | |||||

## RESULT 29

ACH54506/c

ID ACH54506 standard; DNA; 25 BP.

XX

XX ACH54506;

AC

XX

DT 16-OCT-2003 (first entry)

XX

DE DNA target sequence #3642 useful in array for genetic analyses.

XX

KW Gene expression analysis; array; hybridisation; genetic variation;  
KW tag-labelled compound; gene family; in situ hybridisation;  
KW library screening; Southern hybridisation; northern hybridisation;  
KW dot-blot hybridisation; gene sequence; mutation detection;  
KW target sequence; probe; PCR; primer; ss.

XX

OS Unidentified.

XX

FN US2003082596-A1.

XX

PD 01-MAY-2003.

XX

PF 08-AUG-2002; 2002US-00215112.

XX

PR 08-AUG-2001; 2001US-0311040P.

XX

PA (MITT/) MITTMANN M.

XX

PI Mittmann M;

XX

DR WPI; 2003-576608/54.

XX

PT New probe array useful e.g. for monitoring gene expression levels, for  
PT analyzing genetic variations, or for hybridizing tag-labeled compounds,  
PT comprises multiple nucleic acid probes.

XX

PS Claim 1; SEQ ID NO 3642; 9pp; English.

XX

CC The present invention relates to nucleic acid sequences that are  
CC complementary to particular genes, and can be used as probes for a  
CC variety of analyses such as gene expression analysis. Each probe  
CC comprises 9 or more consecutive nucleotides from at least one of 14936  
CC nucleotide sequences defined in the patent, or their perfect sense match,  
CC sense mismatch, antisense match or antisense mismatch oligonucleotides.  
CC The probes may be used in an array comprising at least 10 distinct  
CC nucleic acid probes. The array is useful in monitoring gene expression  
CC levels by hybridisation to a DNA library, in analysing genetic  
CC variations, and in hybridising tag-labelled compounds. The probes are  
CC useful for identifying family members of a gene. The probes are also  
CC useful in situ hybridisations, in screening cDNA or genomic libraries  
CC (or derived subclones) for additional clones containing segments of DNA  
CC that have been previously isolated and sequenced, in Southern, northern,  
CC or dot-blot hybridisation of genomic DNA to identify or detect the  
CC sequence of any gene or detect specific mutations in any gene, and in  
CC mapping the 5' termini of mRNA molecules by primer extensions. The  
CC nucleic acid sequences of the invention are also useful as PCR primers.  
CC The invention provides a large collection of nucleic acid sequences  
CC complementary to particular genes with a wide range of analytical uses.  
CC ACH50865-ACH5260 represent the target sequences of the invention. Note:  
CC The sequence data for this patent was obtained in electronic format  
CC directly from the USPTO web site at seqdata.uspto.gov/psipdsIDentry.html

XX

SQ Sequence 25 BP; 6 A; 3 C; 8 G; 8 T; 0 U; 0 Other;

## Query Match

Best Local Similarity 52.3%; Score 13.6; DB 9; Length 25;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 TCGCAGATCGGTACCTCAAT 26

||||| | |||||

Db 22 TCACAGACGCTACCTCAAT 3

||||| | |||||

## RESULT 30

AAV74227

ID AAV74227 standard; DNA; 34 BP.

XX

XX AAV74227;

AC

XX

Wed Nov 24 08:46:10 2004

```

DT 20-MAR-2003 (revised)
DT 15-MAR-1999 (first entry)
XX
XX
DE CpG-N motif PCR primer Mu- (4+5)R.
DE
DE CpG-N motif; immunostimulation; antigen; CpG-S motif; immunisation;
KW viral antigen; bacterial antigen; parasite; therapeutic; growth factor;
KW toxins; tumour suppressor; cytokine; apoptotic protein; interferon;
XX hormone; clotting factor; ligand; receptor; PCR primer; ss.
XX
OS Synthetic.
XX
XX WO9852581-A1.
XX
XX
XX 26-NOV-1998.
XX
XX 20-MAY-1998; 98WO-US010408.
XX
XX 20-MAY-1997; 97US-0047209P.
XX
XX 20-MAY-1997; 97US-0047233P.
XX
XX (OTTA-) OTTAWA CIVIC HOSPITAL LOEB RES INST.
XX (IOWA) UNIV IOWA RES FOUND.
XX (QIAG-) QIAGEN GMBH.
XX
XX Davis HL, Krieg AM, Schorr J, Wu T;
XX
XX WPI; 1999-059712/05.
XX
XX Use of neutralising CpG and stimulating CpG motifs in DNA vectors - for
XX enhancing the immunostimulatory effect of an antigen or enhancing the
XX expression of a therapeutic polypeptide.
XX
XX Example 1; Page 58; 109pp; English.
XX
XX AAU74209-V74236 are PCR primers used to describe a method for enhancing
XX the immunostimulatory effect of an antigen encoded by nucleic acid
XX contained in a nucleic acid construct. The method involves determining
XX the CpG-N and CpG-S motifs present in the construct, removing
XX neutralising CpG (CpG-N) motifs and optionally inserting stimulatory CpG
XX (CpG-S) motifs in the construct, thereby producing a nucleic acid
XX construct having enhanced immunostimulatory efficacy. The method can be
XX used for immunisation against viral antigens, e.g. from hepatitis B virus
XX (HBV), bacterial antigens or an antigen derived from a parasite. They can
XX also be used for expression of a therapeutic polypeptide, e.g. growth
XX factors, toxins, tumour suppressors, cytokines, apoptotic proteins,
XX interferons, hormones, clotting factors, ligands and receptors. (Updated
XX on 20-MAR-2003 to correct PA field.)
XX
XX Sequence 34 BP; 9 A; 7 C; 10 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 52.3%; Score 13.6; DB 2; Length 34;
XX Best Local Similarity 80.0%; Pred. No. 7.5e+03;
XX Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 7 TCGCAGATCGGTACCTCAAT 26
XX 10 TCGCAGATCGATACCGGAT 29
XX
XX
XX RESULT 31
XX AAC66050
XX ID AAC66050 standard; DNA; 40 BP.
XX
XX AAC66050;
XX
XX 22-FEB-2001 (first entry)
XX
XX E.coli ygbp primer YGBP2A.
XX
XX YJEE; KDTB; YQGF; YGGF; YHBC; YGBP; YGGB; YCHB; YCHB; reverse transcriptase PCR;
KW infection; primer; ss.
XX

```

```

OS Escherichia coli.
XX
XX DE19916176-A1.
XX
XX 12-OCT-2000.
XX
XX 10-APR-1999; 99DE-01016176.
XX
XX 10-APR-1999; 99DE-01016176.
XX
XX (FARB ) BAYER AG.
XX
XX Broetz H, Ehler K, Freiberg C, Spaltmann F, Wieland B;
XX Labischinski H;
XX
XX WPI; 2000-639611/62.
XX
XX Essential genes from bacteria, useful in screening for antimicrobial
XX agents, and related proteins, transformants and antisense sequences.
XX
XX Example 2; Page 26; 28pp; German.
XX
XX This invention describes novel Escherichia coli genes (I) encoding
XX proteins (II) designated YQGF, YHBC, YGGJ, YGBP, YCHB, YGGB, YJEE and
XX KDTB, and genes (Ia) that encode orthologous gene products (IIa) in other
XX microorganisms and which have antibacterial activity. Recombinant
XX microorganisms in which expression of (I) or (Ia) can be regulated are
XX used to identify compounds that bind to the gene products, particularly
XX in affinity selection assays. (II) and (IIa) are potentially useful as
XX substances that bind to (II) or (IIa) are potentially useful as
XX antibacterials for treating a wide range of infections in humans and
XX animals. Sequences antisense to (I) and (Ia) can also be used as
XX antibacterials. The specified genes are widely distributed in bacteria
XX but have no close homologs in eukaryotic cells
XX
XX Sequence 40 BP; 9 A; 12 C; 10 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 52.3%; Score 13.6; DB 3; Length 40;
XX Best Local Similarity 80.0%; Pred. No. 7.7e+03;
XX Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 5 TTTCGACATCGGTACCTCA 24
XX 9 TTATGTGATCGGTACCTCA 28
XX
XX
XX RESULT 32
XX ADG69940/c
XX ID ADG69940 standard; DNA; 24 BP.
XX
XX AC ADG69940;
XX
XX 11-MAR-2004 (first entry)
XX
XX Mouse interleukin-6, IL-6, RT-PCR primer #1.
XX
XX Mouse; interleukin; IL-6; RT-PCR; primer; PCR; reverse transcriptase PCR;
KW cytokine; wild yam; polysaccharide extract; indigestion; anorexia;
XX diarrhoea; diabetes; vaccine; infection; ss.
XX
XX Mus sp.
XX
XX US2003224066-A1.
XX
XX 04-DEC-2003.
XX
XX 30-MAY-2002; 2002US-00160670.
XX
XX 30-MAY-2002; 2002US-00160670.
XX
XX (WURR/) WU R.
XX

```





PI Sawada M;  
XX WPI; 1998-495834/42.  
XX  
XX Microglia with brain affinity - formulable as drug compositions, useful  
PT as carrier for introduction of gene or drugs for treatment of cerebral  
PT diseases.  
XX  
XX Example 1; Page 11; 36pp; Japanese.  
XX  
XX This is the nucleotide sequence of a PCR primer used for amplification in  
CC the method of the invention. The process involves the use of established  
CC microglia as carriers for introducing gene, drugs as well as other  
CC chemical substances e.g. in drug compositions especially to the brain,  
CC particularly useful in the treatment of cerebral diseases. The microglia  
CC can be stably expressed in a vector and have specific affinity to the  
CC brain  
XX  
XX Sequence 25 BP; 7 A; 6 C; 5 G; 7 T; 0 U; 0 Other;  
SQ  
Query Match 51.5%; Score 13.4; DB 2; Length 25;  
Best Local Similarity 73.9%; Pred. No. 9.1e+03;  
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Qy 2 GTCTTTCGACGATCGGTACTTCA 24  
Db 24 GTCTTTCGACGAGGAGGACTTCA 2  
RESULT 35  
AAD24887/c  
ID AAD24887 standard; DNA; 25 BP.  
XX  
XX AAD24887;  
XX  
XX 12-MAR-2002 (first entry)  
XX  
XX Interleukin-6 (IL-6) cDNA amplifying sense RT-PCR primer.  
XX  
XX Cell death; DNA damage; DNA-dependent protein kinase; DNA-PK; necrosis;  
KW immune response; apoptosis; Alzheimer's disease; Parkinson's disease;  
KW rheumatoid arthritis; inflammation; osteoporosis; myocardial infarction;  
KW liver disease; reperfusion injury; carcinoma; multiple sclerosis; stroke;  
KW amyotrophic lateral sclerosis; Acquired Immune Deficiency Syndrome; AIDS;  
KW head injury damage; aplastic anaemia; tumour; organ transplantation;  
KW cerebral infarction; follicular lymphomas; systemic lupus erythematosus;  
KW viral infection; glomerulonephritis; apoptosis; autoimmune disorder;  
KW sepsis; RT-PCR primer; ss.  
XX  
XX Unidentified.  
XX  
XX WO200185910-A2.  
XX  
XX 15-NOV-2001.  
XX  
XX 04-MAY-2001; 2001WO-US014508.  
XX  
XX 05-MAY-2000; 2000US-0202274P.  
XX  
XX 17-JAN-2001; 2001US-0262321P.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
XX  
XX Raz E, Lois AF, Takabayashi K;  
XX  
XX WPI; 2002-062244/08.  
XX  
XX Modulating cell death or reducing DNA damage in eukaryotic cells, useful  
PT for reducing cell death in individual or organ, comprises contacting cell  
PT with agent modulating biological activity of DNA-dependent protein  
PT kinase.  
XX  
XX Example 1; Page 30; 57pp; English.  
XX

CC The invention relates to a method for modulating cell death or reducing  
CC DNA damage in an eukaryotic cell by contacting the cell with an agent  
CC that modulates the biological activity of DNA-dependent protein kinase  
CC (DNA-PK). The invention also relates nucleic acids which modulate the  
CC immune response binding to Ku antigen, resulting in activation of DNA-PK.  
CC The method is useful for modulating cell death or reducing DNA damage in  
CC an eukaryotic cell, for treating any disorder resulting from a genotoxic  
CC insert to a cell e.g., necrosis, apoptosis. The method is also useful for  
CC treating cell death-related indications such as Alzheimer's disease,  
CC Parkinson's disease, rheumatoid arthritis, septic shock, sepsis, stroke,  
CC central nervous system inflammation, osteoporosis, degenerative liver  
CC disease, cerebellar degeneration, reperfusion injury, multiple sclerosis,  
CC amyotrophic lateral sclerosis, myocardial infarction, head injury damage,  
CC acquired immunodeficiency syndrome (AIDS), aplastic anaemia, cerebral  
CC infarction, bypass heart surgery, organ transplantation. The method is  
CC also useful for treating follicular lymphomas, carcinomas, autoimmune  
CC disorders (systemic lupus erythematosus), hormone dependent tumours,  
CC immune mediated glomerulonephritis, apoptosis and viral infections. The  
CC present sequence is a reverse transcription (RT) PCR primer used for  
CC amplifying interleukin-6 (IL-6) cDNA used in the exemplification of the  
CC invention  
XX  
XX Sequence 25 BP; 7 A; 6 C; 5 G; 7 T; 0 U; 0 Other;  
SQ  
Query Match 51.5%; Score 13.4; DB 6; Length 25;  
Best Local Similarity 73.9%; Pred. No. 9.1e+03;  
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Qy 2 GTCTTTCGACGATCGGTACTTCA 24  
Db 24 GTCTTTCGACGAGGAGGACTTCA 2  
RESULT 36  
ACI80464/c  
ID ACI80464 standard; DNA; 25 BP.  
XX  
XX ACI80464;  
XX  
XX 14-OCT-2003 (first entry)  
XX  
XX Human microarray DNA oligonucleotide SEQ ID NO 80455.  
XX  
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;  
KW genetic variation; biallelic marker; polymorphism; human;  
KW cross-species comparison.  
XX  
XX Homo sapiens.  
XX  
XX US2003104410-A1.  
XX  
XX 05-JUN-2003.  
XX  
XX 15-MAR-2002; 2002US-00098263.  
XX  
XX 16-MAR-2001; 2001US-0276759P.  
XX  
XX (AFFY-) AFFYMETRIX INC.  
XX  
XX Mittmann MP;  
XX  
XX WPI; 2003-567953/53.  
XX  
XX New array of nucleic acid probes, useful for in situ hybridization, in  
PT Southern, Northern or dot-blot hybridization to identify or detect the  
PT sequence or specific mutations of any gene.  
XX  
XX Claim 1; SEQ ID NO 80455; 9pp; English.  
XX  
XX The invention discloses a microarray comprising a plurality of nucleic  
CC acid probes including one of 2,018,500 fully defined sequences, or its  
CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
CC Also disclosed is a method of gene expression analysis. The array is used



CC in monitoring gene expression levels by hybridisation to a DNA library,  
 CC in analysis of genetic variation or in hybridisation of tag-labelled  
 CC compounds. The nucleic acid probes are specifically designed for analysis  
 CC of at least one target sequence. The method of analysis comprises  
 CC hybridising at least one or more nucleic acids to at least two or more  
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
 CC probes are attached to a solid support. The analysis comprises monitoring  
 CC gene expression levels, identifying allelic markers or polymorphisms,  
 CC or family members of a gene and a cross-species comparison. Each of the  
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
 CC probes is useful in in situ hybridisation, in Southern, Northern or dot-  
 CC blot hybridisation to identify or detect the sequence or specific  
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
 CC primer extensions or in screening cDNA or genomic libraries or subclones  
 CC for additional subclones containing segments of DNA that have been  
 CC isolated and previously sequenced. The sequence presented is one of the  
 CC nucleic acid probes incorporated in the microarray. Note: The sequence  
 CC data for this patent can also be obtained in electronic format directly  
 CC from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)  
 XX  
 SQ Sequence 25 BP; 6 A; 7 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 51.5%; Score 13.4; DB 9; Length 25;  
 Best Local Similarity 73.9%; Pred. No. 9.1e+03;  
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 Qy 1 CGTCTTTGCGAGATCGGTACCTC 23  
 ||||| || ||||| |||||  
 Db 23 CGTCTCCAGATCGGTCTCTC 1

RESULT 37  
 AAX24768  
 ID AAX24768 standard; DNA; 30 BP.  
 XX  
 AC AAX24768;  
 XX  
 DT 21-JUN-1999 (first entry)  
 XX  
 DE Human glandular kallikrein hKLK2 gene PCR primer 51.70.2.  
 XX  
 KW Enhancer; glandular kallikrein-1; hGK-1; hKLUK2; human; prostate cancer;  
 KW therapy; PCR; primer; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 FN WO9906576-A1.  
 XX  
 PD 11-FEB-1999.  
 XX  
 PF 04-AUG-1998; 98WO-US016312.  
 XX  
 PR 04-AUG-1997; 97US-0054523P.  
 PR 02-MAR-1998; 98US-0076545P.  
 PR 03-AUG-1998; 98US-00127834.  
 XX  
 PA (CALY-) CALYDON INC.  
 XX  
 PI Yu D, Herdenson DR, Schuur ER;  
 XX  
 DR WPI; 1999-153804/13.  
 XX  
 PT New nucleic acid containing the human glandular kallikrein enhancer -  
 PT providing increased expression of heterologous sequences in prostatic  
 PT cells, and related adenoviral vectors for treating prostatic cancer.  
 XX  
 PS Example 2; Page 77; 179pp; English.  
 XX  
 CC Primer 51.70.2 was used with primer 51.70.1 (see AAX24767) to amplify a  
 CC fragment of the 5' flanking region of the hKLUK2 gene. A series of  
 CC constructs was generated by inserting hKLUK2 5' flanking regions upstream  
 CC of a luciferase reporter gene, and the activity of these fragments was

CC compared with that of CN299, a plasmid with the full hKLUK2 promoter (-607  
 CC to +33) driving expression of luciferase. hKLUK2 gene enhancers were  
 CC identified (see AAX24755) that increase the transcription of cis-linked  
 CC coding sequences in prostate cells. Methods of using DNA constructs  
 CC comprising the enhancers to control transcription of heterologous  
 CC polynucleotides are provided. Adenoviral vectors in which one or more  
 CC genes are under transcriptional control of a hKLUK2 transcription  
 CC regulatory element are claimed, and can be used to confer selective  
 CC cytotoxicity in mammalian cells for use e.g. in the treatment of prostate  
 CC cancer  
 XX  
 SQ Sequence 30 BP; 9 A; 8 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 51.5%; Score 13.4; DB 2; Length 30;  
 Best Local Similarity 93.3%; Pred. No. 9.3e+03;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 12 GATCGGTACCTCAAT 26  
 ||||| ||||| |||||  
 Db 1 GATCGGTACCTCACT 15

RESULT 38  
 AAT73409  
 ID AAT73409 standard; DNA; 31 BP.  
 XX  
 AC AAT73409;  
 XX  
 DT 14-JAN-1998 (first entry)  
 XX  
 DE S182 gene mutation detection intron 2/exon 3 boundary.  
 XX  
 KW S182 gene; Alzheimer's disease; polymorphism; mismatch; mutation;  
 KW intronic sequence; polymerase chain reaction; primer; ss.  
 XX  
 OS Synthetic.

Key	Location/Qualifiers
FT intron	1. .21
FT	/tag= a
FT	/number= 2
FT	/note= "End of intron 2"
FT exon	22. .31
FT	/tag= b
FT	/number= 3
FT	/note= "Start of exon 3"

WO9715689-A1.  
 XX  
 PD 01-MAY-1997.  
 XX  
 PF 25-OCT-1996; 96WO-US017132.  
 XX  
 PR 25-OCT-1995; 95US-0007048P.  
 XX  
 PA (UNIW ) UNIV WASHINGTON SCHOOL MED.  
 PA (USF-) UNIV SOUTH FLORIDA.  
 XX  
 PI Hardy JA, Goate AM;  
 XX  
 DR WPI; 1997-259039/23.  
 XX  
 PT Diagnosing Alzheimer's disease by detecting polymorphism in the S182 gene  
 PT - using mismatch polymerase chain reaction primers derived from intronic  
 PT sequences.  
 XX  
 PS Example 2; Fig 1; 30pp; English.

A method has been developed for the detection of polymorphism (mutations)  
 CC in the S182 gene. The mutations are detected using selected mismatch  
 CC polymerase chain reaction (PCR) primers derived from intronic sequences  
 CC of the gene. The present sequence represents the intron 2/ exon 3  
 CC boundary. Mutations in the S182 gene indicate that a subject is

CC susceptible to late onset Alzheimer's disease. The method allows rapid  
CC analysis of many samples by PCR, restriction enzyme digestion and gel  
CC electrophoresis. Use of intronic sequences allows mutations to be  
CC detected in splice donor and acceptor sites (this would be almost  
CC impossible without intronic primers)

XX Sequence 31 BP; 6 A; 8 C; 3 G; 14 T; 0 U; 0 Other;

Query Match 51.5%; Score 13.4; DB 2; Length 31;  
Best Local Similarity 73.9%; Pred. No. 9.4e+03;  
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 TCTTTCGACGATCGGTACTCAA 25  
Db 7 TCTTTCCTTTCAGACCTCAA 29

RESULT 39

ADB23049

ID ADB23049 standard; DNA; 31 BP.

XX ADB23049;

DT 20-NOV-2003 (first entry)

XX Tobacco methionine synthase oligonucleotide #4.

XX ss; plant; methionine synthase; methionine; seed; transformed plant;

XX transgenic; tobacco.

XX Nicotiana tabacum.

XX US2003088886-A1.

XX 08-MAY-2003.

XX 28-JAN-2002; 2002US-00989339.

XX 30-AUG-1995; 95US-0002973P.

XX 27-AUG-1996; 96US-00703829.

XX 19-AUG-1999; 99US-00377431.

XX (FALC/) FALCO S C.

XX (FAMO/) FAMODU O O.

XX (RAFA/) RAFALSKI J A.

XX (RAMA/) RAMAKER M L.

XX (TARC/) TARCZYNSKI M C.

XX (THOR/) THORPE C.

XX Falco SC, Famodu OO, Rafalski JA, Ramaker ML, Tarczynski MC;

PI Thorpe C;

XX WPI; 2003-657990/62.

XX New nucleic acid fragments encoding a plant 5-methyltetra-

XX hydroxyethylglutamate-homocysteine methyl transferase or methionine

XX synthase, useful for producing increased levels of methionine in the

XX seeds of transformed plants.

XX Example 2; Page 42; 69pp; English.

XX The invention relates to an isolated nucleic acid fragment encoding a

XX plant methionine synthase. The nucleic acid fragments and chimeric genes

XX are useful for producing increased levels of methionine in the seeds of

XX transformed plants. The present sequence represents the amino acid

XX sequence of a plant methionine synthase associated oligonucleotide.

QY 12 GATCGGTACTCAAT 26  
Db 1 GATCGGTACTCACT 15

RESULT 40

AAI64730/c

ID AAI64730 standard; DNA; 32 BP.

XX AAI64730;

XX 07-DEC-2001 (first entry)

XX Human line 1-12 PCR primer 4.

XX Human, line 1-12; cytostatic; virucidal; immunomodulatory;  
XX antiinflammatory; haemostatic; malignant tumour; HIV; infection;  
XX human immunodeficiency virus; immunological disease; PCR primer; ss.

XX Homo sapiens.

XX WO200173068-A1.

XX 04-OCT-2001.

XX 26-MAR-2001; 2001WO-CN000495.

XX 27-MAR-2000; 2000CN-00115143.

XX (SHAN-) SHANGHAI BLOWINDOW GENE DEV INC.

XX Mao Y, Xie Y;

XX WPI; 2001-597126/67.

XX Line 1-12 and encoded polynucleotide, used in diagnosis and treatment of  
XX malignant tumors, hemopathy, human immunodeficiency virus infection,  
XX immunological diseases and inflammation.

XX Example 5; Page 17; 33pp; Chinese.

XX The invention relates to human line 1-12 with cytostatic, virucidal,  
XX immunomodulatory, antiinflammatory and haemostatic activity. The protein  
XX and encoding polynucleotide are used in diagnosis and treatment of  
XX malignant tumour, haemopathy, human immunodeficiency virus (HIV)  
XX infection, immunological diseases and various inflammations. The present  
XX sequence is that of a human line 1-12 PCR primer, useful to the invention

XX Sequence 32 BP; 8 A; 7 C; 9 G; 8 T; 0 U; 0 Other;

Query Match 51.5%; Score 13.4; DB 5; Length 32;

Best Local Similarity 73.9%; Pred. No. 9.4e+03;

Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CGTCTTTCGACGATCGGTACTC 23

Db 26 CTTCTTTTCGCAACCGGGAATTC 4

Search completed: November 23, 2004, 17:29:51  
Job time : 160.543 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:59:48 ; Search time 30.0899 Seconds  
(without alignments)  
614.177 Million cell updates/sec

Title: US-10-087-631B-8

Perfect score: 26

Sequence: 1 cgtcttcgcagatcggtacctcaat 26

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 905748

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents NA.\*

1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*

2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*

3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*

4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*

5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*

6: /cgn2\_6/ptodata/1/ina/backfiles.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	15.2	58.5	44	1	US-08-344-695-5
C 2	14.6	56.2	41	2	US-08-365-486A-4
C 3	14.6	56.2	41	3	US-08-880-342-4
C 4	14	53.8	47	4	US-09-641-638-998
C 5	14	53.8	47	4	US-10-170-097-998
C 6	13.6	52.3	34	3	US-09-082-649B-41
C 7	13.4	51.5	25	4	US-09-180-394-3
C 8	13.4	51.5	31	3	US-08-738-381-24
C 9	13.4	51.5	39	3	US-08-845-546-22
C 10	13.2	50.8	32	4	US-09-714-550-6
C 11	13	50.0	30	4	US-09-553-867A-31
C 12	13	50.0	50	1	US-08-171-389-583
C 13	13	50.0	50	1	US-08-123-916-583
C 14	13	50.0	50	2	US-08-475-228A-583
C 15	13	50.0	50	3	US-08-482-080A-583
C 16	13	50.0	50	3	US-09-354-947-583
C 17	13	50.0	50	5	PCT-US93-12388-583
C 18	12.8	49.2	38	1	US-08-485-971-12
C 19	12.8	49.2	38	1	US-08-275-876-12
C 20	12.8	49.2	38	1	US-08-383-754-12
C 21	12.8	49.2	38	1	US-08-485-978-12
C 22	12.8	49.2	38	2	US-08-486-814-12
C 23	12.8	49.2	38	2	US-08-487-472-12
C 24	12.8	49.2	38	3	US-08-485-740-12
C 25	12.8	49.2	38	3	US-09-162-184-12
C 26	12.8	49.2	38	3	US-09-161-902-12
C 27	12.8	49.2	38	3	US-09-489-777A-12

C 28	12.8	49.2	38	5	PCT-US95-08179-12	Sequence 12, Appl
C 29	12.6	48.5	26	4	US-09-976-667-15	Sequence 15, Appl
C 30	12.6	48.5	26	6	RE34606-8	Patent No. RE34,60
C 31	12.4	47.7	28	3	US-09-672-810-15	Sequence 15, Appl
C 32	12.4	47.7	35	3	US-09-455-960-28	Sequence 28, Appl
C 33	12.4	47.7	35	4	US-10-051-325-28	Sequence 28, Appl
C 34	12.4	47.7	37	4	US-08-641-294-4	Sequence 4, Appl
C 35	12.4	47.7	40	6	525658-14	Patent No. 525658
C 36	12.4	47.7	42	3	US-08-879-565-6	Sequence 6, Appl
C 37	12.4	47.7	45	3	US-09-217-228-4	Sequence 4, Appl
C 38	12.2	46.9	18	1	US-08-363-240A-1102	Sequence 1102, Ap
C 39	12.2	46.9	24	3	US-09-165-934-2	Sequence 2, Appli
C 40	12.2	46.9	24	4	US-09-343-494-5	Sequence 5, Appli
C 41	12.2	46.9	31	4	US-09-831-642-59	Sequence 69, Appl
C 42	12.2	46.9	33	4	US-09-828-310-23	Sequence 23, Appl
C 43	12.2	46.9	33	4	US-09-828-310-37	Sequence 37, Appl
C 44	12.2	46.9	33	4	US-09-828-310-44	Sequence 44, Appl
C 45	12.2	46.9	36	4	US-09-173-053-15	Sequence 15, Appl
C 46	12.2	46.9	36	4	US-09-331-793-15	Sequence 15, Appl
C 47	12.2	46.9	38	6	RE34606-9	Patent No. RE34,60
C 48	12.2	46.9	43	3	US-09-351-814-18	Sequence 18, Appl
C 49	12.2	46.9	48	2	US-08-924-695A-27	Sequence 27, Appl
C 50	12	46.2	20	4	US-09-198-452A-4650	Sequence 4650, Ap
C 51	12	46.2	21	1	US-08-171-718-92	Sequence 92, Appl
C 52	12	46.2	21	3	US-08-478-087-32	Sequence 92, Appl
C 53	12	46.2	21	3	US-08-998-416-9	Sequence 9, Appl
C 54	12	46.2	21	3	US-09-415-522-16	Sequence 16, Appl
C 55	12	46.2	21	3	US-09-588-256-14	Sequence 14, Appl
C 56	12	46.2	21	3	US-09-625-188-24	Sequence 24, Appl
C 57	12	46.2	32	4	US-09-527-522-11	Sequence 11, Appl
C 58	12	46.2	32	4	US-10-067-231-11	Sequence 11, Appl
C 59	12	46.2	36	1	US-08-478-039-46	Sequence 46, Appl
C 60	12	46.2	36	1	US-08-476-349A-46	Sequence 46, Appl
C 61	12	46.2	36	3	US-08-523-894-39	Sequence 39, Appl
C 62	12	46.2	38	1	US-08-338-992B-12	Sequence 12, Appl
C 63	12	46.2	38	3	US-09-010-733-12	Sequence 12, Appl
C 64	12	46.2	38	4	US-09-340-798A-46	Sequence 46, Appl
C 65	12	46.2	38	5	PCT-US95-09057-12	Sequence 12, Appl
C 66	12	46.2	43	1	US-08-629-600-18	Sequence 18, Appl
C 67	12	46.2	43	3	US-08-973-131-28	Sequence 28, Appl
C 68	12	46.2	50	4	US-09-863-859-19	Sequence 19, Appl
C 69	11.8	45.4	24	4	US-09-336-946B-67	Sequence 67, Appl
C 70	11.8	45.4	24	4	US-09-362-842-30	Sequence 30, Appl
C 71	11.8	45.4	24	4	US-09-993-170-27	Sequence 27, Appl
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C 73	11.8	45.4	25	3	US-08-729-601A-62	Sequence 62, Appl
C 74	11.8	45.4	25	3	US-09-097-319A-42	Sequence 42, Appl
C 75	11.8	45.4	25	4	US-09-643-971-42	Sequence 42, Appl
C 76	11.8	45.4	27	4	US-09-643-971-42	Sequence 28, Appl
C 77	11.8	45.4	30	4	US-08-693-234-3	Sequence 3, Appli
C 78	11.8	45.4	30	4	US-08-693-234-3	Sequence 4, Appli
C 79	11.8	45.4	31	3	US-08-679-645-417	Sequence 417, App
C 80	11.8	45.4	32	1	US-07-936-163-26	Sequence 26, Appl
C 81	11.8	45.4	32	3	US-08-729-601A-65	Sequence 65, Appl
C 82	11.8	45.4	32	3	US-09-355-434-16	Sequence 16, Appl
C 83	11.8	45.4	32	3	US-09-097-319A-45	Sequence 45, Appl
C 84	11.8	45.4	32	4	US-09-371-772B-14224	Sequence 14224, A
C 85	11.8	45.4	32	4	US-09-643-971-45	Sequence 45, Appl
C 86	11.8	45.4	34	1	US-08-181-271A-58	Sequence 58, Appl
C 87	11.8	45.4	34	1	US-08-449-315-58	Sequence 58, Appl
C 88	11.8	45.4	34	1	US-08-444-803-58	Sequence 58, Appl
C 89	11.8	45.4	34	1	US-08-449-043-58	Sequence 58, Appl
C 90	11.8	45.4	34	1	US-08-456-265A-58	Sequence 58, Appl
C 91	11.8	45.4	34	1	US-08-456-265A-58	Sequence 58, Appl
C 92	11.8	45.4	34	1	US-08-455-244-58	Sequence 58, Appl
C 93	11.8	45.4	34	1	US-08-454-876-58	Sequence 58, Appl
C 94	11.8	45.4	34	2	US-08-457-364-58	Sequence 58, Appl
C 95	11.8	45.4	34	2	US-08-456-262-58	Sequence 58, Appl
C 96	11.8	45.4	34	2	US-08-456-240-58	Sequence 58, Appl
C 97	11.8	45.4	34	2	US-08-455-736-58	Sequence 58, Appl
C 98	11.8	45.4	34	2	US-08-971-217-58	Sequence 58, Appl
C 99	11.8	45.4	34	3	US-09-350-600-58	Sequence 58, Appl
C 100	11.8	45.4	34	4	US-09-906-234-58	Sequence 58, Appl

us-10-087-631b-8.max.rn1

Wed Nov 24 08:46:10 2004

C 101	11.8	45.4	36	1	US-08-066-961-38	Sequence 38, Appl	C 174	11.6	44.6	36	3	US-09-129-740-4	Sequence 4, Appl
C 102	11.8	45.4	36	1	US-08-375-134-4	Sequence 4, Appl	C 175	11.6	44.6	36	3	US-09-568-527-4	Sequence 4, Appl
C 103	11.8	45.4	36	5	PCT-US95-15263-4	Sequence 4, Appl	C 176	11.6	44.6	36	3	US-08-974-549A-498	Sequence 498, Appl
C 104	11.8	45.4	37	3	US-09-424-120-1	Sequence 1, Appl	C 177	11.6	44.6	39	3	US-08-974-549A-500	Sequence 500, Appl
C 105	11.8	45.4	37	3	US-09-424-120-3	Sequence 3, Appl	C 178	11.6	44.6	39	3	US-08-974-549A-502	Sequence 502, Appl
C 106	11.8	45.4	38	1	US-08-181-271A-57	Sequence 57, Appl	C 179	11.6	44.6	39	3	US-08-974-549A-504	Sequence 504, Appl
C 107	11.8	45.4	38	1	US-08-449-315-57	Sequence 57, Appl	C 180	11.6	44.6	39	4	US-08-912-951-265	Sequence 265, Appl
C 108	11.8	45.4	38	1	US-08-449-043-57	Sequence 57, Appl	C 181	11.6	44.6	39	4	US-08-912-951-267	Sequence 267, Appl
C 109	11.8	45.4	38	1	US-08-449-043-57	Sequence 57, Appl	C 182	11.6	44.6	39	4	US-08-912-951-269	Sequence 269, Appl
C 110	11.8	45.4	38	1	US-08-456-265A-57	Sequence 57, Appl	C 183	11.6	44.6	39	4	US-08-912-951-271	Sequence 271, Appl
C 111	11.8	45.4	38	1	US-08-455-244-57	Sequence 57, Appl	C 184	11.6	44.6	39	4	US-09-402-181B-498	Sequence 498, Appl
C 112	11.8	45.4	38	1	US-08-455-244-57	Sequence 57, Appl	C 185	11.6	44.6	39	4	US-09-402-181B-500	Sequence 500, Appl
C 113	11.8	45.4	38	1	US-08-454-876-57	Sequence 57, Appl	C 186	11.6	44.6	39	4	US-09-402-181B-502	Sequence 502, Appl
C 114	11.8	45.4	38	1	US-08-457-364-57	Sequence 57, Appl	C 187	11.6	44.6	39	4	US-09-402-181B-504	Sequence 504, Appl
C 115	11.8	45.4	38	2	US-08-456-262-57	Sequence 57, Appl	C 188	11.6	44.6	39	4	US-09-721-456-498	Sequence 498, Appl
C 116	11.8	45.4	38	2	US-08-456-262-57	Sequence 57, Appl	C 189	11.6	44.6	39	4	US-09-721-456-500	Sequence 500, Appl
C 117	11.8	45.4	38	2	US-08-455-735-57	Sequence 57, Appl	C 190	11.6	44.6	39	4	US-09-721-456-502	Sequence 502, Appl
C 118	11.8	45.4	38	2	US-08-571-217-57	Sequence 57, Appl	C 191	11.6	44.6	39	4	US-09-721-456-504	Sequence 504, Appl
C 119	11.8	45.4	38	2	US-09-350-600-57	Sequence 57, Appl	C 192	11.6	44.6	41	1	US-08-664-449-26	Sequence 26, Appl
C 120	11.8	45.4	38	4	US-09-906-234-57	Sequence 57, Appl	C 193	11.6	44.6	41	1	US-08-664-449-27	Sequence 27, Appl
C 121	11.8	45.4	40	3	US-09-485-737B-6	Sequence 6, Appl	C 194	11.6	44.6	42	4	US-09-622-951-6	Sequence 6, Appl
C 122	11.8	45.4	44	4	US-08-823-823-31	Sequence 31, Appl	C 195	11.6	44.6	44	4	US-08-109-037-30	Sequence 30, Appl
C 123	11.8	45.4	45	1	US-08-447-169A-229	Sequence 229, Appl	C 196	11.6	44.6	44	3	US-08-109-037-118	Sequence 118, Appl
C 124	11.8	45.4	45	1	US-09-860-474-229	Sequence 229, Appl	C 197	11.6	44.6	44	3	US-08-109-037-119	Sequence 119, Appl
C 125	11.8	45.4	47	4	US-09-422-978-162	Sequence 162, Appl	C 198	11.6	44.6	44	3	US-08-109-037-120	Sequence 120, Appl
C 126	11.8	45.4	49	1	US-08-384-708A-114	Sequence 114, Appl	C 199	11.6	44.6	46	1	US-08-171-389-17	Sequence 17, Appl
C 127	11.8	45.4	49	3	US-08-687-421-114	Sequence 114, Appl	C 200	11.6	44.6	46	1	US-08-123-936-17	Sequence 17, Appl
C 128	11.8	45.4	49	3	US-08-442-423-114	Sequence 114, Appl	C 201	11.6	44.6	46	2	US-08-475-228A-17	Sequence 17, Appl
C 129	11.8	45.4	50	1	US-08-207-901-26	Sequence 112, Appl	C 202	11.6	44.6	46	3	US-08-482-080A-17	Sequence 17, Appl
C 130	11.8	45.4	50	3	US-08-687-421-112	Sequence 112, Appl	C 203	11.6	44.6	46	5	US-09-354-947-17	Sequence 17, Appl
C 131	11.8	45.4	50	3	US-08-563-524A-13	Sequence 13, Appl	C 204	11.6	44.6	47	4	PCT-US93-12388-17	Sequence 2653, Appl
C 132	11.8	45.4	50	3	US-08-563-524A-13	Sequence 13, Appl	C 205	11.6	44.6	48	1	US-09-422-978-2653	Sequence 32, Appl
C 133	11.8	45.4	50	3	US-08-563-524A-14	Sequence 14, Appl	C 206	11.6	44.6	48	1	US-08-664-449-32	Sequence 3342, Appl
C 134	11.8	45.4	50	3	US-08-563-524A-15	Sequence 15, Appl	C 207	11.6	44.6	48	1	US-09-198-4459-26	Sequence 1, Appl
C 135	11.8	45.4	50	3	US-08-563-524A-16	Sequence 16, Appl	C 208	11.4	43.8	21	1	US-07-908-679-1	Sequence 26, Appl
C 136	11.8	45.4	50	3	US-08-563-524A-17	Sequence 17, Appl	C 209	11.4	43.8	21	4	US-09-393-858-26	Sequence 26, Appl
C 137	11.8	45.4	50	3	US-08-563-524A-18	Sequence 18, Appl	C 210	11.4	43.8	21	5	US-10-190-279-26	Sequence 1, Appl
C 138	11.8	45.4	50	3	US-08-563-524A-19	Sequence 19, Appl	C 211	11.4	43.8	21	5	PCT-US92-09475-1	Sequence 334, Appl
C 139	11.8	45.4	50	3	US-08-563-524A-19	Sequence 19, Appl	C 212	11.4	43.8	23	4	US-09-216-393B-334	Sequence 422, Appl
C 140	11.6	44.6	50	4	US-08-442-423-112	Sequence 112, Appl	C 213	11.4	43.8	27	1	US-08-758-306-422	Sequence 9, Appl
C 141	11.6	44.6	20	4	US-09-198-452A-2900	Sequence 2900, Appl	C 214	11.4	43.8	28	2	US-09-075-395-9	Sequence 10, Appl
C 142	11.6	44.6	20	4	US-09-112-580-104	Sequence 104, Appl	C 215	11.4	43.8	28	2	US-09-075-395-10	Sequence 24, Appl
C 143	11.6	44.6	24	4	US-09-522-433B-2	Sequence 2, Appl	C 216	11.4	43.8	29	4	US-09-645-593-24	Sequence 28, Appl
C 144	11.6	44.6	29	3	US-09-485-737B-82	Sequence 82, Appl	C 217	11.4	43.8	30	3	US-09-540-014-22	Sequence 47, Appl
C 145	11.6	44.6	30	2	US-08-421-155-7	Sequence 7, Appl	C 218	11.4	43.8	30	3	US-09-540-014-47	Sequence 4, Appl
C 146	11.6	44.6	30	2	US-08-001-157-7	Sequence 12, Appl	C 219	11.4	43.8	31	2	US-08-187-186A-4	Sequence 4, Appl
C 147	11.6	44.6	31	3	US-08-294-386C-12	Sequence 12, Appl	C 220	11.4	43.8	31	2	US-08-442-497C-4	Sequence 4, Appl
C 148	11.6	44.6	31	3	US-08-679-645-496	Sequence 496, Appl	C 221	11.4	43.8	31	4	US-09-333-033-4	Sequence 4, Appl
C 149	11.6	44.6	31	4	US-09-302-357-8	Sequence 8, Appl	C 222	11.4	43.8	32	4	US-10-004-832-4	Sequence 2, Appl
C 150	11.6	44.6	31	5	PCT-US95-10224-12	Sequence 12, Appl	C 223	11.4	43.8	32	4	US-08-744-685-2	Sequence 2, Appl
C 151	11.6	44.6	32	1	US-08-181-271A-60	Sequence 60, Appl	C 224	11.4	43.8	33	4	US-09-970-266-2	Sequence 33, Appl
C 152	11.6	44.6	32	1	US-08-449-315-60	Sequence 60, Appl	C 225	11.4	43.8	33	3	US-09-029-267-33	Sequence 35, Appl
C 153	11.6	44.6	32	1	US-08-449-315-60	Sequence 60, Appl	C 226	11.4	43.8	33	3	US-09-029-267-35	Sequence 50, Appl
C 154	11.6	44.6	32	1	US-08-444-803-60	Sequence 60, Appl	C 227	11.4	43.8	33	3	US-08-169-715-50	Sequence 3, Appl
C 155	11.6	44.6	32	1	US-08-449-043-60	Sequence 60, Appl	C 228	11.4	43.8	33	5	PCT-US92-01358-3	Sequence 4, Appl
C 156	11.6	44.6	32	1	US-08-456-265A-60	Sequence 60, Appl	C 229	11.4	43.8	34	4	US-09-862-847-4	Sequence 10, Appl
C 157	11.6	44.6	32	1	US-08-455-416-60	Sequence 60, Appl	C 230	11.4	43.8	35	3	US-09-178-089-10	Sequence 7, Appl
C 158	11.6	44.6	32	1	US-08-455-416-60	Sequence 60, Appl	C 231	11.4	43.8	35	3	US-09-194-613-7	Sequence 11, Appl
C 159	11.6	44.6	32	1	US-08-454-876-60	Sequence 60, Appl	C 232	11.4	43.8	35	3	US-09-252-586-11	Sequence 11, Appl
C 160	11.6	44.6	32	2	US-08-456-262-60	Sequence 60, Appl	C 233	11.4	43.8	35	4	US-09-142-027A-1	Sequence 4, Appl
C 161	11.6	44.6	32	2	US-08-456-240-60	Sequence 60, Appl	C 234	11.4	43.8	37	4	US-09-463-402-4	Sequence 4, Appl
C 162	11.6	44.6	32	2	US-08-455-736-60	Sequence 60, Appl	C 235	11.4	43.8	37	4	US-09-117-447-4	Sequence 2, Appl
C 163	11.6	44.6	32	2	US-08-455-736-60	Sequence 60, Appl	C 236	11.4	43.8	38	4	US-09-529-239D-41	Sequence 28, Appl
C 164	11.6	44.6	32	2	US-09-350-600-60	Sequence 60, Appl	C 237	11.4	43.8	38	5	PCT-US96-03916-28	Sequence 14, Appl
C 165	11.6	44.6	32	4	US-09-906-234-60	Sequence 60, Appl	C 238	11.4	43.8	44	3	US-08-318-794-14	Sequence 1086, Appl
C 166	11.6	44.6	33	3	US-09-129-740-1	Sequence 1, Appl	C 239	11.4	43.8	47	4	US-08-470-106-14	Sequence 1052, Appl
C 167	11.6	44.6	33	3	US-09-568-527-1	Sequence 1, Appl	C 240	11.4	43.8	47	4	US-09-422-978-1052	Sequence 1086, Appl
C 168	11.6	44.6	33	3	US-08-294-386C-13	Sequence 13, Appl	C 241	11.4	43.8	47	4	US-10-170-097-1086	Sequence 25, Appl
C 169	11.6	44.6	35	1	US-07-814-220-37	Sequence 37, Appl	C 242	11.4	43.8	47	4	US-09-007-005-25	Sequence 25, Appl
C 170	11.6	44.6	35	2	US-07-812-421-37	Sequence 37, Appl	C 243	11.4	43.8	49	3	US-09-244-794A-25	Sequence 25, Appl
C 171	11.6	44.6	35	2	US-09-353-242A-13	Sequence 13, Appl	C 244	11.4	43.8	49	3	US-09-244-796-25	Sequence 25, Appl
C 172	11.6	44.6	35	5	PCT-US95-10224-13	Sequence 13, Appl	C 245	11.4	43.8	49	3	US-09-238-710-25	Sequence 25, Appl
C 173	11.6	44.6	35	5			C 246	11.4	43.8	49	4		

c 247	11.4	43.8	50	3	US-09-315-886C-14	Sequence 14, Appl	c 320	11.2	43.1	40	2	US-08-425-684-6	Sequence 6, Appl
c 248	11.2	43.1	18	3	US-09-071-433-32	Sequence 32, Appl	c 321	11.2	43.1	40	2	US-08-425-684-55	Sequence 55, Appl
c 249	11.2	43.1	19	4	US-09-696-791-238	Sequence 238, Appl	c 322	11.2	43.1	40	2	US-08-675-502-6	Sequence 6, Appl
c 250	11.2	43.1	20	1	US-08-146-422-10	Sequence 10, Appl	c 323	11.2	43.1	40	2	US-08-675-502-55	Sequence 55, Appl
c 251	11.2	43.1	20	1	US-08-146-424-10	Sequence 10, Appl	c 324	11.2	43.1	40	2	US-09-245-802-6	Sequence 6, Appl
c 252	11.2	43.1	20	1	US-08-626-554-26	Sequence 26, Appl	c 325	11.2	43.1	40	4	US-09-245-802-55	Sequence 55, Appl
c 253	11.2	43.1	20	1	US-08-693-709-34	Sequence 34, Appl	c 326	11.2	43.1	42	3	US-09-248-574A-2	Sequence 2, Appl
c 254	11.2	43.1	20	3	US-09-339-757-33	Sequence 33, Appl	c 327	11.2	43.1	42	4	US-09-248-574A-2	Sequence 2, Appl
c 255	11.2	43.1	20	4	US-09-198-452A-2584	Sequence 2584, Ap	c 328	11.2	43.1	42	4	US-09-503-632-2	Sequence 2, Appl
c 256	11.2	43.1	20	4	US-09-198-452A-6523	Sequence 6523, Ap	c 329	11.2	43.1	42	4	US-09-503-632-2	Sequence 2, Appl
c 257	11.2	43.1	24	2	US-08-948-717A-2	Sequence 2, Appl	c 330	11.2	43.1	43	1	US-08-316-293-43	Sequence 43, Appl
c 258	11.2	43.1	26	3	US-09-202-712-26	Sequence 26, Appl	c 331	11.2	43.1	47	2	US-08-422-333-5	Sequence 5, Appl
c 259	11.2	43.1	28	1	US-07-988-194A-17	Sequence 17, Appl	c 332	11.2	43.1	47	2	US-08-422-333-6	Sequence 6, Appl
c 260	11.2	43.1	28	1	US-08-258-152-19	Sequence 19, Appl	c 333	11.2	43.1	47	4	US-09-478-189-179	Sequence 179, App
c 261	11.2	43.1	28	1	US-08-076-299A-19	Sequence 19, Appl	c 334	11.2	43.1	47	4	US-09-422-978-65	Sequence 65, Appl
c 262	11.2	43.1	28	2	US-08-438-582-19	Sequence 19, Appl	c 335	11.2	43.1	47	4	US-09-422-978-1443	Sequence 1443, Ap
c 263	11.2	43.1	28	2	US-09-035-593-8	Sequence 8, Appl	c 336	11.2	43.1	49	2	US-08-392-771-3	Sequence 3, Appl
c 264	11.2	43.1	28	2	US-08-859-998-1149	Sequence 1149, Ap	c 337	11.2	43.1	50	2	US-08-583-276-3	Sequence 3, Appl
c 265	11.2	43.1	28	3	US-08-266-596-19	Sequence 19, Appl	c 338	11.2	43.1	50	3	US-08-985-162-1696	Sequence 1696, Ap
c 266	11.2	43.1	28	3	US-08-479-737-17	Sequence 17, Appl	c 339	11.2	43.1	50	4	US-08-956-171B-2020	Sequence 2020, Ap
c 267	11.2	43.1	28	3	US-09-225-928-1149	Sequence 1149, Ap	c 340	11.2	43.1	50	4	US-09-401-063-1696	Sequence 1696, Ap
c 268	11.2	43.1	28	4	US-08-475-442A-17	Sequence 17, Appl	c 341	11.2	43.1	50	4	US-08-781-986A-2020	Sequence 2020, Ap
c 269	11.2	43.1	28	4	US-09-225-201B-1149	Sequence 1149, Ap	c 342	11.2	42.3	20	4	US-09-331-359-6	Sequence 6, Appl
c 270	11.2	43.1	28	4	US-09-944-411-19	Sequence 19, Appl	c 343	11.2	42.3	21	1	US-09-198-452A-4777	Sequence 4777, Ap
c 271	11.2	43.1	28	4	US-08-608-958-26	Sequence 26, Appl	c 344	11.2	42.3	21	1	US-07-747-785-2	Sequence 2, Appl
c 272	11.2	43.1	28	4	US-09-608-958-32	Sequence 32, Appl	c 345	11.2	42.3	21	3	US-09-195-817-3	Sequence 3, Appl
c 273	11.2	43.1	28	4	US-08-608-958-33	Sequence 33, Appl	c 346	11.2	42.3	21	4	US-09-379-615-3	Sequence 3, Appl
c 274	11.2	43.1	29	2	US-07-814-220-38	Sequence 38, Appl	c 347	11.2	42.3	24	1	US-08-361-920-80	Sequence 80, Appl
c 275	11.2	43.1	29	2	US-07-812-421-38	Sequence 38, Appl	c 348	11.2	42.3	24	1	US-08-479-939-80	Sequence 80, Appl
c 276	11.2	43.1	29	3	US-09-189-462-43	Sequence 43, Appl	c 349	11.2	42.3	24	1	US-08-483-432-80	Sequence 80, Appl
c 277	11.2	43.1	29	4	US-08-863-040-43	Sequence 43, Appl	c 350	11.2	42.3	24	4	US-09-687-538B-17	Sequence 17, Appl
c 278	11.2	43.1	31	3	US-09-023-221A-13	Sequence 13, Appl	c 351	11.2	42.3	25	3	US-10-309-437-17	Sequence 17, Appl
c 279	11.2	43.1	31	3	US-08-282-352A-13	Sequence 13, Appl	c 352	11.2	42.3	25	3	US-08-544-381B-99	Sequence 99, Appl
c 280	11.2	43.1	31	3	US-08-679-645-284	Sequence 284, Ap	c 353	11.2	42.3	25	3	US-09-014-065-11	Sequence 11, Appl
c 281	11.2	43.1	32	3	US-08-931-952-7	Sequence 7, Appl	c 354	11.2	42.3	25	4	US-09-495-406-27	Sequence 27, Appl
c 282	11.2	43.1	32	3	US-08-272-247-7	Sequence 7, Appl	c 355	11.2	42.3	25	4	US-09-816-028A-41	Sequence 41, Appl
c 283	11.2	43.1	32	5	PCT-US95-08560-7	Sequence 7, Appl	c 356	11.2	42.3	26	3	US-10-303-162-41	Sequence 41, Appl
c 284	11.2	43.1	34	3	US-08-711-218-10	Sequence 10, Appl	c 357	11.2	42.3	26	3	US-09-005-298-40	Sequence 40, Appl
c 285	11.2	43.1	34	3	US-09-485-737B-95	Sequence 95, Appl	c 358	11.2	42.3	26	4	US-08-768-619-40	Sequence 40, Appl
c 286	11.2	43.1	34	4	US-09-479-479-18	Sequence 18, Appl	c 359	11.2	42.3	27	2	US-08-892-880-8	Sequence 8, Appl
c 287	11.2	43.1	34	4	US-09-297-851-18	Sequence 18, Appl	c 360	11.2	42.3	27	3	US-09-314-847A-13	Sequence 13, Appl
c 288	11.2	43.1	35	3	US-08-133-321-12	Sequence 12, Appl	c 361	11.2	42.3	27	4	US-10-037-677A-15	Sequence 15, Appl
c 289	11.2	43.1	36	4	US-09-545-814-38	Sequence 38, Appl	c 362	11.2	42.3	28	1	US-08-601-435-5	Sequence 5, Appl
c 290	11.2	43.1	37	3	US-09-035-665-1	Sequence 1, Appl	c 363	11.2	42.3	28	2	US-08-930-274-13	Sequence 13, Appl
c 291	11.2	43.1	38	1	US-08-485-971-15	Sequence 15, Appl	c 364	11.2	42.3	28	2	US-08-930-274-14	Sequence 14, Appl
c 292	11.2	43.1	38	1	US-08-485-971-15	Sequence 15, Appl	c 365	11.2	42.3	28	2	US-08-931-047-5	Sequence 5, Appl
c 293	11.2	43.1	38	1	US-08-275-876-14	Sequence 14, Appl	c 366	11.2	42.3	28	2	US-08-783-202-5	Sequence 5, Appl
c 294	11.2	43.1	38	1	US-08-275-876-15	Sequence 15, Appl	c 367	11.2	42.3	28	3	US-09-165-827C-4	Sequence 4, Appl
c 295	11.2	43.1	38	1	US-08-383-754-15	Sequence 15, Appl	c 368	11.2	42.3	29	2	US-09-165-827C-8	Sequence 8, Appl
c 296	11.2	43.1	38	1	US-08-485-978-14	Sequence 14, Appl	c 369	11.2	42.3	29	4	US-08-892-880-10	Sequence 10, Appl
c 297	11.2	43.1	38	1	US-08-485-978-15	Sequence 15, Appl	c 370	11.2	42.3	29	5	PCT-US93-05240-1	Sequence 9, Appl
c 298	11.2	43.1	38	1	US-08-485-978-15	Sequence 15, Appl	c 371	11.2	42.3	29	5	PCT-US93-05240-1	Sequence 9, Appl
c 299	11.2	43.1	38	2	US-08-486-814-14	Sequence 14, Appl	c 372	11.2	42.3	30	4	US-08-896-537A-10	Sequence 10, Appl
c 300	11.2	43.1	38	2	US-08-486-814-15	Sequence 15, Appl	c 373	11.2	42.3	30	4	US-09-912-935-45	Sequence 45, Appl
c 301	11.2	43.1	38	2	US-08-432-871C-10	Sequence 10, Appl	c 374	11.2	42.3	31	1	US-08-466-033-150	Sequence 150, App
c 302	11.2	43.1	38	2	US-08-487-472-14	Sequence 14, Appl	c 375	11.2	42.3	31	1	US-08-444-733-150	Sequence 150, App
c 303	11.2	43.1	38	2	US-08-487-472-15	Sequence 15, Appl	c 376	11.2	42.3	31	2	US-08-464-134-150	Sequence 150, App
c 304	11.2	43.1	38	3	US-08-485-740-14	Sequence 14, Appl	c 377	11.2	42.3	31	2	US-08-461-361-150	Sequence 150, App
c 305	11.2	43.1	38	3	US-08-485-740-15	Sequence 15, Appl	c 378	11.2	42.3	31	2	US-08-485-910-150	Sequence 150, App
c 306	11.2	43.1	38	3	US-09-162-184-14	Sequence 14, Appl	c 379	11.2	42.3	31	2	US-09-018-576-8	Sequence 8, Appl
c 307	11.2	43.1	38	3	US-09-162-184-15	Sequence 15, Appl	c 380	11.2	42.3	31	2	US-09-018-576-9	Sequence 9, Appl
c 308	11.2	43.1	38	3	US-09-161-902-14	Sequence 14, Appl	c 381	11.2	42.3	31	3	US-09-248-137-8	Sequence 8, Appl
c 309	11.2	43.1	38	3	US-09-161-902-15	Sequence 15, Appl	c 382	11.2	42.3	31	3	US-09-248-137-9	Sequence 9, Appl
c 310	11.2	43.1	38	3	US-09-489-777A-14	Sequence 14, Appl	c 383	11.2	42.3	33	1	US-08-173-510B-52	Sequence 52, Appl
c 311	11.2	43.1	38	3	US-09-489-777A-15	Sequence 15, Appl	c 384	11.2	42.3	33	2	US-08-458-218-52	Sequence 52, Appl
c 312	11.2	43.1	38	4	US-09-270-956-10	Sequence 10, Appl	c 385	11.2	42.3	33	2	US-08-450-497-52	Sequence 52, Appl
c 313	11.2	43.1	38	5	PCT-US95-08179-14	Sequence 14, Appl	c 386	11.2	42.3	34	1	US-07-931-473B-324	Sequence 324, App
c 314	11.2	43.1	39	3	US-09-485-740-15	Sequence 15, Appl	c 387	11.2	42.3	34	1	US-07-714-131C-324	Sequence 324, App
c 315	11.2	43.1	39	3	US-08-445-463B-84	Sequence 84, Appl	c 388	11.2	42.3	34	1	US-08-412-110-324	Sequence 324, App
c 316	11.2	43.1	39	3	US-08-445-464C-84	Sequence 84, Appl	c 389	11.2	42.3	34	1	US-08-409-442A-324	Sequence 324, App
c 317	11.2	43.1	39	4	US-09-402-631A-31	Sequence 31, Appl	c 390	11.2	42.3	34	2	US-08-469-609A-324	Sequence 324, App
c 318	11.2	43.1	39	4	US-08-044-857D-84	Sequence 84, Appl	c 391	11.2	42.3	34	2	US-08-821-782-16	Sequence 16, Appl
c 319	11.2	43.1	39	5	PCT-US94-03437-84	Sequence 84, Appl	c 392	11.2	42.3	34	3	US-09-143-190-324	Sequence 324, App
												US-09-292-435A-16	Sequence 16, Appl

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393	11	42.3	34	3	US-09-502-344-324	Sequence 324, App	466	10.8	41.5	24	3	US-08-949-155-17	Sequence 17, Appl
394	11	42.3	35	4	US-09-614-034-11	Sequence 11, Appl	467	10.8	41.5	24	3	US-08-949-155-19	Sequence 19, Appl
395	11	42.3	35	4	US-09-614-034-12	Sequence 12, Appl	C 468	10.8	41.5	24	3	US-09-230-804-24	Sequence 24, Appl
396	11	42.3	35	4	US-09-614-034-13	Sequence 13, Appl	C 469	10.8	41.5	24	3	US-08-981-653-4	Sequence 4, Appl
397	11	42.3	35	4	US-09-614-034-17	Sequence 17, Appl	470	10.8	41.5	24	3	US-09-819-964-17	Sequence 17, Appl
398	11	42.3	35	4	US-09-614-034-21	Sequence 21, Appl	471	10.8	41.5	24	3	US-09-819-964-19	Sequence 19, Appl
399	11	42.3	35	4	US-09-614-034-33	Sequence 33, Appl	472	10.8	41.5	24	3	US-09-033-556-18	Sequence 18, Appl
400	11	42.3	36	1	US-08-445-640-33	Sequence 5, Appl	C 473	10.8	41.5	25	1	US-08-155-746-9	Sequence 9, Appl
401	11	42.3	36	2	US-08-438-864-5	Sequence 5, Appl	C 474	10.8	41.5	25	1	US-08-341-148-11	Sequence 11, Appl
402	11	42.3	36	2	US-08-474-379C-74	Sequence 33, Appl	C 475	10.8	41.5	25	1	US-08-341-148-21	Sequence 21, Appl
403	11	42.3	36	3	US-08-170-558-33	Sequence 74, Appl	C 476	10.8	41.5	25	4	US-09-648-254-27	Sequence 27, Appl
404	11	42.3	36	3	US-08-146-249A-74	Sequence 33, Appl	C 477	10.8	41.5	25	5	PCT-US94-00771-9	Sequence 9, Appl
405	11	42.3	36	3	US-08-447-314-33	Sequence 33, Appl	C 478	10.8	41.5	25	5	PCT-US94-14096-11	Sequence 11, Appl
406	11	42.3	36	3	US-08-445-461-33	Sequence 74, Appl	C 479	10.8	41.5	27	3	US-09-005-165-10	Sequence 10, Appl
407	11	42.3	36	3	US-08-206-188B-74	Sequence 5, Appl	C 480	10.8	41.5	27	3	US-09-253-396A-42	Sequence 42, Appl
408	11	42.3	36	3	US-08-628-747-5	Sequence 5, Appl	C 481	10.8	41.5	27	4	US-09-305-681-50	Sequence 50, Appl
409	11	42.3	36	3	US-08-402-253-5	Sequence 5, Appl	C 482	10.8	41.5	28	4	US-10-080-505-57	Sequence 57, Appl
410	11	42.3	36	3	US-08-443-866B-5	Sequence 36, Appl	C 483	10.8	41.5	30	1	US-08-411-795B-157	Sequence 157, Appl
411	11	42.3	36	4	US-09-864-866-39	Sequence 39, Appl	484	10.8	41.5	30	1	US-08-341-148-22	Sequence 22, Appl
412	11	42.3	36	4	US-09-864-866-39	Sequence 27, Appl	485	10.8	41.5	30	1	US-08-341-148-23	Sequence 23, Appl
413	11	42.3	37	3	US-09-320-878-27	Sequence 27, Appl	486	10.8	41.5	30	1	US-08-469-319A-157	Sequence 157, Appl
414	11	42.3	37	4	US-09-141-908-24	Sequence 24, Appl	487	10.8	41.5	30	1	US-08-764-114-157	Sequence 157, Appl
415	11	42.3	37	4	US-09-657-440-27	Sequence 27, Appl	488	10.8	41.5	30	4	US-08-469-419-157	Sequence 157, Appl
416	11	42.3	37	6	5198342-8	Patent No. 5198342	C 489	10.8	41.5	30	4	US-09-593-359-10	Sequence 10, Appl
417	11	42.3	38	3	US-09-182-859-28	Sequence 28, Appl	490	10.8	41.5	30	4	US-09-937-832-11	Sequence 11, Appl
418	11	42.3	38	4	US-09-537-168-27	Sequence 27, Appl	491	10.8	41.5	30	4	US-09-937-832-11	Sequence 11, Appl
419	11	42.3	38	4	US-09-672-459-28	Sequence 28, Appl	492	10.8	41.5	30	5	PCT-US94-14096-23	Sequence 23, Appl
420	11	42.3	38	4	US-10-186-042-28	Sequence 28, Appl	493	10.8	41.5	32	5	US-09-022-461-3	Sequence 3, Appl
421	11	42.3	41	1	US-07-931-473B-274	Sequence 274, App	494	10.8	41.5	32	3	US-09-138-024-12	Sequence 12, Appl
422	11	42.3	41	1	US-07-714-131C-274	Sequence 274, App	495	10.8	41.5	32	3	US-09-404-066-12	Sequence 12, Appl
423	11	42.3	41	1	US-08-412-110-274	Sequence 274, App	496	10.8	41.5	32	3	US-09-573-322-12	Sequence 12, Appl
424	11	42.3	41	1	US-08-409-442A-274	Sequence 274, App	497	10.8	41.5	32	4	US-09-151-376-70	Sequence 70, Appl
425	11	42.3	41	2	US-08-469-609A-274	Sequence 274, App	498	10.8	41.5	32	4	US-08-173-510B-52	Sequence 52, Appl
426	11	42.3	41	3	US-09-143-190-274	Sequence 274, App	499	10.8	41.5	33	1	US-08-458-218-52	Sequence 21, Appl
427	11	42.3	41	3	US-09-502-344-274	Sequence 274, App	500	10.8	41.5	33	1	US-08-690-102A-21	Sequence 21, Appl
428	11	42.3	43	1	US-08-720-899-24	Sequence 24, Appl	501	10.8	41.5	33	1	US-08-463-224-20	Sequence 20, Appl
429	11	42.3	43	1	US-08-459-610-24	Sequence 24, Appl	C 502	10.8	41.5	33	2	US-08-463-377-20	Sequence 20, Appl
430	11	42.3	43	2	US-08-343-804-24	Sequence 24, Appl	C 503	10.8	41.5	33	2	US-08-450-497-52	Sequence 52, Appl
431	11	42.3	43	2	US-09-153-310-23	Sequence 23, Appl	504	10.8	41.5	33	2	US-08-874-678-22	Sequence 22, Appl
432	11	42.3	43	4	US-09-636-368-13	Sequence 13, Appl	C 505	10.8	41.5	33	3	US-09-127-902-21	Sequence 21, Appl
433	11	42.3	45	1	US-07-931-473B-307	Sequence 307, App	C 506	10.8	41.5	33	3	US-09-227-717-9	Sequence 9, Appl
434	11	42.3	47	1	US-07-714-131C-307	Sequence 307, App	507	10.8	41.5	33	3	US-09-155-107-33	Sequence 33, Appl
435	11	42.3	47	1	US-08-412-110-307	Sequence 307, App	508	10.8	41.5	33	3	US-09-348-886-22	Sequence 22, Appl
436	11	42.3	47	1	US-08-409-442A-307	Sequence 307, App	C 509	10.8	41.5	33	3	US-09-589-287B-40	Sequence 40, Appl
437	11	42.3	47	2	US-08-459-609A-307	Sequence 307, App	C 510	10.8	41.5	33	4	US-09-589-286A-40	Sequence 40, Appl
438	11	42.3	47	3	US-08-910-632-80	Sequence 80, Appl	C 511	10.8	41.5	33	4	US-09-589-286A-40	Sequence 40, Appl
439	11	42.3	47	3	US-09-143-190-307	Sequence 307, App	C 512	10.8	41.5	33	4	PCT-US95-09641-21	Sequence 21, Appl
440	11	42.3	47	4	US-09-502-344-307	Sequence 307, App	C 513	10.8	41.5	33	5	US-08-792-832A-13	Sequence 13, Appl
441	11	42.3	47	4	US-09-422-978-1156	Sequence 1156, App	514	10.8	41.5	34	3	US-08-559-390-245	Sequence 245, App
442	11	42.3	48	4	US-09-422-978-13324	Sequence 3324, App	515	10.8	41.5	36	1	US-08-411-796-245	Sequence 251, App
443	11	42.3	48	4	US-08-786-531B-10	Sequence 10, Appl	C 516	10.8	41.5	36	1	US-08-411-796-251	Sequence 7, Appl
444	11	42.3	48	4	US-09-454-204A-25	Sequence 25, Appl	C 517	10.8	41.5	36	2	US-08-921-382-7	Sequence 11, Appl
445	11	42.3	49	4	US-09-331-793-56	Sequence 56, Appl	518	10.8	41.5	36	2	US-08-921-382-11	Sequence 245, App
446	11	42.3	50	1	US-07-727-814B-6	Sequence 6, Appl	C 519	10.8	41.5	36	2	US-08-471-039-251	Sequence 251, App
447	10.8	41.5	14	3	US-08-258-614-6	Sequence 11, Appl	C 520	10.8	41.5	36	3	US-09-098-628-69	Sequence 69, Appl
448	10.8	41.5	18	4	US-08-687-580B-11	Sequence 11, Appl	C 521	10.8	41.5	36	3	US-09-098-628-69	Sequence 245, App
449	10.8	41.5	18	4	US-09-608-958-14	Sequence 14, Appl	C 522	10.8	41.5	36	4	US-08-559-390-251	Sequence 7, Appl
450	10.8	41.5	20	2	US-08-608-958-14	Sequence 14, Appl	C 523	10.8	41.5	36	4	US-09-386-380-7	Sequence 11, Appl
451	10.8	41.5	20	3	US-08-256-426B-287	Sequence 287, App	524	10.8	41.5	36	4	US-09-386-380-11	Sequence 245, App
452	10.8	41.5	20	4	US-09-418-641-64	Sequence 64, Appl	C 525	10.8	41.5	36	5	PCT-US93-11198-245	Sequence 251, App
453	10.8	41.5	20	4	US-09-112-580-99	Sequence 6622, App	C 526	10.8	41.5	36	5	PCT-US93-11198-245	Sequence 31, Appl
454	10.8	41.5	20	4	US-09-112-580-99	Sequence 99, Appl	C 527	10.8	41.5	36	5	PCT-US93-11198-245	Sequence 54, Appl
455	10.8	41.5	20	4	US-09-418-980-15	Sequence 15, Appl	C 528	10.8	41.5	37	2	US-08-700-670A-31	Sequence 23, Appl
456	10.8	41.5	21	3	US-08-701-582D-22	Sequence 18, Appl	C 529	10.8	41.5	37	4	US-09-313-221A-54	Sequence 30, Appl
457	10.8	41.5	22	1	US-08-891-463-18	Sequence 14, Appl	C 530	10.8	41.5	38	5	PCT-US92-01015-23	Patent No. RE34,60
458	10.8	41.5	22	2	US-08-696-944-14	Sequence 23, Appl	C 531	10.8	41.5	39	6	RE34606-26	Sequence 16, Appl
459	10.8	41.5	22	4	US-09-433-579-23	Sequence 78, Appl	C 532	10.8	41.5	40	3	US-09-590-061-16	Sequence 9, Appl
460	10.8	41.5	22	4	US-09-574-779B-78	Sequence 79, Appl	C 533	10.8	41.5	40	3	US-09-329-920-9	Sequence 16, Appl
461	10.8	41.5	22	4	US-09-574-779B-78	Sequence 3, Appl	C 534	10.8	41.5	40	4	US-09-894-788-16	Sequence 50, Appl
462	10.8	41.5	24	1	US-08-657-175-3	Sequence 43, Appl	C 535	10.8	41.5	42	2	US-08-428-197-50	
463	10.8	41.5	24	3	US-08-589-028-43	Sequence 43, Appl	C 536	10.8	41.5				
464	10.8	41.5	24	3	US-08-784-582-43	Sequence 43, Appl	C 537	10.8	41.5				
465	10.8	41.5	24	3	US-08-785-271-43	Sequence 334, App	538	10.8	41.5				

C 539	10.8	41.5	42	3	US-08-879-565-9	Sequence 9, Appli	612	10.6	40.8	30	3	US-08-951-923-28	Sequence 28, Appl
C 540	10.8	41.5	42	4	US-09-138-277C-5	Sequence 5, Appli	613	10.6	40.8	30	3	US-08-848-793-13	Sequence 13, Appl
C 541	10.8	41.5	42	5	PCT-US93-10555-50	Sequence 50, Appli	614	10.6	40.8	30	3	US-08-322-678-13	Sequence 13, Appl
C 542	10.8	41.5	44	1	US-07-931-473B-248	Sequence 248, App	615	10.6	40.8	30	4	US-07-969-863-23	Sequence 23, Appl
C 543	10.8	41.5	44	1	US-07-714-131C-248	Sequence 248, App	616	10.6	40.8	30	4	US-09-741-744A-100	Sequence 100, App
C 544	10.8	41.5	44	1	US-08-412-110-248	Sequence 248, App	C 617	10.6	40.8	31	1	US-08-466-033-113	Sequence 113, App
C 545	10.8	41.5	44	1	US-08-409-442A-248	Sequence 248, App	C 618	10.6	40.8	31	1	US-08-444-733-113	Sequence 113, App
C 546	10.8	41.5	44	2	US-08-469-609A-248	Sequence 248, App	C 619	10.6	40.8	31	2	US-08-464-133-113	Sequence 113, App
C 547	10.8	41.5	44	3	US-09-143-190-248	Sequence 248, App	C 620	10.6	40.8	31	2	US-08-461-361-113	Sequence 113, App
C 548	10.8	41.5	44	3	US-09-502-344-248	Sequence 248, App	C 621	10.6	40.8	31	2	US-08-485-910-113	Sequence 113, App
C 549	10.8	41.5	47	4	US-09-641-638-1207	Sequence 1207, Ap	C 622	10.6	40.8	31	2	US-08-859-998-182	Sequence 182, App
C 550	10.8	41.5	47	4	US-10-170-097-1207	Sequence 1207, Ap	C 623	10.6	40.8	31	2	US-09-225-928-182	Sequence 182, App
C 551	10.8	41.5	48	1	US-08-014-153D-14	Sequence 14, Appl	C 624	10.6	40.8	31	4	US-09-225-201B-182	Sequence 182, App
C 552	10.8	41.5	48	3	US-08-532-657A-46	Sequence 46, Appl	C 625	10.6	40.8	31	5	PCT-US95-06266-94	Sequence 94, Appl
C 553	10.8	41.5	48	3	US-09-248-998-46	Sequence 46, Appl	C 626	10.6	40.8	32	1	US-08-222-616-40	Sequence 40, Appl
C 554	10.8	41.5	48	4	US-09-248-998-46	Sequence 46, Appl	C 627	10.6	40.8	32	1	US-08-442-542-41	Sequence 41, Appl
C 555	10.8	41.5	48	4	US-09-610-651-46	Sequence 46, Appl	C 628	10.6	40.8	32	3	US-08-765-469-41	Sequence 41, Appl
C 556	10.8	41.5	49	4	US-09-395-937-29	Sequence 29, Appl	C 629	10.6	40.8	32	3	US-09-312-285-9	Sequence 9, Appli
C 557	10.8	41.5	50	4	US-09-907-794A-168	Sequence 168, App	C 630	10.6	40.8	32	3	US-09-312-286-9	Sequence 9, Appli
C 558	10.8	41.5	50	4	US-09-905-125A-168	Sequence 168, App	C 631	10.6	40.8	32	3	US-09-312-038-9	Sequence 9, Appli
C 559	10.8	41.5	50	4	US-09-902-775A-168	Sequence 168, App	C 632	10.6	40.8	32	3	US-08-446-648-40	Sequence 40, Appl
C 560	10.8	41.5	50	4	US-09-906-700-168	Sequence 168, App	C 633	10.6	40.8	32	4	US-09-728-764-9	Sequence 9, Appli
C 561	10.8	41.5	50	4	US-09-903-603A-168	Sequence 168, App	C 634	10.6	40.8	32	4	US-09-312-304B-7	Sequence 7, Appli
C 562	10.6	40.8	17	1	US-07-717-332D-4	Sequence 4, Appli	C 635	10.6	40.8	32	4	US-09-728-792-9	Sequence 9, Appli
C 563	10.6	40.8	17	3	US-08-673-645-263	Sequence 263, App	C 636	10.6	40.8	32	4	US-09-850-964-9	Sequence 9, Appli
C 564	10.6	40.8	18	1	US-08-390-850-1128	Sequence 1128, Ap	C 637	10.6	40.8	32	4	US-09-982-610-40	Sequence 40, Appl
C 565	10.6	40.8	18	1	US-08-435-634-1128	Sequence 1128, Ap	C 638	10.6	40.8	32	4	US-09-532-806-10	Sequence 10, Appl
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C 567	10.6	40.8	20	4	US-09-844-634-49	Sequence 49, Appl	C 640	10.6	40.8	33	1	US-08-049-473-8	Sequence 8, Appli
C 568	10.6	40.8	20	4	US-09-198-452A-2885	Sequence 2885, Ap	C 641	10.6	40.8	33	1	US-08-312-648-8	Sequence 8, Appli
C 569	10.6	40.8	20	4	US-09-198-452A-5930	Sequence 5930, Ap	C 642	10.6	40.8	33	3	US-08-793-408-10	Sequence 10, Appl
C 570	10.6	40.8	20	4	US-09-198-452A-5996	Sequence 5996, Ap	C 643	10.6	40.8	33	3	US-09-139-762A-10	Sequence 10, Appl
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C 572	10.6	40.8	20	4	US-08-983-605-235	Sequence 235, App	C 645	10.6	40.8	33	3	US-08-837-034-36	Sequence 36, Appl
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C 574	10.6	40.8	21	3	US-09-376-781-20	Sequence 20, Appl	C 647	10.6	40.8	33	3	US-09-382-616A-29	Sequence 29, Appl
C 575	10.6	40.8	21	4	US-09-105-058C-16	Sequence 16, Appl	C 648	10.6	40.8	33	4	US-09-813-781-41	Sequence 41, Appl
C 576	10.6	40.8	22	4	US-08-983-605-115	Sequence 115, App	C 649	10.6	40.8	33	4	US-09-728-466-27	Sequence 27, Appl
C 577	10.6	40.8	23	1	US-07-616-022C-11	Sequence 11, Appl	C 650	10.6	40.8	34	4	US-09-728-466-29	Sequence 29, Appl
C 578	10.6	40.8	24	1	US-08-399-675-16	Sequence 16, Appl	C 651	10.6	40.8	33	5	PCT-US94-04190-8	Sequence 8, Appli
C 579	10.6	40.8	24	1	US-08-233-030-18	Sequence 18, Appl	C 652	10.6	40.8	33	6	5316943-4	Patent No. 5316943
C 580	10.6	40.8	24	2	US-08-809-297-36	Sequence 36, Appl	C 653	10.6	40.8	34	1	US-08-468-036-42	Sequence 42, Appl
C 581	10.6	40.8	24	3	US-09-345-217-24	Sequence 24, Appl	C 654	10.6	40.8	34	2	US-08-376-843-42	Sequence 42, Appl
C 582	10.6	40.8	24	4	US-09-845-129-24	Sequence 24, Appl	C 655	10.6	40.8	34	4	US-09-595-344-16	Sequence 16, Appl
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C 584	10.6	40.8	25	4	US-09-538-709-299	Sequence 299, App	C 657	10.6	40.8	35	1	US-08-401-908-22	Sequence 22, Appl
C 585	10.6	40.8	25	4	US-10-132-920B-24	Sequence 24, Appl	C 658	10.6	40.8	35	2	US-08-474-379C-70	Sequence 70, Appl
C 586	10.6	40.8	26	1	US-08-627-845-9	Sequence 9, Appli	C 659	10.6	40.8	36	3	US-09-146-249A-70	Sequence 70, Appl
C 587	10.6	40.8	26	1	US-08-627-845-9	Sequence 9, Appli	C 660	10.6	40.8	36	3	US-08-206-188B-70	Sequence 70, Appl
C 588	10.6	40.8	26	4	US-09-050-739-117	Sequence 117, App	C 661	10.6	40.8	36	3	US-09-522-666-23	Sequence 23, Appl
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C 590	10.6	40.8	27	3	US-08-584-040-551	Sequence 551, App	C 663	10.6	40.8	37	1	US-08-077-252B-8	Sequence 8, Appli
C 591	10.6	40.8	27	3	US-08-584-040-6706	Sequence 6706, Ap	C 664	10.6	40.8	37	1	US-08-899-575-134	Sequence 134, App
C 592	10.6	40.8	27	3	US-08-584-040-7136	Sequence 7136, Ap	C 665	10.6	40.8	37	1	US-08-899-575-134	Sequence 134, App
C 593	10.6	40.8	27	4	US-09-009-893A-12	Sequence 12, Appl	C 666	10.6	40.8	37	3	US-09-002-753A-8	Sequence 8, Appli
C 594	10.6	40.8	27	4	US-09-009-893A-18	Sequence 18, Appl	C 667	10.6	40.8	37	4	US-09-657-274-8	Sequence 8, Appli
C 595	10.6	40.8	27	4	US-09-454-204A-23	Sequence 23, Appl	C 668	10.6	40.8	37	5	PCT-US94-06687-8	Sequence 8, Appli
C 596	10.6	40.8	27	4	US-09-489-155-12	Sequence 12, Appl	C 669	10.6	40.8	37	5	PCT-US95-08743-134	Sequence 134, App
C 597	10.6	40.8	27	4	US-09-489-155-18	Sequence 18, Appl	C 670	10.6	40.8	38	2	US-08-432-871C-10	Sequence 10, Appl
C 598	10.6	40.8	27	4	US-09-642-894A-4	Sequence 4, Appli	C 671	10.6	40.8	38	2	US-08-570-155-6	Sequence 6, Appli
C 599	10.6	40.8	29	3	US-09-446-504-92	Sequence 92, Appl	C 672	10.6	40.8	38	4	US-09-270-956-10	Sequence 10, Appl
C 600	10.6	40.8	29	3	US-09-712-266-92	Sequence 92, Appl	C 673	10.6	40.8	38	5	PCT-US95-02861-6	Sequence 6, Appli
C 601	10.6	40.8	29	4	US-09-786-684-7	Sequence 7, Appli	C 674	10.6	40.8	40	1	US-08-105-483-66	Sequence 66, Appl
C 602	10.6	40.8	29	4	US-09-078-972A-6	Sequence 6, Appli	C 675	10.6	40.8	40	1	US-08-117-083-4	Sequence 4, Appli
C 603	10.6	40.8	29	4	US-09-291-289-27	Sequence 27, Appl	C 676	10.6	40.8	40	1	US-08-709-209-66	Sequence 66, Appl
C 604	10.6	40.8	29	4	US-09-786-684-7	Sequence 7, Appli	C 677	10.6	40.8	40	1	US-08-458-101-66	Sequence 66, Appl
C 605	10.6	40.8	29	4	US-09-623-551-24	Sequence 24, Appl	C 678	10.6	40.8	40	3	US-08-961-083-358	Sequence 358, App
C 606	10.6	40.8	29	4	US-09-623-551-25	Sequence 25, Appl	C 679	10.6	40.8	40	3	US-09-633-566-2	Sequence 2, Appli
C 607	10.6	40.8	30	1	US-08-479-487-17	Sequence 17, Appl	C 680	10.6	40.8	40	4	US-09-536-784-358	Sequence 358, App
C 608	10.6	40.8	30	1	US-08-322-677A-13	Sequence 13, Appl	C 681	10.6	40.8	40	4	US-09-628-730-19	Sequence 19, Appl
C 609	10.6	40.8	30	1	US-08-322-676-13	Sequence 13, Appl	C 682	10.6	40.8	40	4	US-09-628-730-36	Sequence 36, Appl
C 610	10.6	40.8	30	3	US-08-898-218-13	Sequence 13, Appl	C 683	10.6	40.8	40	4	US-09-863-179-6	Sequence 6, Appli
C 611	10.6	40.8	30	3	US-08-951-923-12	Sequence 12, Appl	C 684	10.6	40.8	40	6	5198342-9	Patent No. 5198342



685	10.6	40.8	41	3	US-08-813-507-1	Sequence 1, Appl	28	1	US-08-032-846-24	Sequence 24, Appl
686	10.6	40.8	41	3	US-08-813-507-123	Sequence 123, App	28	3	US-08-474-636-24	Sequence 24, Appl
687	10.6	40.8	41	3	US-09-464-453-1	Sequence 1, Appl	28	3	US-07-971-834-13	Sequence 13, Appl
688	10.6	40.8	41	3	US-09-464-453-123	Sequence 123, App	29	1	US-08-348-961-2	Sequence 2, Appl
689	10.6	40.8	42	4	US-09-997-956-3	Sequence 3, Appl	29	1	US-08-222-177A-460	Sequence 460, Appl
690	10.6	40.8	44	1	US-08-093-741-58	Sequence 58, Appl	29	3	US-08-422-459-25	Sequence 25, Appl
691	10.6	40.8	44	1	US-08-720-012-58	Sequence 58, Appl	29	3	US-08-716-873-39	Sequence 39, Appl
692	10.6	40.8	45	2	US-08-560-098A-25	Sequence 25, Appl	29	3	US-09-001-472-6	Sequence 6, Appl
693	10.6	40.8	46	2	US-08-730-563-69	Sequence 69, Appl	29	3	US-09-368-431-39	Sequence 39, Appl
694	10.6	40.8	46	3	US-09-371-774-69	Sequence 69, Appl	29	3	US-09-414-006-25	Sequence 25, Appl
695	10.6	40.8	47	2	US-08-986-306-57	Sequence 57, Appl	29	4	US-07-971-834-7	Sequence 7, Appl
696	10.6	40.8	47	2	US-08-996-306-60	Sequence 60, Appl	29	4	US-07-971-834-8	Sequence 8, Appl
697	10.6	40.8	47	3	US-09-338-907-57	Sequence 57, Appl	29	4	US-09-775-827A-6	Sequence 39, Appl
698	10.6	40.8	47	3	US-09-338-907-60	Sequence 60, Appl	29	4	US-09-951-217-39	Sequence 17, Appl
699	10.6	40.8	47	3	US-09-218-207-57	Sequence 57, Appl	30	1	US-08-147-696E-17	Sequence 17, Appl
700	10.6	40.8	47	3	US-09-218-207-60	Sequence 60, Appl	30	1	US-08-147-696E-32	Sequence 32, Appl
701	10.6	40.8	47	4	US-09-641-638-1051	Sequence 1051, Ap	30	1	US-08-147-890-8	Sequence 8, Appl
702	10.6	40.8	47	4	US-09-422-978-2410	Sequence 2410, Ap	30	1	US-08-484-334-17	Sequence 17, Appl
703	10.6	40.8	47	4	US-09-422-978-2626	Sequence 2626, Ap	30	1	US-08-484-334-32	Sequence 32, Appl
704	10.6	40.8	47	4	US-09-422-978-3536	Sequence 3536, Ap	30	3	US-09-013-092-17	Sequence 17, Appl
705	10.6	40.8	47	4	US-09-422-978-3924	Sequence 3924, Ap	30	3	US-09-013-092-32	Sequence 32, Appl
706	10.6	40.8	47	4	US-10-170-097-1051	Sequence 1051, Ap	30	3	US-09-280-999-17	Sequence 17, Appl
707	10.6	40.8	49	2	US-08-414-657D-4	Sequence 4, Appl	30	3	US-09-280-999-32	Sequence 32, Appl
708	10.6	40.8	49	4	US-09-135-080-29	Sequence 29, Appl	30	3	US-09-026-408-8	Sequence 8, Appl
709	10.6	40.8	50	4	US-09-849-069-15	Sequence 15, Appl	30	3	US-09-545-244A-1	Sequence 1, Appl
710	10.4	40.0	13	3	US-09-091-058-16	Sequence 16, Appl	30	4	US-09-402-631A-13	Sequence 13, Appl
711	10.4	40.0	16	3	US-09-187-946-14	Sequence 14, Appl	30	4	US-09-173-053-10	Sequence 10, Appl
712	10.4	40.0	17	3	US-09-523-323-62	Sequence 62, Appl	30	4	US-07-971-834-10	Sequence 10, Appl
713	10.4	40.0	17	3	US-09-091-058-17	Sequence 17, Appl	30	4	US-09-846-028-22	Sequence 22, Appl
714	10.4	40.0	20	2	US-08-778-494B-113	Sequence 113, App	30	4	US-08-896-537A-8	Sequence 8, Appl
715	10.4	40.0	21	1	US-07-602-608-20	Sequence 20, Appl	30	4	US-09-902-684-8	Sequence 8, Appl
716	10.4	40.0	21	1	US-08-263-578-20	Sequence 20, Appl	31	1	US-07-867-106-16	Sequence 16, Appl
717	10.4	40.0	21	1	US-08-440-103-10	Sequence 10, Appl	31	1	US-08-147-696E-18	Sequence 18, Appl
718	10.4	40.0	21	1	US-08-440-542-10	Sequence 10, Appl	31	1	US-08-032-846-12	Sequence 12, Appl
719	10.4	40.0	21	1	US-08-426-792-27	Sequence 27, Appl	31	1	US-08-334-18	Sequence 18, Appl
720	10.4	40.0	21	1	US-08-231-368-10	Sequence 10, Appl	31	2	US-08-626-169-9	Sequence 9, Appl
721	10.4	40.0	21	1	US-08-440-210-10	Sequence 10, Appl	31	2	US-08-466-120-4	Sequence 4, Appl
722	10.4	40.0	21	3	US-09-048-604-10	Sequence 10, Appl	31	2	US-08-602-359A-9	Sequence 9, Appl
723	10.4	40.0	21	4	US-09-452-638-15	Sequence 15, Appl	31	3	US-09-013-092-18	Sequence 18, Appl
724	10.4	40.0	22	1	US-08-423-315-5	Sequence 5, Appl	31	3	US-09-164-907-9	Sequence 9, Appl
725	10.4	40.0	22	3	US-08-716-190-17	Sequence 17, Appl	31	3	US-09-280-999-18	Sequence 18, Appl
726	10.4	40.0	22	3	US-09-358-972-281	Sequence 281, App	31	3	US-08-474-636-12	Sequence 12, Appl
727	10.4	40.0	22	3	US-09-406-065-14	Sequence 14, Appl	31	3	US-08-032-846-12	Sequence 12, Appl
728	10.4	40.0	22	3	US-09-790-417-1	Sequence 1, Appl	31	3	US-08-474-636-12	Sequence 12, Appl
729	10.4	40.0	22	4	US-09-790-417-281	Sequence 281, App	31	4	US-09-828-303-40	Sequence 40, Appl
730	10.4	40.0	22	4	US-08-778-494B-112	Sequence 112, App	31	4	US-09-940-244-376	Sequence 376, App
731	10.4	40.0	23	1	US-08-173-510B-29	Sequence 29, Appl	31	4	US-09-721-908-31	Sequence 31, Appl
732	10.4	40.0	23	1	US-08-458-218-29	Sequence 29, Appl	32	2	US-08-889-909A-15	Sequence 15, Appl
733	10.4	40.0	24	1	US-08-816-605-4	Sequence 4, Appl	32	2	US-08-697-631A-1	Sequence 1, Appl
734	10.4	40.0	24	2	US-08-816-605-6	Sequence 6, Appl	32	3	US-08-997-803-10	Sequence 10, Appl
735	10.4	40.0	24	2	US-08-450-497-29	Sequence 29, Appl	32	3	US-08-845-546-17	Sequence 17, Appl
736	10.4	40.0	24	2	US-09-866-108A-13783	Sequence 13783, A	32	3	PCT-US96-00547-37	Sequence 37, Appl
737	10.4	40.0	24	2	US-09-866-108A-13784	Sequence 13784, A	32	3	US-08-557-128-16	Sequence 16, Appl
738	10.4	40.0	24	4	US-09-866-108A-13785	Sequence 13785, A	32	3	US-09-156-163A-15	Sequence 15, Appl
739	10.4	40.0	24	4	US-09-866-108A-13786	Sequence 13786, A	32	4	US-09-982-308B-15	Sequence 15, Appl
740	10.4	40.0	25	2	US-08-671-975A-14	Sequence 14, Appl	32	4	US-09-758-282B-23	Sequence 23, Appl
741	10.4	40.0	25	4	US-09-758-282B-34	Sequence 34, Appl	32	4	US-09-577-304A-23	Sequence 23, Appl
742	10.4	40.0	25	4	US-09-866-108A-13783	Sequence 13783, A	32	4	US-09-577-304A-23	Sequence 23, Appl
743	10.4	40.0	25	4	US-09-866-108A-13784	Sequence 13784, A	32	4	US-09-577-304A-23	Sequence 23, Appl
744	10.4	40.0	25	4	US-09-866-108A-13785	Sequence 13785, A	32	4	US-09-577-304A-23	Sequence 23, Appl
745	10.4	40.0	25	4	US-09-866-108A-13786	Sequence 13786, A	32	4	US-09-577-304A-23	Sequence 23, Appl
746	10.4	40.0	25	4	US-09-866-108A-13787	Sequence 13787, A	34	1	US-08-484-334-29	Sequence 29, Appl
747	10.4	40.0	25	4	US-09-866-108A-13788	Sequence 13788, A	34	1	US-08-147-696E-29	Sequence 29, Appl
748	10.4	40.0	25	4	US-09-577-304A-34	Sequence 34, Appl	34	1	US-08-484-334-29	Sequence 29, Appl
749	10.4	40.0	25	4	US-10-004-993A-2	Sequence 2, Appl	34	2	US-08-888-366-33	Sequence 33, Appl
750	10.4	40.0	26	1	US-08-120-827-60	Sequence 60, Appl	34	2	US-09-013-092-29	Sequence 29, Appl
751	10.4	40.0	26	1	US-08-478-675-60	Sequence 60, Appl	34	3	US-09-013-092-29	Sequence 29, Appl
752	10.4	40.0	27	3	US-08-985-162-1347	Sequence 1347, Ap	34	3	US-08-767-128-42	Sequence 42, Appl
753	10.4	40.0	27	3	US-08-985-162-1489	Sequence 1489, Ap	34	3	US-08-767-128-42	Sequence 42, Appl
754	10.4	40.0	27	3	US-08-985-162-1489	Sequence 1489, Ap	34	3	US-08-767-128-42	Sequence 42, Appl
755	10.4	40.0	27	3	US-08-985-162-1489	Sequence 1489, Ap	34	3	US-08-767-128-42	Sequence 42, Appl
756	10.4	40.0	27	3	US-08-985-162-1489	Sequence 1489, Ap	34	3	US-08-767-128-42	Sequence 42, Appl
757	10.4	40.0	27	3	US-08-985-162-1489	Sequence 1489, Ap	34	3	US-08-767-128-42	Sequence 42, Appl
758	10.4	40.0	27	3	US-08-985-162-1489	Sequence 1489, Ap	34	3	US-08-767-128-42	Sequence 42, Appl
759	10.4	40.0	27	3	US-08-985-162-1489	Sequence 1489, Ap	34	3	US-08-767-128-42	Sequence 42, Appl
760	10.4	40.0	27	3	US-08-985-162-1489	Sequence 1489, Ap	34	3	US-08-767-128-42	Sequence 42, Appl
761	10.4	40.0	27	3	US-08-985-162-1489	Sequence 1489, Ap	34	3	US-08-767-128-42	Sequence 42, Appl
762	10.4	40.0	27	3	US-08-985-162-1489	Sequence 1489, Ap	34	3	US-08-767-128-42	Sequence 42, Appl
763	10.4	40.0	27	3	US-08-985-162-1489	Sequence 1489, Ap	34	3	US-08-767-128-42	Sequence 42, Appl
764	10.4	40.0	27	3	US-08-985-162-1489	Sequence 1489, Ap	34	3	US-08-767-128-42	Sequence 42, Appl
765	10.4	40.0	27	3	US-08-985-162-1489	Sequence 1489, Ap	34	3	US-08-767-128-42	Sequence 42, Appl
766	10.4	40.0	27	3	US-08-985-162-1489	Sequence 1489, Ap	34	3	US-08-767-128-42	Sequence 42, Appl
767	10.4	40.0	27	3	US-08-985-162-1489	Sequence 1489, Ap	34	3	US-08-767-128-42	Sequence 42, Appl
768	10.4	40.0	27	3	US-08-985-162-1489	Sequence 1489, Ap	34	3	US-08-767-128-42	Sequence 42, Appl
769	10.4	40.0	27	3	US-08-985-162-1489	Sequence 1489, Ap	34	3	US-08-767-128-42	Sequence 42, Appl
770	10.4	40.0	27	3	US-08-985-162-1489	Sequence 1489, Ap	34	3	US-08-767-128-42	Sequence 42, Appl
771	10.4	40.0	27	3	US-08-985-162-1489	Sequence 1489, Ap	34	3	US-08-767-128-42	Sequence 42, Appl
772	10.4	40.0	27	3	US-08-985-162-1489	Sequence 1489, Ap	34	3	US-08-767-128-42	Sequence 42, Appl
773	10.4	40.0	27	3	US-08-985-162-1489	Sequence 1489, Ap	34	3	US-08-767-128-42	Sequence 42, Appl
774	10.4	40.0	27	3	US-08-985-162-1489	Sequence 1489, Ap	34	3	US-08-767-128-42	Sequence 42, Appl
775	10.4	40.0	27	3	US-08-985-162-1489	Sequence 1489, Ap	34	3	US-08-767-128-42	Sequence 42, Appl
776	10.4	40.0	27	3	US-08-985-162-1489	Sequence 1489, Ap	34	3	US-08-767-128-42	Sequence 42, Appl
777	10.4	40.0	27	3	US-08-985-162-1489	Sequence 1489, Ap	34	3	US-08-767-128-42	Sequence 42, Appl
778	10.4	40.0	27	3	US-08-985-162-1489	Sequence 1489, Ap	34	3	US-08-767-128-42	Sequence 42, Appl
779	10.4	40.0	27	3	US-08-985-162-1489	Sequence 1489, Ap	34	3	US-08-767-128-42	Sequence 42, Appl
780	10.4	40.0	27	3	US-08-985-162-1489	Sequence 1489, Ap	34	3	US-08-767-128-42	Sequence 42, Appl
781	10.4	40.0	27	3	US-08-985-162-1489	Sequence 1489, Ap	34	3	US-08-767-128-42	Sequence 42, Appl
782	10.4	40.0	27	3	US-08-985-162-1489	Sequence 1489, Ap	34	3	US-08-767-128-42	Sequence 42, Appl
783	10.4	40.0	27	3	US-08-985-162-1489	Sequence 1489, Ap	34	3	US-08-767-128-42	Sequence 42, Appl
784	10.4	40.0	27	3	US-08-985-162-1489	Sequence 1489, Ap	34	3	US-08-767-128-42	Sequence 42, Appl
785	10.4	40.0	27	3	US-08-985-162-1489	Sequence 1489, Ap	34	3	US-08-767-128-42	Sequence 42, Appl
786	10.4	40.0	27	3	US-08-985-162-1489	Sequence 1489, Ap	34	3	US-08-767-128-42	Sequence 42, Appl
787	10.4	40.0	27	3	US-08-985-162-1489	Sequence 1489, Ap	34	3	US-08-767-128-42	Sequence 42, Appl





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Query Match          58.5%; Score 15.2; DB 1; Length 44;
Best Local Similarity 85.0%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels

      y      6 TTCGCAGATCGGTACCTCAA 25
      ||||| ||||| ||||| ||||| |||||
      b      26 TTCACAGTTCGGTACTTGAA 7

RESULT 2
US-08-365-486A-4/c
Sequence 4, Application US/08365486A
Patent No. 5834306
GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESS: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,486A
FILING DATE: 23-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: ET-1 primer F
US-08-365-486A-4

Query Match          56.2%; Score 14.6; DB 2; Length 41;
Best Local Similarity 81.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 4; Indels

Qy      2 GTCTTTCCGAGATCGGTAACT 22
      ||||| ||||| ||||| ||||| |||||
Db      30 GTCTTTCCCTATCGGTAACT 10

RESULT 3
US-08-880-342-4/c
Sequence 4, Application US/08880342
Patent No. 6218179
GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESS: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,486A
FILING DATE: 23-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: ET-1 primer F
US-08-365-486A-4

```

APPLICANT: Green, Christopher J.  
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Avenue, Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/880,342  
FILING DATE: 23-JUN-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/IB95/00996  
FILING DATE: 13-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/365,486  
FILING DATE: 23-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Sholtz, Charles K.  
REGISTRATION NUMBER: 38,615  
REFERENCE/DOCKET NUMBER: 8255-0018.30  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 41 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: ET-1 primer F  
US-08-880-342-4

Query Match 56.2%; Score 14.6; DB 3; Length 41;  
Best Local Similarity 81.0%; Pred. No. 3.2e+02;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GTCTTTCGACATCGGTACCT 22  
||||| |  
Db 30 GTCTTTCCTATCGGTACCT 10

RESULT 4  
US-09-641-638-998/c  
; Sequence 998, Application US/09641638  
; Patent No. 6432648  
; GENERAL INFORMATION:  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Bougueleret, Lydie  
; APPLICANT: Chumakov, Ilya  
; APPLICANT: Cohen, Annick  
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING  
; TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM  
; FILE REFERENCE: GENSET.051CPI  
; CURRENT FILING DATE: 2000-08-16  
; PRIOR APPLICATION NUMBER: US/09/641,638  
; PRIOR FILING DATE: 2000-02-11  
; PRIOR APPLICATION NUMBER: US 09/502,330  
; PRIOR FILING DATE: 2000-02-11  
; PRIOR APPLICATION NUMBER: US 60/133,200  
; PRIOR FILING DATE: 1999-05-07

APPLICANT: Green, Christopher J.  
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Avenue, Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/880,342  
FILING DATE: 23-JUN-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/IB95/00996  
FILING DATE: 13-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/365,486  
FILING DATE: 23-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Sholtz, Charles K.  
REGISTRATION NUMBER: 38,615  
REFERENCE/DOCKET NUMBER: 8255-0018.30  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 41 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: ET-1 primer F  
US-08-880-342-4

Query Match 53.8%; Score 14; DB 4; Length 47;  
Best Local Similarity 70.8%; Pred. No. 6.5e+02;  
Matches 17; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 2 GTCTTTCGACATCGGTACCTCAA 25  
||||| |  
Db 43 GTCTTTCACAGATAGGAGGTGAA 20

RESULT 5  
US-10-170-097-998/c  
; Sequence 998, Application US/10170097  
; Patent No. 6794143  
; GENERAL INFORMATION:  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Bougueleret, Lydie  
; APPLICANT: Chumakov, Ilya  
; APPLICANT: Cohen, Annick  
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING  
; TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM  
; FILE REFERENCE: GEN-T114XC2DI  
; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: US/10/170,097  
; PRIOR FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: US 09/641,638  
; PRIOR FILING DATE: 2000-08-16  
; PRIOR APPLICATION NUMBER: US 09/502,330  
; PRIOR FILING DATE: 2000-02-11  
; PRIOR APPLICATION NUMBER: US 60/133,200  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: US 09/275,267  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: US 60/119,917  
; PRIOR FILING DATE: 1999-02-12  
; NUMBER OF SEQ ID NOS: 1304  
; SOFTWARE: Patent.pm  
; SEQ ID NO 998  
; LENGTH: 47  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 24  
; OTHER INFORMATION: 10-482-145 : polymorphic base A or G  
US-10-170-097-998

Query Match 53.8%; Score 14; DB 4; Length 47;  
Best Local Similarity 70.8%; Pred. No. 6.5e+02;  
Matches 17; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 2 GTCTTTCGACATCGGTACCTCAA 25  
||||| |  
Db 43 GTCTTTCACAGATAGGAGGTGAA 20

RESULT 6  
US-09-082-649B-41  
; Sequence 41, Application US/09082649B

Query Match 53.8%; Score 14; DB 4; Length 47;  
Best Local Similarity 70.8%; Pred. No. 6.5e+02;  
Matches 17; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 2 GTCTTTCGACATCGGTACCTCAA 25  
||||| |  
Db 43 GTCTTTCACAGATAGGAGGTGAA 20

Patent No. 6339068  
GENERAL INFORMATION:  
APPLICANT: Davis, Heather L.  
APPLICANT: Krieg, Arthur M.  
APPLICANT: Schorr, Joachim  
APPLICANT: Wu, Tong  
TITLE OF INVENTION: Vectors and Methods for Immunization or Therapeutic Protocols  
FILE REFERENCE: C1039/7009  
CURRENT APPLICATION NUMBER: US/09/082,649B  
CURRENT FILING DATE: 1998-05-20  
PRIOR APPLICATION NUMBER: US 60/047,233  
PRIOR FILING DATE: 1997-05-20  
PRIOR APPLICATION NUMBER: US 60/047,209  
PRIOR FILING DATE: 1997-05-20  
NUMBER OF SEQ ID NOS: 85  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 41  
LENGTH: 34  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic oligonucleotide  
US-09-082-649B-41

Query Match 52.3%; Score 13.6; DB 3; Length 34;  
Best Local Similarity 80.0%; Pred. No. 9.9e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 TCGCAGATCGGTACCTCAAT 26  
|||||  
DB 10 TCGCAGATCGATACCAGGAT 29

RESULT 7  
US-09-180-394-3/c  
Sequence 3, Application US/09180394  
Patent No. 6673605  
GENERAL INFORMATION:  
APPLICANT: M. Sawada  
TITLE OF INVENTION: ESTABLISHED CELL LINE OF MICROGLIA  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Peter F. Corless  
STREET: Pike, Bronstein, Roberts & Cushman, LLP 130 Water St.  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109-4280  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/180,394  
FILING DATE: 1998-11-05  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP98/00949  
FILING DATE: 1998-03-05  
ATTORNEY/AGENT INFORMATION:  
NAME: Peter F. Corless  
REGISTRATION NUMBER: 33,860  
REFERENCE/DOCKET NUMBER: 1526-48781  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)-523-3400  
TELEFAX: (617)-523-6440  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Synthetic DNA  
US-09-180-394-3

Query Match 51.5%; Score 13.4; DB 4; Length 25;  
Best Local Similarity 73.9%; Pred. No. 1.2e+03;  
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 GTCTTCGACATCGGTACTTCA 24  
|||||  
DB 24 GTCTTCGACAGAGAACTTCA 2

RESULT 8  
US-08-738-381-24  
Sequence 24, Application US/08738381  
Patent No. 6083694  
GENERAL INFORMATION:  
APPLICANT: John A. Hardy, Alison M. Goate  
TITLE OF INVENTION: Method for Elucidation and Detection of Polymorphisms, Splice Variants and Proximal Coding Using Intronic Sequences of the Mutations Alzheimer's S182 Gene  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road, P.O. Box 1539  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB  
MEDIUM TYPE: STORAGE  
COMPUTER: IBM 486  
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/738,381  
FILING DATE: Herewith  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/007,048  
FILING DATE: October 25, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: William T. Han  
REGISTRATION NUMBER: 34,344  
REFERENCE/DOCKET NUMBER: P50388  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5024  
TELEFAX: 610-270-5090  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: No  
US-08-738-381-24

Query Match 51.5%; Score 13.4; DB 3; Length 31;  
Best Local Similarity 73.9%; Pred. No. 1.2e+03;  
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 TCTTTCGACATCGGTACTTCAA 25  
|||||  
DB 7 TCTTTCCTTTTCAGAACCTCAA 29

RESULT 9  
US-08-845-546-22/c  
Sequence 22, Application US/08845546

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; FEATURE:
; US-09-714-550-6
;
Query Match 50.8%; Score 13.2; DB 4; Length 32;
Best Local Similarity 69.2%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 8; Indels 0;

QY 1 CGCTTTTCGAGATCGGTACCTCAAT 26
Db 3 CGCCAATTCATTTCAGTACCTCAAT 28
      ||| ||| ||| ||| ||| ||| |||
      ||| ||| ||| ||| ||| ||| |||

RESULT 11
US-09-553-867A-31
; Sequence 31, Application US/09553867A
; Patent No. 6476188
; GENERAL INFORMATION:
; APPLICANT: Young, Michael W
; APPLICANT: Kloss, Brian
; APPLICANT: Blau, Justin
; APPLICANT: Price, Jeffrey
; APPLICANT: Takahashi, Joseph S.
; APPLICANT: Philip, Lowrey L.
; TITLE OF INVENTION: A NOVEL CLOCK GENE AND METHODS OF USE THEREOF
; FILE REFERENCE: 600-1-221NCP
; CURRENT APPLICATION NUMBER: US/09/553,867A
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/090,068
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 09/335,983
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer.
US-09-553-867A-31

Query Match 50.0%; Score 13; DB 4; Length 30;
Best Local Similarity 76.2%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0;

QY 2 GCTTTTCGAGATCGGTACCT 22
Db 9 GTCCTTCGAGATATCTACCT 29
      ||| ||| ||| ||| |||
      ||| ||| ||| ||| |||

RESULT 12
US-08-171-389-583/c
; Sequence 583, Application US/08171389
; Patent No. 5578444
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
; APPLICANT: Cantor, Charles R.
; APPLICANT: Andrews, Beth M.
; APPLICANT: Turin, Lisa M.
; APPLICANT: Fry, Kirk E.
; TITLE OF INVENTION: Sequence-Directed DNA Binding
; TITLE OF INVENTION: Molecules, Compositions and Methods
; NUMBER OF SEQUENCES: 641
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Pembscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/171.389
; FILING DATE:
; PRIOR APPLICATION DATA:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 08/123,936
; FILING DATE: 17-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/996,783
; FILING DATE: 23-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/723,618
; FILING DATE: 27-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/081,070
; FILING DATE: 22-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4600-0175/G19P3
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 583:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Adenovirus type-2 L11a (start site)
; INDIVIDUAL ISOLATE: 25954)
; US-08-171-389-583
;
; Query Match 50.0%; Score 13; DB 1; Length 50;
; Best Local Similarity 76.2%; Pred. NO. 2.1e+03;
; Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
;
; Qy 4 CTTTCGAGATCGGTACCTCA 24
; Db 34 CCTTCGCAAAATTTGTACCTGA 14
;
; RESULT 13
; US-08-123-936-583/c
; Sequence 583, Application US/08123936
; Patent No. 5726014
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
; APPLICANT: Cantor, Charles R.
; APPLICANT: Andrews, Beth M.
; APPLICANT: Turin, Lisa M.
; APPLICANT: Fry, Kirk E.
; TITLE OF INVENTION: Screening Assay for the Detection of
; TITLE OF INVENTION: DNA-Binding Molecules
; NUMBER OF SEQUENCES: 640
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; US-08-171-389-583
; Query Match 50.0%; Score 13; DB 1; Length 50;
; Best Local Similarity 76.2%; Pred. NO. 2.1e+03;
; Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
;
; Qy 4 CTTTCGAGATCGGTACCTCA 24
; Db 34 CCTTCGCAAAATTTGTACCTGA 14
;
; RESULT 14
; US-08-475-228A-583/c
; Sequence 583, Application US/08475228A
; Patent No. 5869241
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
; APPLICANT: Cantor, Charles R.
; APPLICANT: Andrews, Beth M.
; APPLICANT: Turin, Lisa M.
; APPLICANT: Fry, Kirk E.
; TITLE OF INVENTION: Sequence-Directed DNA Binding
; TITLE OF INVENTION: Molecules, Compositions and Methods
; NUMBER OF SEQUENCES: 664
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; US-08-475-228A-583
; Query Match 50.0%; Score 13; DB 1; Length 50;
; Best Local Similarity 76.2%; Pred. NO. 2.1e+03;
; Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
;
; Qy 4 CTTTCGAGATCGGTACCTCA 24
; Db 34 CCTTCGCAAAATTTGTACCTGA 14
;
; RESULT 15
; US-08-475-228A-583/c
; Sequence 583, Application US/08475228A
; Patent No. 5869241
; GENERAL INFORMATION:
; APPLICANT: Edwards, Cynthia A.
; APPLICANT: Cantor, Charles R.
; APPLICANT: Andrews, Beth M.
; APPLICANT: Turin, Lisa M.
; APPLICANT: Fry, Kirk E.
; TITLE OF INVENTION: Sequence-Directed DNA Binding
; TITLE OF INVENTION: Molecules, Compositions and Methods
; NUMBER OF SEQUENCES: 664
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genelabs Technologies, Inc.
; STREET: 505 Penobscot Drive
; CITY: Redwood City
; STATE: CA
; COUNTRY: USA
; ZIP: 94063
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;

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; APPLICATION NUMBER: US 07/723,618  
; FILING DATE: 27-JUN-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/081,070  
; FILING DATE: 22-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stratford, Carol A.  
; REGISTRATION NUMBER: 34,444  
; REFERENCE/DOCKET NUMBER: 4600-0175.21/G19P3D2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 324-0880  
; TELEFAX: (415) 324-0960  
; INFORMATION FOR SEQ ID NO: 583:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 50 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: Adenovirus type-2 LI1a (start site  
; INDIVIDUAL ISOLATE: 25954)  
; US-08-475-228A-583

Query Match 50.0%; Score 13; DB 2; Length 50;  
Best Local Similarity 76.2%; Pred. No. 2.1e+03;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 CTTTCGCAGATCGGTACTCA 24  
| | | | | | | | | | | | | | | | | |  
Db 34 CTTTCGCAAAATTTGTACTGA 14

RESULT 15  
US-08-482-080A-583/c  
; Sequence 583, Application US/08482080A  
; Patent No. 6010849  
; GENERAL INFORMATION:  
; APPLICANT: Edwards, Cynthia A.  
; APPLICANT: Cantor, Charles R.  
; APPLICANT: Andrews, Beth M.  
; APPLICANT: Turin, Lisa M.  
; APPLICANT: Fry, Kirk E.  
; TITLE OF INVENTION: Sequence-Directed DNA Binding  
; NUMBER OF SEQUENCES: 664  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genelabs Technologies, Inc.  
; STREET: 505 Penobscot Drive  
; CITY: Redwood City  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94063  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/482,080A  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/171,389  
; FILING DATE: 20-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/123,936  
; FILING DATE: 17-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/996,783  
; FILING DATE: 23-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/723,618

; FILING DATE: 27-JUN-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/081,070  
; FILING DATE: 22-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brady, John F.  
; REGISTRATION NUMBER: 39,118  
; REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 324-0880  
; TELEFAX: (650) 324-0960  
; INFORMATION FOR SEQ ID NO: 583:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 50 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: Adenovirus type-2 LI1a (start site  
; INDIVIDUAL ISOLATE: 25954)  
; US-08-482-080A-583

Query Match 50.0%; Score 13; DB 3; Length 50;  
Best Local Similarity 76.2%; Pred. No. 2.1e+03;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 CTTTCGCAGATCGGTACTCA 24  
| | | | | | | | | | | | | | | | | |  
Db 34 CTTTCGCAAAATTTGTACTGA 14

RESULT 16  
US-09-354-947-583/c  
; Sequence 583, Application US/09354947  
; Patent No. 6384208  
; GENERAL INFORMATION:  
; APPLICANT: Edwards, Cynthia A.  
; APPLICANT: Cantor, Charles R.  
; APPLICANT: Andrews, Beth M.  
; APPLICANT: Turin, Lisa M.  
; APPLICANT: Fry, Kirk E.  
; TITLE OF INVENTION: Sequence-Directed DNA Binding  
; NUMBER OF SEQUENCES: 664  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genelabs Technologies, Inc.  
; STREET: 505 Penobscot Drive  
; CITY: Redwood City  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94063  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/354,947  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/482,080  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/171,389  
; FILING DATE: 20-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/123,936  
; FILING DATE: 17-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/996,783  
; FILING DATE: 23-DEC-1992  
; PRIOR APPLICATION DATA:

RESULT 17  
PCT-US93-12388-593/c  
Sequence 583, Application PC/TUS9312388  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Sequence-Directed DNA Binding  
TITLE OF INVENTION: Molecules, Compositions and Methods  
NUMBER OF SEQUENCES: 641  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genelabs Technologies, Inc.  
STREET: 505 Penobscot Drive  
CITY: Redwood City  
STATE: CA  
COUNTRY: USA  
ZIP: 94063  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/12388  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA: US 08/123,936  
APPLICATION NUMBER: 17-SEP-1993  
FILING DATE: 17-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/996,783  
FILING DATE: 23-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Fabian, Gary R.  
REGISTRATION NUMBER: 33,875  
REFERENCE/DOCKET NUMBER: 4600-0175.41/G19PCT12  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 583:  
SEQUENCE CHARACTERISTICS:



TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 38 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-485-971-12

Query Match 49.2%; Score 12.8; DB 1; Length 38;  
Best Local Similarity 70.8%; Pred. No. 2.6e+03;  
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 3 TCTTTCCGAGATCGGTACTCTCAAT 26  
Db 36 TCTATCACTGATAGGGAACCTCTAT 13

RESULT 19

US-08-275-876-12/c  
Sequence 12, Application US/08275876  
Patent No. 5654168  
GENERAL INFORMATION:  
APPLICANT: Bujard, Hermann  
APPLICANT: Gossen, Manfred  
TITLE OF INVENTION: Tetracycline-Inducible Transcriptional  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/275,876  
FILING DATE:  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US  
FILING DATE: 01-JULY-94  
CLASSIFICATION: 436  
ATTORNEY/AGENT INFORMATION:  
NAME: DeConti, Giulio A. Jr.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: BBI-009CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 38 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-275-876-12

Query Match 49.2%; Score 12.8; DB 1; Length 38;  
Best Local Similarity 70.8%; Pred. No. 2.6e+03;  
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 3 TCTTTCCGAGATCGGTACTCTCAAT 26  
Db 36 TCTATCACTGATAGGGAACCTCTAT 13

RESULT 20

US-08-383-754-12/c  
Sequence 12, Application US/08383754  
Patent No. 5789156  
GENERAL INFORMATION:  
APPLICANT: Bujard, Hermann  
APPLICANT: Gossen, Manfred  
TITLE OF INVENTION: Tetracycline-Regulated Transcriptional  
TITLE OF INVENTION: Inhibitors  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/383,754  
FILING DATE:  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/275,876  
FILING DATE: 15-JULY-94  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/270,637  
FILING DATE: 01-JULY-94  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/260,452  
FILING DATE: 14-JUNE-94  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/076,327  
FILING DATE: 14-JUNE-93  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/076,726  
FILING DATE: 14-JUNE-93  
CLASSIFICATION: 436  
ATTORNEY/AGENT INFORMATION:  
NAME: DeConti, Giulio A. Jr.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: BBI-009CP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 38 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-383-754-12

Query Match 49.2%; Score 12.8; DB 1; Length 38;  
Best Local Similarity 70.8%; Pred. No. 2.6e+03;  
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 3 TCTTTCCGAGATCGGTACTCTCAAT 26  
Db 36 TCTATCACTGATAGGGAACCTCTAT 13

RESULT 21

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US-08-485-978-12/c
Sequence 12, Application US/08485978
Patent No. 5814618
GENERAL INFORMATION:
APPLICANT: Bujard, Hermann
APPLICANT: Gossen, Manfred
TITLE OF INVENTION: Methods for Regulating Gene Expression
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,978
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/383,754
FILING DATE: 03-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/275,876
FILING DATE: 15-JULY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/270,637
FILING DATE: 01-JULY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,452
FILING DATE: 14-JUNE-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/076,327
FILING DATE: 14-JUNE-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/076,726
FILING DATE: 14-JUNE-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A. Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-009CP6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-485-978-12
Query Match 49.2%; Score 12.8; DB 1; Length 38;
Best Local Similarity 70.8%; Pred. No. 2.6e+03;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 3 TCTTTTCGACATCGGTACCTCAAT 26
Db 36 TCTATCACTGATAGGGACTCTAT 13

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RESULT 23

US-08-487-472-12/c  
; Sequence 12, Application US/08487472  
; Patent No. 5912411  
; GENERAL INFORMATION:  
; APPLICANT: Bujard, Hermann  
; APPLICANT: Gossen, Manfred  
; TITLE OF INVENTION: Animal Transgenic for a Tetracycline- Inducible Transcription  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, Suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/487,472  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/383,754  
; FILING DATE: 03-FEB-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/275,876  
; FILING DATE: 15-JULY-1994  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/270,637  
; FILING DATE: 01-JULY-94  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/260,452  
; FILING DATE: 14-JUNE-1994  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/076,327  
; FILING DATE: 14-JUNE-1993  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/076,726  
; FILING DATE: 14-JUNE-1993  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DeConti, Giulio A. Jr.  
; REGISTRATION NUMBER: 31,503  
; REFERENCE/DOCKET NUMBER: BBI-009CP3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 38 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-487-472-12

Query Match 49.2%; Score 12.8; DB 2; Length 38;  
Best Local Similarity 70.8%; Pred. No. 2.6e+03;  
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 TCTTTCCGACATCGTACTCAAT 26

Db 36 TCTATCACTGATGGGAACCTCTAT 13

RESULT 24

US-08-485-740-12/c  
; Sequence 12, Application US/08485740  
; Patent No. 6004941  
; GENERAL INFORMATION:  
; APPLICANT: Bujard, Hermann  
; APPLICANT: Gossen, Manfred  
; TITLE OF INVENTION: Methods for Regulating Gene Expression  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, Suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,740  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/383,754  
; FILING DATE: 03-FEB-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/275,876  
; FILING DATE: 15-JULY-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/270,637  
; FILING DATE: 01-JULY-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/260,452  
; FILING DATE: 14-JUNE-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/076,327  
; FILING DATE: 14-JUNE-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/076,726  
; FILING DATE: 14-JUNE-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DeConti, Giulio A. Jr.  
; REGISTRATION NUMBER: 31,503  
; REFERENCE/DOCKET NUMBER: BBI-009CP5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 38 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-485-740-12

Query Match 49.2%; Score 12.8; DB 3; Length 38;  
Best Local Similarity 70.8%; Pred. No. 2.6e+03;  
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 TCTTTCCGACATCGTACTCAAT 26

Db 36 TCTATCACTGATGGGAACCTCTAT 13

Db 36 TCTATCACTGATAGGAACTCTAT 13

RESULT 25

US-09-162-184-12/c

; Sequence 12, Application US/09162184A

; Patent No. 6136954

GENERAL INFORMATION:

APPLICANT: Bujard, Hermann

Gossen, Manfred

TITLE OF INVENTION: Tetracycline-Inducible Transcriptional

Activator Fusion Proteins

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/162,184A

FILING DATE: 28-Sep-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/383,754

FILING DATE: 03-FEB-1995

APPLICATION NUMBER: US 08/275,876

FILING DATE: 15-JULY-1994

APPLICATION NUMBER: US 08/270,637

FILING DATE: 01-JULY-1994

APPLICATION NUMBER: US 08/260,452

FILING DATE: 14-JUNE-1994

APPLICATION NUMBER: US 08/076,327

FILING DATE: 14-JUNE-1993

APPLICATION NUMBER: US 08/076,726

FILING DATE: 14-JUNE-1993

ATTORNEY/AGENT INFORMATION:

NAME: DeConti, Giulio A. Jr.

REGISTRATION NUMBER: 31,503

REFERENCE/DOCKET NUMBER: BBI-009C6CN

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)742-4214

TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-162-184-12

Query Match 49.2%; Score 12.8; DB 3; Length 38;

Best Local Similarity 70.8%; Pred. No. 2.6e+03;

Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 TCTTTCGACATCGGTACTCAAT 26

Db 36 TCTATCACTGATAGGAACTCTAT 13

RESULT 26

US-09-161-902-12/c

; Sequence 12, Application US/09161902

; Patent No. 6242667

GENERAL INFORMATION:

APPLICANT: Bujard, Hermann

Gossen, Manfred

TITLE OF INVENTION: Tetracycline-Inducible Transcriptional

Activator Fusion Proteins

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/161,902

FILING DATE: 08/08/1998

CLASSIFICATION: US 08/270,637

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/275,876

FILING DATE: 15-JULY-1994

CLASSIFICATION: US 08/260,452

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/270,637

FILING DATE: 01-JULY-94

CLASSIFICATION: US 08/260,452

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/076,327

FILING DATE: 14-JUNE-1993

CLASSIFICATION: US 08/076,726

FILING DATE: 14-JUNE-1993

ATTORNEY/AGENT INFORMATION:

NAME: DeConti, Giulio A. Jr.

REGISTRATION NUMBER: 31,503

REFERENCE/DOCKET NUMBER: BBI-009CP3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-161-902-12

Query Match 49.2%; Score 12.8; DB 3; Length 38;

Best Local Similarity 70.8%; Pred. No. 2.6e+03;

Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 TCTTTCGACATCGGTACTCAAT 26

Db 36 TCTATCACTGATAGGAACTCTAT 13

RESULT 27

US-09-489-777A-12/c

; Sequence 12, Application US/09489777A

; Patent No. 6271348

GENERAL INFORMATION:

APPLICANT: Bujard, Hermann

Gossen, Manfred

TITLE OF INVENTION: Tetracycline-Inducible Transcriptional

Activator Fusion Proteins

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street, Suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/161,902

FILING DATE: 08/08/1998

CLASSIFICATION: US 08/270,637

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/275,876

FILING DATE: 15-JULY-1994

CLASSIFICATION: US 08/260,452

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/270,637

FILING DATE: 01-JULY-94

CLASSIFICATION: US 08/260,452

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/076,327

FILING DATE: 14-JUNE-1993

CLASSIFICATION: US 08/076,726

FILING DATE: 14-JUNE-1993

ATTORNEY/AGENT INFORMATION:

NAME: DeConti, Giulio A. Jr.

REGISTRATION NUMBER: 31,503

REFERENCE/DOCKET NUMBER: BBI-009CP3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-161-902-12

Query Match 49.2%; Score 12.8; DB 3; Length 38;

Best Local Similarity 70.8%; Pred. No. 2.6e+03;

Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 TCTTTCGACATCGGTACTCAAT 26

Db 36 TCTATCACTGATAGGAACTCTAT 13

RESULT 28

US-09-489-777A-12/c

; Sequence 12, Application US/09489777A

; Patent No. 6271348

GENERAL INFORMATION:

APPLICANT: Bujard, Hermann

Gossen, Manfred

TITLE OF INVENTION: Tetracycline-Inducible Transcriptional

Activator Fusion Proteins

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street, Suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/161,902

FILING DATE: 08/08/1998

CLASSIFICATION: US 08/270,637

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/275,876

FILING DATE: 15-JULY-1994

CLASSIFICATION: US 08/260,452

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/270,637

FILING DATE: 01-JULY-94

CLASSIFICATION: US 08/260,452

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/076,327

FILING DATE: 14-JUNE-1993

CLASSIFICATION: US 08/076,726

FILING DATE: 14-JUNE-1993

ATTORNEY/AGENT INFORMATION:

NAME: DeConti, Giulio A. Jr.

REGISTRATION NUMBER: 31,503

REFERENCE/DOCKET NUMBER: BBI-009CP3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-161-902-12

Query Match 49.2%; Score 12.8; DB 3; Length 38;

Best Local Similarity 70.8%; Pred. No. 2.6e+03;

Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 TCTTTCGACATCGGTACTCAAT 26

Db 36 TCTATCACTGATAGGAACTCTAT 13



```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cloning Oligonucleotide
US-09-976-667-15

Query Match
Best Local Similarity 48.5%; Score 12.6; DB 4; Length 26;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 TCTTTCGAGATCGGTACC 21
DB 21 TCTTTCGAGATCGGTACC 3

RESULT 30
RE34606-8
; Patent No. RE34,606
; APPLICANT: ESTELL, DAVID A.; WELLS, JAMES A.; BOTT,
; RICHARD R.
; TITLE OF INVENTION: MODIFIED ENZYMES AND METHODS FOR
; MAKING SAME
; NUMBER OF SEQUENCES: 27
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/556,918
; FILING DATE: 20-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 614,612
; FILING DATE: 29-MAY-1984
; SEQ ID NO: 8
; LENGTH: 48
RE34606-8

Query Match
Best Local Similarity 48.5%; Score 12.6; DB 6; Length 48;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 CGCAGATCGGTACTCAAT 26
DB 2 CGTACACGGTACGTCAAT 20

RESULT 31
US-09-672-810-15
; Sequence 15, Application US/09672810
; Patent No. 6617450
; GENERAL INFORMATION:
; APPLICANT: STOCKER, PENNY J.
; APPLICANT: STEINEL-CRESPI, DOROTHY T.
; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
; FILE REFERENCE: G0307/7018
; CURRENT APPLICATION NUMBER: US/09/672,810
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/156,921
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/158,818
; PRIOR FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide based on Macaca fascicularis
US-09-672-810-15

Query Match
Best Local Similarity 47.7%; Score 12.4; DB 4; Length 28;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 CGCAGATCGGTACTCAAT 26
DB 2 CGTACACGGTACGTCAAT 20

RESULT 32
US-09-455-960-28/c
; Sequence 28, Application US/09455960
; Patent No. 6361776
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compositions isolated from M. vaccae and
; TITLE OF INVENTION: their use in modulation of immune responses.
; FILE REFERENCE: 11000.1047
; CURRENT APPLICATION NUMBER: US/09/455,960
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-455-960-28

Query Match
Best Local Similarity 47.7%; Score 12.4; DB 3; Length 35;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CGTCTTTCGAGATCGGTACTCT 22
DB 29 CGTCTTTCGAGATCGGTACTCT 8

RESULT 33
US-10-051-325-28/c
; Sequence 28, Application US/10051325
; Patent No. 6716430
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compositions isolated from M. vaccae and
; TITLE OF INVENTION: their use in modulation of immune responses.
; FILE REFERENCE: 11000.1047/c1
; CURRENT APPLICATION NUMBER: US/10/051,325
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 09/455,960
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-10-051-325-28

Query Match
Best Local Similarity 47.7%; Score 12.4; DB 4; Length 35;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CGTCTTTCGAGATCGGTACTCT 22
DB 29 CGTCTTTCGAGATCGGTACTCT 8

RESULT 34
US-08-641-294-4
; Sequence 4, Application US/08641294
; Patent No. 6635479
; GENERAL INFORMATION:
; APPLICANT: Hippenmeyer, Paul J.
; APPLICANT: Highkin, Maureen K.

```

;; TITLE OF INVENTION: Production of Recombinant Proteins Using  
;; TITLE OF INVENTION: Herpes Virus Promoters and VP16 Transactivators  
;; NUMBER OF SEQUENCES: 12  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Dennis A. Bennett, Monsanto Co., A3SG  
;; STREET: 800 N. Lindbergh  
;; CITY: St. Louis  
;; STATE: Missouri  
;; COUNTRY: USA  
;; ZIP: 63198  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/641,294  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/290,050  
;; FILING DATE:  
;; APPLICATION NUMBER: US/07/850,700  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Bennett, Dennis A.  
;; REGISTRATION NUMBER: 34,547  
;; REFERENCE/DOCKET NUMBER: 07-21(690)A  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (314)694-5402  
;; TELEFAX: (314)694-9009  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 37 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
US-08-641-294-4

Query Match 47.7%; Score 12.4; DB 4; Length 37;  
Best Local Similarity 92.9%; Pred. No. 4.1e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 GATCGGTACCTCAA 25  
Db 1 GATCGGTACCGCAA 14

RESULT 35  
5256558-14/c  
; Patent No. 5256558  
; APPLICANT: CORUZZI, GLORIA M.; TSAI, FONG-YING  
; TITLE OF INVENTION: GENE ENCODING PLANT ASPARAGINE SYNTHETASE  
; NUMBER OF SEQUENCES: 17  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/514,816  
; FILING DATE: 26-APR-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 347,302  
; FILING DATE: 03-MAY-1989  
; SEQ ID NO: 14:  
; LENGTH: 40  
5256558-14

Query Match 47.7%; Score 12.4; DB 6; Length 40;  
Best Local Similarity 72.7%; Pred. No. 4.1e+03;  
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CGTCTTTCCGACATCGGTACCT 22  
Db 28 GGTCTGTCACACTGCTAGATACCT 7

RESULT 36  
US-08-879-565-6/c  
; Sequence 6; Application US/08879565A  
; Patent No. 6093573  
; GENERAL INFORMATION:  
; APPLICANT: Beamer, Lesa J.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Eisenberg, David  
; TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF  
; FILE REFERENCE: 1103/11034US01  
; CURRENT APPLICATION NUMBER: US/08/879,565A  
; CURRENT FILING DATE: 1997-06-20  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 42  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide complementary to SEQ ID NO:5  
US-08-879-565-6

Query Match 47.7%; Score 12.4; DB 3; Length 42;  
Best Local Similarity 72.7%; Pred. No. 4.1e+03;  
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 GTCTTTCCGACATCGGTACCTC 23  
Db 30 GTCCTTCTCCCTTCGTCCTC 9

RESULT 37  
US-09-217-228-4  
; Sequence 4, Application US/09217228  
; Patent No. 6323178  
; GENERAL INFORMATION:  
; APPLICANT: Butler, Jon P.  
; APPLICANT: Hale, John E.  
; APPLICANT: Heath Jr., William F.  
; APPLICANT: Schoner, Brigitte E.  
; APPLICANT: Helman, Mark L.  
; APPLICANT: Becker, Gerald W.  
; APPLICANT: Varshavsky, Alexander D.  
; TITLE OF INVENTION: Beta-lipotropin and Uses Thereof  
; FILE REFERENCE: X-12139  
; CURRENT APPLICATION NUMBER: US/09/217,228  
; CURRENT FILING DATE: 1998-12-21  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 45  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: Oligonucleotide linker  
US-09-217-228-4

Query Match 47.7%; Score 12.4; DB 3; Length 45;  
Best Local Similarity 72.7%; Pred. No. 4.2e+03;  
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 TCTTTCCGACATCGGTACCTCA 24  
Db 8 TCTATCGAAGGTCTGTGACCTCA 29

RESULT 38  
US-08-363-240A-1102/c  
; Sequence 1102, Application US/08363240A  
; Patent No. 5705388

GENERAL INFORMATION:  
APPLICANT: Couture, Larry  
APPLICANT: McSwiggen, James  
APPLICANT: Bisgaier, Charles  
APPLICANT: Pape, Michael  
TITLE OF INVENTION: METHOD AND REAGENT FOR PREVENTION, INHIBITION OF PROGRESSION AND REGRESSION OF VASCULAR DISEASES  
TITLE OF INVENTION: OF VASCULAR DISEASES  
NUMBER OF SEQUENCES: 1243  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/363,240A  
FILING DATE: December 23, 1994  
PRIOR APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 210/096  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1102:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-363-240A-1102  
Query Match 46.9%; Score 12.2; DB 1; Length 18;  
Best Local Similarity 82.4%; Pred. No. 4.6e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 6 TTTCGAGATCGGTACCT 22  
DB 17 TTTCGAGATCGTCCCT 1  
RESULT 39  
US-09-165-934-2/c  
Sequence 2, Application US/09165934  
Patent No. 6284496  
GENERAL INFORMATION:  
APPLICANT: Litman, Gary W.  
APPLICANT: Hawke, No. 62844961 A.  
APPLICANT: Haire, Robert N.  
APPLICANT: Strong, Scott J.  
TITLE OF INVENTION: DNA VECTOR FOR DETERMINING THE PRESENCE OF OUT-OF-READING-FRAME MUTATIONS  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kohn & Associates  
STREET: 30500 No. 6284496thwestern Hwy., Suite 410  
CITY: Farmington Hills  
STATE: Michigan  
COUNTRY: US

ZIP: 48334  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/165,934  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Montgomery, Ilene N.  
REGISTRATION NUMBER: 38,972  
REFERENCE/DOCKET NUMBER: 0152.00298  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (248) 539-5050  
TELEFAX: (248) 539-5055  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-09-165-934-2  
Query Match 46.9%; Score 12.2; DB 3; Length 24;  
Best Local Similarity 82.4%; Pred. No. 4.8e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 9 GCAGATCGGTACCTCAA 25  
DB 23 GCAGATCGATATCTCGA 7  
RESULT 40  
US-09-343-494-5/c  
Sequence 5, Application US/09343494  
Patent No. 6413741  
GENERAL INFORMATION:  
APPLICANT: Jegla, Timothy J.  
APPLICANT: Wickenden, Alan  
APPLICANT: ICAGEN, Incorporated  
TITLE OF INVENTION: Human Elk, a Voltage-Gated Potassium Channel Subunit  
FILE REFERENCE: 018512-001320US  
CURRENT APPLICATION NUMBER: US/09/343,494  
CURRENT FILING DATE: 1999-06-30  
EARLIER APPLICATION NUMBER: US 60/091,469  
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EARLIER APPLICATION NUMBER: US 60/116,621  
EARLIER FILING DATE: 1999-01-21  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 24  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: amplification  
US-09-343-494-5  
Query Match 46.9%; Score 12.2; DB 4; Length 24;  
Best Local Similarity 82.4%; Pred. No. 4.8e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 CGTCTTTCGACATCGG 17  
DB 18 CGTCTTCAGCAGATGGG 2



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